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Efficient expression of modified human papillomavirus 16 e6/e7 fusion protein and the antitumor efficacy in a mouse model.

Biol Pharm Bull. 2004 Mar;27(3):303-7.

PMID: 14993792 [PubMed - indexed for MEDLINE]

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☐ 2: [Daemen T, Pries F, Bungener L, Kraak M, Regts J, Wilschut J.](#) [Related Articles, Links](#)



Genetic immunization against cervical carcinoma: induction of cytotoxic T lymphocyte activity with a recombinant alphavirus vector expressing human papillomavirus type 16 E6 and E7.

Gene Ther. 2000 Nov;7(21):1859-66.

PMID: 11110419 [PubMed - indexed for MEDLINE]

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☐ 3: [Daemen T, Regts J, Holtrop M, Wilschut J.](#) [Related Articles, Links](#)



Immunization strategy against cervical cancer involving an alphavirus vector expressing high levels of a stable fusion protein of human papillomavirus 16 E6 and E7.

Gene Ther. 2002 Jan;9(2):85-94.

PMID: 11857066 [PubMed - indexed for MEDLINE]

☐ 4: [Pokorna D, Mackova J, Duskova M, Rittich S, Ludvikova V, Smahel M.](#) [Related Articles, Links](#)



Combined immunization with fusion genes of mutated E7 gene of human papillomavirus type 16 did not enhance antitumor effect.

J Gene Med. 2005 Jun;7(6):696-707.

PMID: 15712328 [PubMed - indexed for MEDLINE]

☐ 5: [Chu NR, Wu HB, Wu T, Boux LJ, Siegel MI, Mizzen LA.](#) [Related Articles, Links](#)



Immunotherapy of a human papillomavirus (HPV) type 16 E7-expressing tumour by administration of fusion protein comprising Mycobacterium bovis bacille Calmette-Guerin (BCG) hsp65 and HPV16 E7.

Clin Exp Immunol. 2000 Aug;121(2):216-25.

PMID: 10931134 [PubMed - indexed for MEDLINE]

☐ 6: [Cassetti MC, McElhiney SP, Shahabi V, Pullen JK, Le Poole IC, Eiben GL, Smith LR, Kast WM.](#) [Related Articles, Links](#)










Antitumor efficacy of Venezuelan equine encephalitis virus replicon particles encoding mutated HPV16 E6 and E7 genes.








Vaccine. 2004 Jan 2;22(3-4):520-7.

PMID: 14670335 [PubMed - indexed for MEDLINE]

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- ☐ **7:** [Smahel M, Sima P, Ludvikova V, Vonka V.](#) Related Articles, Links
 **Modified HPV16 E7 Genes as DNA Vaccine against E7-Containing Oncogenic Cells.**
Virology. 2001 Mar 15;281(2):231-8.
PMID: 11277695 [PubMed - indexed for MEDLINE]
- ☐ **8:** [Ressing ME, Sette A, Brandt RM, Ruppert J, Wentworth PA, Hartman M, Oseroff C, Grey HM, Melief CJ, Kast WM.](#) Related Articles, Links
 **Human CTL epitopes encoded by human papillomavirus type 16 E6 and E7 identified through in vivo and in vitro immunogenicity studies of HLA-A*0201-binding peptides.**
J Immunol. 1995 Jun 1;154(11):5934-43.
PMID: 7538538 [PubMed - indexed for MEDLINE]
- ☐ **9:** [Chu NR, Wu HB, Wu TC, Boux LJ, Mizzen LA, Siegel MI.](#) Related Articles, Links
 **Immunotherapy of a human papillomavirus type 16 E7-expressing tumor by administration of fusion protein comprised of Mycobacterium bovis BCG Hsp65 and HPV16 E7.**
Cell Stress Chaperones. 2000 Nov;5(5):401-5.
PMID: 11189443 [PubMed - indexed for MEDLINE]
- ☐ **10:** [De Bruijn ML, Schuurhuis DH, Vierboom MP, Vermeulen H, de Cock KA, Ooms ME, Ressing ME, Toebes M, Franken KL, Drijfhout JW, Ottenhoff TH, Offringa R, Melief CJ.](#) Related Articles, Links
 **Immunization with human papillomavirus type 16 (HPV16) oncoprotein-loaded dendritic cells as well as protein in adjuvant induces MHC class I-restricted protection to HPV16-induced tumor cells.**
Cancer Res. 1998 Feb 15;58(4):724-31.
PMID: 9485027 [PubMed - indexed for MEDLINE]
- ☐ **11:** [Kim TY, Myoung HJ, Kim JH, Moon IS, Kim TG, Ahn WS, Sin JI.](#) Related Articles, Links
 **Both E7 and CpG-oligodeoxynucleotide are required for protective immunity against challenge with human papillomavirus 16 (E6/E7) immortalized tumor cells: involvement of CD4+ and CD8+ T cells in protection.**
Cancer Res. 2002 Dec 15;62(24):7234-40.
PMID: 12499264 [PubMed - indexed for MEDLINE]
- ☐ **12:** [Daemen T, Riezebos-Brilman A, Regts J, Dontje B, van der Zee A, Wilschut J.](#) Related Articles, Links
 **Superior therapeutic efficacy of alphavirus-mediated immunization against human papilloma virus type 16 antigens in a murine tumour model: effects of the route of immunization.**
Antivir Ther. 2004 Oct;9(5):733-42.
PMID: 15535411 [PubMed - indexed for MEDLINE]
- ☐ **13:** [Baez-Astua A, Herraez-Hernandez E, Garbi N, Pasolli HA, Juarez V, Zur Hausen H, Cid-Arregui A.](#) Related Articles, Links
 **Low-dose adenovirus vaccine encoding chimeric hepatitis B virus surface antigen-human papillomavirus type 16 E7 proteins induces enhanced E7-specific antibody and cytotoxic T-cell responses.**
J Virol. 2005 Oct;79(20):12807-17.
PMID: 16188983 [PubMed - indexed for MEDLINE]

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- ☐ **14:** [Lasaro MO, Diniz MO, Reyes-Sandoval A, Ertl HC, Ferreira LC.](#) Related Articles, Links
 Anti-tumor DNA vaccines based on the expression of human papillomavirus-16 E6/E7 oncoproteins genetically fused with the glycoprotein D from herpes simplex virus-1.
Microbes Infect. 2005 Dec;7(15):1541-50. Epub 2005 Sep 9.
PMID: 16213178 [PubMed - indexed for MEDLINE]
- ☐ **15:** [Sun Q, Tang SC, Pater MM, Pater A.](#) Related Articles, Links
 Different HPV16 E6/E7 oncogene expression patterns in epithelia reconstructed from HPV16-immortalized human endocervical cells and genital keratinocytes.
Oncogene. 1997 Nov 13;15(20):2399-408.
PMID: 9395236 [PubMed - indexed for MEDLINE]
- ☐ **16:** [Azoury-Ziadeh R, Herd K, Fernando GJ, Frazer IH, Tindle RW.](#) Related Articles, Links
 T-helper epitopes identified within the E6 transforming protein of cervical cancer-associated human papillomavirus type 16.
Viral Immunol. 1999;12(4):297-312.
PMID: 10630789 [PubMed - indexed for MEDLINE]
- ☐ **17:** [Indrova M, Reinis M, Bubenik J, Jandlova T, Bieblova J, Vonka V, Velek J.](#) Related Articles, Links
 Immunogenicity of dendritic cell-based HPV16 E6/E7 peptide vaccines: CTL activation and protective effects.
Folia Biol (Praha). 2004;50(6):184-93.
PMID: 15709713 [PubMed - indexed for MEDLINE]
- ☐ **18:** [Fernando GJ, Murray B, Zhou J, Frazer IH.](#) Related Articles, Links
 Expression, purification and immunological characterization of the transforming protein E7, from cervical cancer-associated human papillomavirus type 16.
Clin Exp Immunol. 1999 Mar;115(3):397-403.
PMID: 10193409 [PubMed - indexed for MEDLINE]
- ☐ **19:** [Peng S, Ji H, Trimble C, He L, Tsai YC, Yeatermeyer J, Boyd DA, Hung CF, Wu TC.](#) Related Articles, Links
 Development of a DNA vaccine targeting human papillomavirus type 16 oncoprotein E6.
J Virol. 2004 Aug;78(16):8468-76.
PMID: 15280455 [PubMed - indexed for MEDLINE]
- ☐ **20:** [Kadish AS, Ho GY, Burk RD, Wang Y, Romney SL, Ledwidge R, Angeletti RH.](#) Related Articles, Links
 Lymphoproliferative responses to human papillomavirus (HPV) type 16 proteins E6 and E7: outcome of HPV infection and associated neoplasia.
J Natl Cancer Inst. 1997 Sep 3;89(17):1285-93.
PMID: 9293919 [PubMed - indexed for MEDLINE]

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☐ 1. Document ID: CN 1160463 C, CN 1381583 A

L4: Entry 1 of 3

File: DWPI

Aug 4, 2004

DERWENT-ACC-NO: 2003-258260

DERWENT-WEEK: 200612

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TITLE: Human papillomavirus E6/E7 fusion gene and its efficient expression carrier and fusion protein vaccine

INVENTOR: ZHAO, Q

PRIORITY-DATA: 2002CN-0117143 (April 24, 2002)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
<u>CN 1160463 C</u>	August 4, 2004		000	C12N015/62
<u>CN 1381583 A</u>	November 27, 2002		000	C12N015/62

INT-CL (IPC): A61 K 48/00; A61 P 35/00; C07 K 19/00; C12 N 15/62; C12 N 15/63

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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☐ 2. Document ID: NZ 505108 A, WO 9933868 A2, AU 9924191 A, ZA 9811848 A, EP 1040123 A2, BR 9814487 A, CZ 200002376 A3, AU 729336 B, HU 200100526 A2, JP 2001527091 W

L4: Entry 2 of 3

File: DWPI

Oct 25, 2002

DERWENT-ACC-NO: 1999-405485

DERWENT-WEEK: 200274

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TITLE: Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to induce immune response to HPV

INVENTOR: DALEMANS, W L J; GERARD, C M G

PRIORITY-DATA: 1997GB-0027262 (December 24, 1997)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
<u>NZ 505108 A</u>	October 25, 2002		000	A61K039/02
<u>WO 9933868 A2</u>	July 8, 1999	E	062	C07K014/00

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<u>AU 9924191 A</u>	July 19, 1999		000
<u>ZA 9811848 A</u>	July 26, 2000		063 C07K000/00
<u>EP 1040123 A2</u>	October 4, 2000	E	000 C07K014/00
<u>BR 9814487 A</u>	October 10, 2000		000 C07K014/00
<u>CZ 200002376 A3</u>	November 15, 2000		000 C07K014/01
<u>AU 729336 B</u>	February 1, 2001		000 C07K014/00
<u>HU 200100526 A2</u>	June 28, 2001		000 A61K039/12
<u>JP 2001527091 W</u>	December 25, 2001		093 C07K014/025

INT-CL (IPC): A61 K 38/16; A61 K 39/00; A61 K 39/02; A61 K 39/09; A61 K 39/102;
A61 K 39/12; A61 K 39/385; A61 K 39/39; A61 P 35/00; C07 K 0/00; C07 K 14/00;
C07 K 14/01; C07 K 14/025; C07 K 14/285; C07 K 14/315; C07 K 19/00; C12 N 15/09

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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☐ 3. Document ID: DE 69824013 T2, WO 9910375 A2, AU 9892639 A, ZA 9807591 A, NO 200000850 A, EP 1007551 A2, BR 9812139 A, CZ 200000634 A3, CN 1276833 A, HU 200004327 A2, AU 732946 B, MX 2000001813 A1, KR 2001023193 A, JP 2001513986 W, US 6342224 B1, NZ 502632 A, US 20020182221 A1, EP 1007551 B1, DE 69824013 E, ES 2221198 T3

L4: Entry 3 of 3

File: DWPI

Jun 2, 2005

DERWENT-ACC-NO: 1999-190587

DERWENT-WEEK: 200537

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TITLE: Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for treatment or prophylaxis of HPV induced lesions

INVENTOR: BRUCK, C; DELISSE, A E F ; GERARD, C M G ; LOMBARDO-BENCHEIKH, A ; SILVA, T C ; CABEZON, S T ; CABEZON SILVA, T ; FERNANDE DELISSE, A E ; GHISLAINE GERARD, C M

PRIORITY-DATA: 1997GB-0017953 (August 22, 1997)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
<u>DE 69824013 T2</u>	June 2, 2005		000	C07K014/025
<u>WO 9910375 A2</u>	March 4, 1999	E	095	C07K014/00
<u>AU 9892639 A</u>	March 16, 1999		000	C07K014/00
<u>ZA 9807591 A</u>	April 26, 2000		096	C07K000/00
<u>NO 200000850 A</u>	April 14, 2000		000	C07K019/00
<u>EP 1007551 A2</u>	June 14, 2000	E	000	C07K014/00
<u>BR 9812139 A</u>	July 18, 2000		000	C07K014/00
<u>CZ 200000634 A3</u>	January 17, 2001		000	C07K014/00
<u>CN 1276833 A</u>	December 13, 2000		000	C12N015/62
<u>HU 200004327 A2</u>	March 28, 2001		000	C07K014/00
<u>AU 732946 B</u>	May 3, 2001		000	C07K014/00
<u>MX 2000001813 A1</u>	October 1, 2000		000	C07K014/00
<u>KR 2001023193 A</u>	March 26, 2001		000	C12N015/62

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<u>JP 2001513986 W</u>	September 11, 2001	131	C12N015/09
<u>US 6342224 B1</u>	January 29, 2002	000	A61K039/00
<u>NZ 502632 A</u>	March 28, 2002	000	C07K014/285
<u>US 20020182221 A1</u>	December 5, 2002	000	A61K039/12
<u>EP 1007551 B1</u>	May 19, 2004	E 000	C07K014/025
<u>DE 69824013 E</u>	June 24, 2004	000	C07K014/025
<u>ES 2221198 T3</u>	December 16, 2004	000	C07K014/025

NZ 502632 A , US 20020182221 A1 INT-CL (IPC): A61 K 9/107; A61 K 38/02;
A61 K 39/00; A61 K 39/12; A61 K 39/145; A61 K 39/39; A61 P 35/00; A61 P 37/00;
C07 H 14/00; C07 H 21/04; C07 K 0/00; C07 K 1/00; C07 K 14/00; C07 K 14/025;
C07 K 14/08; C07 K 14/11; C07 K 14/285; C07 K 16/08; C07 K 17/00; C07 K 19/00;
C12 N 1/15; C12 N 1/19; C12 N 1/20; C12 N 1/21; C12 N 5/00; C12 N 5/02; C12 N 5/10;
C12 N 15/00; C12 N 15/09; C12 N 15/62; C12 N 15/63; C12 N 15/70; C12 N 15/74;
C12 P 21/02; C12 P 21/04

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☐ 1. Document ID: US 6558670 B1

L10: Entry 1 of 6

File: USPT

May 6, 2003

US-PAT-NO: 6558670

DOCUMENT-IDENTIFIER: US 6558670 B1

TITLE: Vaccine adjuvants

DATE-ISSUED: May 6, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Friede; Martin	Court St Etienne			BE
Hermand; Philippe	Court St Etienne			BE

US-CL-CURRENT: [424/184.1](#); [424/278.1](#), [424/283.1](#), [514/25](#)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Figures	Abstract	Claims	KMC	Drawings
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☐ 2. Document ID: US 6544518 B1

L10: Entry 2 of 6

File: USPT

Apr 8, 2003

US-PAT-NO: 6544518

DOCUMENT-IDENTIFIER: US 6544518 B1

TITLE: Vaccines

DATE-ISSUED: April 8, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Friede; Martin	Farnham			GB
Garcon; Nathalie	Wavre			BE
Gerard; Catherine Marie Ghislaine	Rhode Saint Genese			BE
Hermand; Philippe	Court-Saint-Etienne			BE

US-CL-CURRENT: [424/184.1](#); [424/208.1](#), [424/228.1](#), [424/229.1](#), [424/231.1](#), [424/249.1](#),
[424/278.1](#), [424/283.1](#), [514/25](#)

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☐ 3. Document ID: US 6342224 B1

L10: Entry 3 of 6

File: USPT

Jan 29, 2002

US-PAT-NO: 6342224

DOCUMENT-IDENTIFIER: US 6342224 B1

TITLE: Recombinant papillomavirus vaccine and method for production and treatment

DATE-ISSUED: January 29, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bruck; Claudine	Rixensart			BE
Silva; Teresa Cabezon	Lenkebeek			BE
Fernande Delisse; Anne-Marie Eva	Gosselies			BE
Ghislaine Gerard; Catherine Marie	Rhode Saint Genese			BE
Lombardo-Bencheikh; Angela	Wavre			BE

US-CL-CURRENT: 424/192.1; 424/185.1, 424/186.1, 424/204.1, 435/252.3, 435/320.1,
435/325, 435/69.3, 435/69.7, 530/350, 536/23.4, 536/23.72

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw. De
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☐ 4. Document ID: US 6306397 B1

L10: Entry 4 of 6

File: USPT

Oct 23, 2001

US-PAT-NO: 6306397

DOCUMENT-IDENTIFIER: US 6306397 B1

TITLE: Variants of human papilloma virus antigens

DATE-ISSUED: October 23, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Edwards; Stirling John	Northcote			AU
Cox; John Cooper	Bullengarook			AU
Webb; Elizabeth Ann	Eltham			AU
Frazer; Ian	St. Lucia			AU

US-CL-CURRENT: 424/192.1; 424/186.1, 424/204.1, 435/235.1, 435/69.1, 435/69.7,
536/23.1, 536/23.72, 536/24.3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw. De
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☐ 5. Document ID: US 6303128 B1

L10: Entry 5 of 6

File: USPT

Oct 16, 2001

US-PAT-NO: 6303128

DOCUMENT-IDENTIFIER: US 6303128 B1

TITLE: Method for protein expression

DATE-ISSUED: October 16, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Webb; Elizabeth Ann	Eltham			AU
Edwards; Stirling John	Northcote			AU

US-CL-CURRENT: [424/199.1](#); [424/192.1](#), [435/235.1](#), [435/320.1](#), [435/325](#), [435/69.1](#),
[435/69.7](#)

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☐ 6. Document ID: US 6004557 A

L10: Entry 6 of 6

File: USPT

Dec 21, 1999

US-PAT-NO: 6004557

DOCUMENT-IDENTIFIER: US 6004557 A

TITLE: Variants of human papillomavirus antigens

DATE-ISSUED: December 21, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Edwards; Stirling John	Caburg			AU
Cox; John Cooper	Bullengarook			AU
Webb; Elizabeth Ann	Eltham			AU
Frazer; Ian	St. Lucia.			AU

US-CL-CURRENT: [424/192.1](#); [424/186.1](#), [424/199.1](#), [424/204.1](#), [435/235.1](#), [435/320.1](#),
[435/69.1](#), [435/69.7](#), [536/23.1](#), [536/23.72](#) , [536/24.3](#)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw. De
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☐ 1: [Cassetti MC, McElhiney SP, Shahabi V, Pullen JK, Le Poole IC, Eiben GL, Smith LR, Kast WM.](#) Related Articles, Links

Antitumor efficacy of Venezuelan equine encephalitis virus replicon particles encoding mutated HPV16 E6 and E7 genes. Vaccine. 2004 Jan 2;22(3-4):520-7. PMID: 14670335 [PubMed - indexed for MEDLINE]

☐ 2: [Velders MP, McElhiney S, Cassetti MC, Eiben GL, Higgins T, Kovacs GR, Elmishad AG, Kast WM, Smith LR.](#) Related Articles, Links

Eradication of established tumors by vaccination with Venezuelan equine encephalitis virus replicon particles delivering human papillomavirus 16 E7 RNA. Cancer Res. 2001 Nov 1;61(21):7861-7. PMID: 11691804 [PubMed - indexed for MEDLINE]

☐ 3: [Eiben GL, Velders MP, Schreiber H, Cassetti MC, Pullen JK, Smith LR, Kast WM.](#) Related Articles, Links

Establishment of an HLA-A*0201 human papillomavirus type 16 tumor model to determine the efficacy of vaccination strategies in HLA-A*0201 transgenic mice. Cancer Res. 2002 Oct 15;62(20):5792-9. PMID: 12384540 [PubMed - indexed for MEDLINE]

☐ 4: [Zhou X, Qian X, Zhao Q, Lu Y, Xiong M.](#) Related Articles, Links

Efficient expression of modified human papillomavirus 16 e6/e7 fusion protein and the antitumor efficacy in a mouse model. Biol Pharm Bull. 2004 Mar;27(3):303-7. PMID: 14993792 [PubMed - indexed for MEDLINE]

☐ 5: [Peng S, Ji H, Trimble C, He L, Tsai YC, Yeatermeyer J, Boyd DA, Hung CF, Wu TC.](#) Related Articles, Links

Development of a DNA vaccine targeting human papillomavirus type 16 oncoprotein E6. J Virol. 2004 Aug;78(16):8468-76. PMID: 15280455 [PubMed - indexed for MEDLINE]


☐ 6: [Pushko P, Parker M, Ludwig GV, Davis NL, Johnston RE, Smith JF.](#) Related Articles, Links

Replicon-helper systems from attenuated Venezuelan equine encephalitis virus: expression of heterologous genes in vitro and immunization against heterologous pathogens in vivo.

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Virology. 1997 Dec 22;239(2):389-401.
PMID: 9434729 [PubMed - indexed for MEDLINE]

- ☐ 7: [Smahel M, Sima P, Ludvikova V, Vonka V.](#) [Related Articles, Links](#)

 Modified HPV16 E7 Genes as DNA Vaccine against E7-Containing Oncogenic Cells.


Virology. 2001 Mar 15;281(2):231-8.
PMID: 11277695 [PubMed - indexed for MEDLINE]

- ☐ 8: [Ressing ME, Sette A, Brandt RM, Ruppert J, Wentworth PA, Hartman M, Oseroff C, Grey HM, Melief CJ, Kast WM.](#) [Related Articles, Links](#)

 Human CTL epitopes encoded by human papillomavirus type 16 E6 and E7 identified through in vivo and in vitro immunogenicity studies of HLA-A*0201-binding peptides.


J Immunol. 1995 Jun 1;154(11):5934-43.
PMID: 7538538 [PubMed - indexed for MEDLINE]

- ☐ 9: [Greenstone HL, Nieland JD, de Visser KE, De Bruijn ML, Kimbauer R, Roden RB, Lowy DR, Kast WM, Schiller JT.](#) [Related Articles, Links](#)

 Chimeric papillomavirus virus-like particles elicit antitumor immunity against the E7 oncoprotein in an HPV16 tumor model.


Proc Natl Acad Sci U S A. 1998 Feb 17;95(4):1800-5.
PMID: 9465097 [PubMed - indexed for MEDLINE]

- ☐ 10: [Daemen T, Pries F, Bungener L, Kraak M, Regts J, Wilschut J.](#) [Related Articles, Links](#)

 Genetic immunization against cervical carcinoma: induction of cytotoxic T lymphocyte activity with a recombinant alphavirus vector expressing human papillomavirus type 16 E6 and E7.


Gene Ther. 2000 Nov;7(21):1859-66.
PMID: 11110419 [PubMed - indexed for MEDLINE]

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 Cancer immunotherapy using Sindbis virus replicon particles encoding a VP22-antigen fusion.


Hum Gene Ther. 2002 Mar 1;13(4):553-68.
PMID: 11874633 [PubMed - indexed for MEDLINE]

- ☐ 12: [Pokorna D, Mackova J, Duskova M, Rittich S, Ludvikova V, Smahel M.](#) [Related Articles, Links](#)

 Combined immunization with fusion genes of mutated E7 gene of human papillomavirus type 16 did not enhance antitumor effect.


J Gene Med. 2005 Jun;7(6):696-707.
PMID: 15712328 [PubMed - indexed for MEDLINE]

- ☐ 13: [Daemen T, Regts J, Holtrop M, Wilschut J.](#) [Related Articles, Links](#)

 Immunization strategy against cervical cancer involving an alphavirus vector expressing high levels of a stable fusion protein of human papillomavirus 16 E6 and E7.

Gene Ther. 2002 Jan;9(2):85-94.
PMID: 11857066 [PubMed - indexed for MEDLINE]

- ☐ 14: [Chu NR, Wu HB, Wu T, Boux LJ, Siegel MI, Mizzen LA.](#) [Related Articles, Links](#)

 Immunotherapy of a human papillomavirus (HPV) type 16 E7-expressing tumour by administration of fusion protein comprising Mycobacterium

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bovis bacille Calmette-Guerin (BCG) hsp65 and HPV16 E7.
Clin Exp Immunol. 2000 Aug;121(2):216-25.
PMID: 10931134 [PubMed - indexed for MEDLINE]

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T-helper epitopes identified within the E6 transforming protein of cervical cancer-associated human papillomavirus type 16.

Viral Immunol. 1999;12(4):297-312.

PMID: 10630789 [PubMed - indexed for MEDLINE]

- ☐ 16: [Melero I, Singhal MC, McGowan P, Haugen HS, Blake J, Hellstrom KE, Yang G, Clegg CH, Chen L.](#) Related Articles, Links



Immunological ignorance of an E7-encoded cytolytic T-lymphocyte epitope in transgenic mice expressing the E7 and E6 oncogenes of human papillomavirus type 16.

J Virol. 1997 May;71(5):3998-4004.

PMID: 9094677 [PubMed - indexed for MEDLINE]

- ☐ 17: [Daemen T, Riezebos-Brilman A, Regts J, Dontje B, van der Zee A, Wilschut J.](#) Related Articles, Links



Superior therapeutic efficacy of alphavirus-mediated immunization against human papilloma virus type 16 antigens in a murine tumour model: effects of the route of immunization.

Antivir Ther. 2004 Oct;9(5):733-42.

PMID: 15535411 [PubMed - indexed for MEDLINE]

- ☐ 18: [Wakabayashi MT, Da Silva DM, Potkul RK, Kast WM.](#) Related Articles, Links



Comparison of human papillomavirus type 16 L1 chimeric virus-like particles versus L1/L2 chimeric virus-like particles in tumor prevention.

Intervirology. 2002;45(4-6):300-7.

PMID: 12566713 [PubMed - indexed for MEDLINE]

- ☐ 19: [Indrova M, Reinis M, Bubenik J, Jandlova T, Bieblova J, Vonka V, Velek J.](#) Related Articles, Links



Immunogenicity of dendritic cell-based HPV16 E6/E7 peptide vaccines: CTL activation and protective effects.

Folia Biol (Praha). 2004;50(6):184-93.

PMID: 15709713 [PubMed - indexed for MEDLINE]

- ☐ 20: [Lasaro MO, Diniz MO, Reyes-Sandoval A, Ertl HC, Ferreira LC.](#) Related Articles, Links



Anti-tumor DNA vaccines based on the expression of human papillomavirus-16 E6/E7 oncoproteins genetically fused with the glycoprotein D from herpes simplex virus-1.

Microbes Infect. 2005 Dec;7(15):1541-50. Epub 2005 Sep 9.

PMID: 16213178 [PubMed - indexed for MEDLINE]

Items 1 - 20 of 489

Page

1

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☐ 1. Document ID: US 6558670 B1

L10: Entry 1 of 6

File: USPT

May 6, 2003

US-PAT-NO: 6558670

DOCUMENT-IDENTIFIER: US 6558670 B1

TITLE: Vaccine adjuvants

DATE-ISSUED: May 6, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Friede; Martin	Court St Etienne			BE
Hermand; Philippe	Court St Etienne			BE

US-CL-CURRENT: [424/184.1](#); [424/278.1](#), [424/283.1](#), [514/25](#)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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☐ 2. Document ID: US 6544518 B1

L10: Entry 2 of 6

File: USPT

Apr 8, 2003

US-PAT-NO: 6544518

DOCUMENT-IDENTIFIER: US 6544518 B1

TITLE: Vaccines

DATE-ISSUED: April 8, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Friede; Martin	Farnham			GB
Garcon; Nathalie	Wavre			BE
Gerard; Catherine Marie Ghislaine	Rhode Saint Genese			BE
Hermand; Philippe	Court-Saint-Etienne			BE

US-CL-CURRENT: [424/184.1](#); [424/208.1](#), [424/228.1](#), [424/229.1](#), [424/231.1](#), [424/249.1](#), [424/278.1](#), [424/283.1](#), [514/25](#)

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Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw D
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☐ 3. Document ID: US 6342224 B1

L10: Entry 3 of 6

File: USPT

Jan 29, 2002

US-PAT-NO: 6342224

DOCUMENT-IDENTIFIER: US 6342224 B1

TITLE: Recombinant papillomavirus vaccine and method for production and treatment

DATE-ISSUED: January 29, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bruck; Claudine	Rixensart			BE
Silva; Teresa Cabezon	Lenkebeek			BE
Fernande Delisse; Anne-Marie Eva	Gosselies			BE
Ghislaine Gerard; Catherine Marie	Rhode Saint Genese			BE
Lombardo-Bencheikh; Angela	Wavre			BE

US-CL-CURRENT: 424/192.1; 424/185.1, 424/186.1, 424/204.1, 435/252.3, 435/320.1,
435/325, 435/69.3, 435/69.7, 530/350, 536/23.4, 536/23.72

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw D
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☐ 4. Document ID: US 6306397 B1

L10: Entry 4 of 6

File: USPT

Oct 23, 2001

US-PAT-NO: 6306397

DOCUMENT-IDENTIFIER: US 6306397 B1

TITLE: Variants of human papilloma virus antigens

DATE-ISSUED: October 23, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Edwards; Stirling John	Northcote			AU
Cox; John Cooper	Bullengarook			AU
Webb; Elizabeth Ann	Eltham			AU
Frazer; Ian	St. Lucia			AU

US-CL-CURRENT: 424/192.1; 424/186.1, 424/204.1, 435/235.1, 435/69.1, 435/69.7,
536/23.1, 536/23.72, 536/24.3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw D
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☐ 5. Document ID: US 6303128 B1

L10: Entry 5 of 6

File: USPT

Oct 16, 2001

US-PAT-NO: 6303128

DOCUMENT-IDENTIFIER: US 6303128 B1

TITLE: Method for protein expression

DATE-ISSUED: October 16, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Webb; Elizabeth Ann	Eltham			AU
Edwards; Stirling John	Northcote			AU

US-CL-CURRENT: 424/199.1; 424/192.1, 435/235.1, 435/320.1, 435/325, 435/69.1,
435/69.7

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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☐ 6. Document ID: US 6004557 A

L10: Entry 6 of 6

File: USPT

Dec 21, 1999

US-PAT-NO: 6004557

DOCUMENT-IDENTIFIER: US 6004557 A

TITLE: Variants of human papillomavirus antigens

DATE-ISSUED: December 21, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Edwards; Stirling John	Caburg			AU
Cox; John Cooper	Bullengarook			AU
Webb; Elizabeth Ann	Eltham			AU
Frazer; Ian	St. Lucia.			AU

US-CL-CURRENT: 424/192.1; 424/186.1, 424/199.1, 424/204.1, 435/235.1, 435/320.1,
435/69.1, 435/69.7, 536/23.1, 536/23.72 , 536/24.3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw D
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E6/E7 fusion

6

This Page Blank (uspto)

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This Page Blank (uspto)

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<input type="checkbox"/>	L8	US-6342224-B1.did.	1
	<i>DB=EPAB; PLUR=YES; OP=ADJ</i>		
<input type="checkbox"/>	L7	WO-9910375-A2.did.	1
<input type="checkbox"/>	L6	WO-9910375-A2.did.	1
<input type="checkbox"/>	L5	CN-1381583-A.did.	0
	<i>DB=DWPI; PLUR=YES; OP=ADJ</i>		
<input type="checkbox"/>	L4	E6/E7 fusion	3
	<i>DB=PGPB; PLUR=YES; OP=ADJ</i>		
<input type="checkbox"/>	L3	E6/E7 fusion	12
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OM protein - protein search, using sw model

Run on: May 27, 2006, 04:59:57 ; Search time 228.273 Seconds

(without alignments)
196.288 Million cell updates/secTitle: US-10-530-253-14ED
Perfect score: 517
Sequence: 1 MHGDTPLHEHYMDLQPERTT.....LEDLMGTCIGVXPSQKP 98Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

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3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*
9: geneseqp20058:*
10: geneseqp20068:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	99.4	248	AD044070	Ad044070 Amino aci
2	513	99.2	98	AE13079	AE13079 HPV16 E7
3	513	99.2	220	AA25378	AA25378 HPV fusio
4	513	99.2	220	AA20634	AA20634 Prot.D1/3
5	513	99.2	230	AED52640	AED52640 Fusion pr
6	513	99.2	248	AD044068	Ad044068 Amino aci
7	513	99.2	805	ADA27366	Ada27366 HPV-16 L2
8	513	99.2	805	ADA92544	Ada92544 HPV-16 L2
9	513	99.2	805	ADA14293	Ada14293 HPV-16 L2
10	513	99.2	805	AAE38618	AAE38618 HPV-16 L2
11	512	99.0	98	AAR22767	Aar22767 HPV E7 pe
12	512	99.0	98	AAR42361	Aar42361 Human pap
13	512	99.0	98	AAW46886	AAW46886 Amino aci
14	512	99.0	98	AAW58474	AAW58474 Human pap
15	512	99.0	98	AAW57721	AAW57721 Human pap
16	512	99.0	98	AAW58421	AAW58421 Human pap
17	512	99.0	98	AAU01718	AAu01718 Human pap
18	512	99.0	98	AAU72607	AAu72607 Human pap
19	512	99.0	98	AAW67546	AAW67546 Amino aci
20	512	99.0	98	AAW86332	AAW86332 HPV 16 E7
21	512	99.0	98	AAU77713	AAu77713 Human pap
22	512	99.0	98	AAU10810	AAu10810 Human pap
23	512	99.0	98	ABB82375	Abb82375 Wild-type

24	512	99.0	98	AAO16630	AAo16630 Human pap
25	512	99.0	98	ADP09516	ADp09516 Human pap
26	512	99.0	98	ADP18632	ADp18632 Human pap
27	512	99.0	98	ADL90076	ADl90076 Human pap
28	512	99.0	98	ADM32916	Adm32916 Amino aci
29	512	99.0	98	AD044073	Ad044073 Amino aci
30	512	99.0	98	ADN49005	Adn49005 Human pap
31	512	99.0	98	ADU66362	Adu66362 Human pap
32	512	99.0	98	ADX15532	Adx15532 Human pap
33	512	99.0	98	ADY16903	ADy16903 Human pap
34	512	99.0	98	AEA40816	Aea40816 Ant1-apop
35	512	99.0	98	AE11989	AEb11989 HPV16 E7
36	512	99.0	98	AEC6392	Aec6392 HPV prote
37	512	99.0	98	AEC98871	Aec98871 HPV16 En
38	512	99.0	98	AED13078	Aed13078 HPV16 E7
39	512	99.0	98	AED64360	Aed64360 Human pap
40	512	99.0	98	AEE94089	Aee94089 HPV16 E7
41	512	99.0	99	ADQ88451	Adq88451 HPV16 E7
42	512	99.0	99	ADY92615	Ady92615 HPV16 E7
43	512	99.0	121	AA831608	Aab31608 Amino aci
44	512	99.0	198	AA831616	Aab31616 Novel Pve
45	512	99.0	212	ADT75831	Adt75831 Novel Pve
46	512	99.0	220	AAW25375	AAW25375 HPV fusio
47	512	99.0	220	AAW02631	AAW02631 ProtdCh1
48	512	99.0	220	AED52631	Aed52631 Fusion pr
49	512	99.0	239	AAW25380	AAW25380 HPV fusio
50	512	99.0	239	AAW02636	AAW02636 Fusion pr
51	512	99.0	239	AED52644	Aed52644 Amino aci
52	512	99.0	248	AD044066	Ad044066 Amino aci
53	512	99.0	253	AAW43480	AAW43480 Amino ter
54	512	99.0	253	AAW01502	AAW01502 Amino ter
55	512	99.0	253	AAW97612	AAW97612 Amino ter
56	512	99.0	253	AAW11132	AAW11132 CTAA4/E7
57	512	99.0	253	AAW81586	AAW81586 CTAA4/E7
58	512	99.0	253	AAW87562	AAW87562 CTAA4-E7
59	512	99.0	256	ADR47005	Adr47005 Human pap
60	512	99.0	256	AER40157	Aer40157 Human pap
61	512	99.0	266	AAW97561	AAW97561 Human pap
62	512	99.0	288	AAU02129	AAU02129 Flt-3 lig
63	512	99.0	295	AAW31615	Aab31615 Amino aci
64	512	99.0	324	AAW31613	Aab31613 Amino aci
65	512	99.0	334	AAW022926	AAW022926 HbAg-E7
66	512	99.0	349	AEA40828	Aea40828 Ant1-apop
67	512	99.0	349	AEA40831	Aea40831 Ant1-apop
68	512	99.0	371	AAW25377	AAW25377 HPV fusio
69	512	99.0	371	AAW02633	AAW02633 Prot.D1/3
70	512	99.0	371	AAW02638	AAW02638 Fusion pr
71	512	99.0	390	AAW25381	AAW25381 HPV fusio
72	512	99.0	390	AAW02637	AAW02637 CLYTA-E6E
73	512	99.0	390	AED52646	Aed52646 Fusion pr
74	512	99.0	421	AAW50663	AAW50663 Thioedox
75	512	99.0	493	AAW31610	Aab31610 Amino aci
76	512	99.0	638	AAW03790	Aab03790 Heat choc
77	512	99.0	639	AAW31609	Aab31609 Amino aci
78	512	99.0	641	AAW31619	Aab31619 Amino aci
79	512	99.0	647	AAW31620	Aab31620 Amino aci
80	511	98.8	98	ADF18635	Adf18635 Human pap
81	511	98.8	248	AD044064	Ad044064 Amino aci
82	510	98.6	248	AD044062	Ad044062 Amino aci
83	509	98.5	248	AD044060	Ad044060 Amino aci
84	507	98.1	98	AAW50703	AAW50703 HPV16 E7
85	507	98.1	98	AAW49453	AAW49453 HPV 16E7
86	507	98.1	98	AAW02639	AAW02639 HPV-16 pr
87	507	98.1	111	AAW022923	AAW022923 Human pap
88	505	97.7	262	AAW27724	AAW27724 HPV 16 E7
89	504	97.5	98	AAW08020	AAW08020 Human pap
90	504	97.5	98	ADJ32548	Adj32548 Human pap
91	503	97.3	98	AAW31607	Aab31607 Amino aci
92	503	97.3	490	ADZ42209	Adz42209 N. mening
93	503	97.3	648	AAW31614	Aab31614 Amino aci
94	503	97.3	711	AAW31617	Aab31617 Amino aci
95	503	97.3	724	AAW31618	Aab31618 Amino aci
96	500	96.7	99	ABB81111	Abb81111 HPV E7 an

97	500	96.7	99	5	ABB82376	Modified
98	500	96.7	99	7	ADE21865	HPV-16 E7
99	500	96.7	99	8	AD005276	Human pap
100	500	96.7	99	8	AD066377	Human pap

ALIGNMENTS

RESULT 1

ADO44070 standard; protein; 248 AA.

ADO44070;

15-JUL-2004 (first entry)

Amino acid sequence of a fusion protein designated E7E6PentM.

E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;

cervical cancer; immune response; lower gastrointestinal tract cancer;

anal cancer; reproductive system cancer; penile cancer; vulvar cancer;

gene; 98.

Human papillomavirus type 16.

Synthetic.

WO2004030636-A2.

15-APR-2004.

02-OCT-2003; 2003WO-US031726.

03-OCT-2002; 2002US-0415929P.

(AMHP) WYETH HOLDINGS CORP.

Smith L, Cassecci MC;

WPI; 2004-316328/29.

N-PSDB; ADO44071.

New polypeptide comprising human papillomavirus E6 and E7 polypeptides,

useful for treating or preventing human papillomavirus (HPV)-associated

cancers, e.g. cervical cancer.

Claim 22; Page 75-76; 101pp; English.

The present sequence represents a fusion protein, comprising E7 and E6

polypeptides from human papillomavirus type 16 (HPV16). The fusion

protein is designated E7E6PentM, and comprises an E7 amino terminus

(where residues 24, 26 and 91 have been replaced with glycine) and an E6

carboxy terminus (where residues 63 and 106 have been replaced with

glycine). E7E6PentM is representative of fusion proteins of the

invention. The specification describes human papillomavirus E6 and E7

polypeptides, where the E7 polypeptide has mutations at any one or more

of the amino acids corresponding to amino acids 24, 26 or 91 of the

sequence given in ADO44073 and the E6 polypeptide has no mutations or has

mutations at any one or more of the amino acids corresponding to amino

acids 63 or 106 of the sequence given in ADO44072. The polypeptides of

the invention are useful for treating or preventing human papillomavirus

(HPV)-associated cancers, such as cervical cancer. The fusion proteins

and nucleic acids encoding the fusion proteins are useful for generating

immune responses against HPV. They are also useful for treating lower

gastrointestinal tract cancers, e.g. anal cancer, and other cancers of

the reproductive system, including penile and vulvar cancer.

Sequence 248 AA;

Query Match 99.4%; Score 514; DB 8; Length 248;

Best Local Similarity 96.9%; Pred. No. 3.9e-57;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MHGDTPLHEMYMDLOPETTDLYXXYXQLNDSSEDEIDGPAQAEPPRAHYNIIVTFCK	60
Db	1	MHGDTPLHEMYMDLOPETTDLYXXYXQLNDSSEDEIDGPAQAEPPRAHYNIIVTFCK	60
Qy	61	CDSTLRFCVQSTHVDIRTLIEDLMGTIGIVPICSGKP	98
Db	61	CDSTLRFCVQSTHVDIRTLIEDLMGTIGIVPICSGKP	98

RESULT 2

AED13079 standard; protein; 98 AA.

AED13079;

15-DEC-2005 (first entry)

HPV16 E7 variant protein sequence.

mutagen; vaccine; antigen; virucide; antibacterial.

Human papillomavirus type 16.

FR2868781-A1.

14-OCT-2005.

13-APR-2004; 2004FR-00003848.

13-APR-2004; 2004FR-00003848.

(IMMU-) IMMUTEP.

Triebel F;

WPI; 2005-678227/70.

N-PSDB; AED13077.

Therapeutic vaccine, for viral and bacterial conditions, comprises an

antigen protein and a viral or bacterial protein, coupled together by

stable hydrogen or covalence bonds in biological media.

Disclosure; Fig 1; 51pp; French.

The invention relates to a novel vaccine composed of an antigen protein

and a second protein as an s-(methyl mercury)-L-cysteine (CMH class II)

ligand. The second protein is taken from a group including human

Lymphocyte Activation Gene (hLAG)-3. The first protein is a viral or

bacterial antigen, a tumor antigen, parasitic antigen, or their mixtures.

The viral antigens can be for hepatitis B (HBV), human papillomavirus

(HPV), hepatitis C (HCV), human immunodeficiency virus (HIV), Epstein-

Barr virus (EBV), cytomegalovirus (CMV), and their combinations. The

bacterial antigens can be intracellular bacteria of tuberculosis, leprosy

and listeria. A vaccine of the invention has virucide, and antibacterial

activity. The present sequence represents the HPV16 variant E7 protein

sequence.

Sequence 98 AA;

Query Match 99.2%; Score 513; DB 9; Length 98;

Best Local Similarity 96.9%; Pred. No. 1.6e-57;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 3

AAV25378
ID AAV25378 standard; protein; 220 AA.
XX
AC AAV25378;
XX
DT 06-SEP-1999 (first entry)
XX
DE HPV fusion protein DI/3-E7-Mutated (C24G, E26Q)/HPV16.
XX
KW Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KM immunological fusion partner; Cpg oligonucleotide; immune response;
KM HPV antigen; prevention; treatment.
XX
OS Synthetic.
OS Human papillomavirus.
XX
PN WO933868-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1998; 98WO-EP008563.
XX
PR 24-DEC-1997; 97GB-00027262.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Dalemans WJ, Gerard CMG;
XX
DR WPI; 1999-405485/34.
XX
DR N-PSDB; AAX78794.
XX
PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PS Induce immune response to HPV.
XX
PS Example V; Page 51; 62pp; English.
XX
CC AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAV25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory Cpg
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours
XX
SQ Sequence 220 AA;
XX
Query Match 99.2%; Score 513; DB 2; Length 220;
Best Local Similarity 96.9%; Pred. No. 4.6e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 MGGDTPTLHEVMDLQPEETDLYXXQLNDSSEEDIDGPAGAPDRAHYNIIVTFCK 60
DB 114 MGGDTPTLHEVMDLQPEETDLYXXQLNDSSEEDIDGPAGAPDRAHYNIIVTFCK 173
QY 61 CDSTLRICVQSTHVDIRTELDLMGTIGIYPCISQKP 98
DB 174 CDSTLRICVQSTHVDIRTELDLMGTIGIYPCISQKP 211

RESULT 4
AAV02634
ID AAV02634 standard; protein; 220 AA.
XX
AC AAV02634;
XX
DT 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)
XX
DE Prot. DI/3-E7-mut (C24G, E26Q)/HPV16 protein.
XX
KM Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KM tumour; lesion; benign; malignant; virus; infection.
XX

OS Human papillomavirus.
OS Haemophilus influenzae.
OS Chimeric.
XX
PN WO910375-A2.
XX
PD 04-MAR-1999.
XX
PF 17-AUG-1998; 98WO-EP005285.
XX
PR 22-AUG-1997; 97GB-00017953.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
XX
PI Lombardo-Bencheikh A;
XX
DR WPI; 1999-190587/16.
XX
DR N-PSDB; AAX29783.
XX
PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT treatment or prophylaxis of HPV induced lesions.
XX
PS Disclosure; Fig 8; 95pp; English.
XX
CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B protein
CC D. The sequence also contains a histidine tag at the C-terminus of the
CC encoded protein. The protein can be used in a vaccine, for immuno-
CC therapeutically treating HPV induced tumour lesions (benign or malignant)
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 220 AA;
XX
Query Match 99.2%; Score 513; DB 2; Length 220;
Best Local Similarity 96.9%; Pred. No. 4.6e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 MGGDTPTLHEVMDLQPEETDLYXXQLNDSSEEDIDGPAGAPDRAHYNIIVTFCK 60
DB 114 MGGDTPTLHEVMDLQPEETDLYXXQLNDSSEEDIDGPAGAPDRAHYNIIVTFCK 173
QY 61 CDSTLRICVQSTHVDIRTELDLMGTIGIYPCISQKP 98
DB 174 CDSTLRICVQSTHVDIRTELDLMGTIGIYPCISQKP 211

RESULT 5
AED52640
ID AED52640 standard; protein; 220 AA.
XX
AC AED52640;
XX
DT 29-DEC-2005 (first entry)
XX
DE Fusion protein DI/3-E7-Ris (HPV16), C137G/E139Q.
XX
KW Fusion protein; vaccine; papilloma; cyostatic; papillomavirus infection;
KM virucide; uterine cervix tumor; E7; mutain; D protein.
XX
OS Haemophilus influenzae; strain 772.
OS Human papillomavirus type 16.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Misc-difference 137 /note= "Wild-type Cys substituted by Gly"
FT FT Misc-difference 139 /note= "Wild-type Gln substituted by Gln"
FT FT

PN IN9801903-14.
 XX
 PD 04-MAR-2005.
 XX
 PF 24-AUG-1998; 98IN-CH001903.
 XX
 PR 22-AUG-1997; 97EP-00179535.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Tyrell AMR;
 XX
 DR WPI: 2005-557648/57.
 XX
 DR N-PSDB; AED52639.
 XX
 PT Vaccine.
 PS
 SQ Example 8; Fig 8; 96pp; English.
 CC The invention relates to human Papilloma virus (HPV) fusion proteins,
 CC linked to an immunological fusion partner that provides T helper epitopes
 CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
 CC are useful in the treatment or prophylaxis of HPV induced lesions
 CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
 CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
 CC Haemophilus influenzae D protein (20-127), the C-terminus of
 CC Streptococcus pneumoniae Lyta protein (glycA) or choredoxin. The present
 CC sequence represents a mutated HPV-H. Influenzae D protein, fusion protein
 CC of the invention.
 XX
 SQ Sequence 220 AA;

Query March 99.2%; Score 513; DB 9; Length 220;
 Best Local Similarity 96.9%; Pred. No. 4.6e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDPPTLHEYMLDLPETTDLYXXYXQLNDSSEEDSIDGPAGQAEPRRAHYNIVTFCK 60
 DB 114 MHGDPPTLHEYMLDLPETTDLYGYQLNDSSEEDSIDGPAGQAEPRRAHYNIVTFCK 173
 QY 61 CDSTLRLCVOSTHYDRTLELDLMTGLGIYXPCSQKP 98
 DB 174 CDSTLRLCVOSTHYDRTLELDLMTGLGIYPCISQKP 211

RESULT 6
 ADO44068
 ID ADO44068 standard; protein; 248 AA.
 XX
 AC ADO44068;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Amino acid sequence of a fusion protein designated E7E6TeM.
 XX
 KW E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
 KW cervical cancer; immune response; lower gastrointestinal tract cancer;
 KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
 XX
 OS Human papillomavirus type 16.
 OS Synthetic.
 XX
 PN WO2004030636-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 02-OCT-2003; 2003WO-US031726.
 XX
 PR 03-OCT-2002; 2002US-0415929P.
 XX
 PA (AMHP) WYETH HOLDINGS CORP.
 XX
 PI Smith L, Caesetti MC;

XX
 DR WPI: 2004-316328/29.
 XX
 DR N-PSDB; ADO44069.
 XX
 PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.
 XX
 PF
 PS Claim 22; Page 73-74; 101pp; English.
 CC
 CC The present sequence represents a fusion protein, comprising E7 and E6
 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
 CC protein is designated E7E6TeM, and comprises an E7 amino terminus (where
 CC residues 24 and 26 have been replaced with glycine) and an E6 carboxy
 CC terminus (where residues 63 and 106 have been replaced with glycine).
 CC E7E6TeM is representative of fusion proteins of the invention. The
 CC specification describes human papillomavirus E6 and E7 polypeptides,
 CC where the E7 polypeptide has mutations at any one or more of the amino
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of
 CC there sequence given in ADO44072. The polypeptides of the invention are
 CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.
 XX
 SQ Sequence 248 AA;

Query March 99.2%; Score 513; DB 8; Length 248;
 Best Local Similarity 96.9%; Pred. No. 5.3e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDPPTLHEYMLDLPETTDLYXXYXQLNDSSEEDSIDGPAGQAEPRRAHYNIVTFCK 60
 DB 1 MHGDPPTLHEYMLDLPETTDLYGYQLNDSSEEDSIDGPAGQAEPRRAHYNIVTFCK 60
 QY 61 CDSTLRLCVOSTHYDRTLELDLMTGLGIYXPCSQKP 98
 DB 61 CDSTLRLCVOSTHYDRTLELDLMTGLGIYPCISQKP 98

RESULT 7
 ADA27366
 ID ADA27366 standard; protein; 805 AA.
 XX
 AC ADA27366;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.
 XX
 KW cell line; American Type Culture Collection PTA-4047; ATCC-4047;
 KW baculoviruses; viral recombinant protein; virus-like particle; vaccine;
 KW diagnostic reagent; human papillomavirus type 16; HPV-16; L2/E7/E2;
 KW fusion protein.
 XX
 OS Synthetic.
 OS Human papillomavirus type 16.
 XX
 PN WO2003068804-A2.
 XX
 PD 21-AUG-2003.
 XX
 PF 14-FEB-2003; 2003WO-US004516.
 XX
 PR 14-FEB-2002; 2002US-0356113P.
 PR 14-FEB-2002; 2002US-0356118P.
 PR 14-FEB-2002; 2002US-0356119P.
 PR 14-FEB-2002; 2002US-0356123P.
 PR 14-FEB-2002; 2002US-0356126P.

PR 14-FEB-2002; 2002US-0356133P.
 PR 14-FEB-2002; 2002US-0356135P.
 PR 14-FEB-2002; 2002US-0356150P.
 PR 14-FEB-2002; 2002US-0356151P.
 PR 14-FEB-2002; 2002US-0356152P.
 PR 14-FEB-2002; 2002US-0356154P.
 PR 14-FEB-2002; 2002US-0356156P.
 PR 14-FEB-2002; 2002US-0356157P.
 PR 14-FEB-2002; 2002US-0356161P.
 PR 14-FEB-2002; 2002US-0356162P.
 XX
 PA (NOVA-) NOVAVAX INC.
 XX
 PI Robinson RA;
 DR WPI; 2003-646475/61.
 DR N-PSDB; ADA27374.
 XX
 PT New insect cell line designated ATCC PTA-4047, useful for replicating
 PT baculoviruses to produce large amounts of recombinant proteins of
 PT medical, pharmaceutical and veterinary importance.
 XX
 PS Disclosure; Page 59-60; 63pp; English.
 XX
 CC The present invention describes a cell line comprising a cell that is a
 CC clone, derivative, mutant and/or transfectant of a cell line designated
 CC American Type Culture Collection (ATCC) PTA-4047. The cell upon culture
 CC grows continuously and retains the identifying characteristics of the
 CC cell line designated ATCC-4047. Also described is a process of making a
 CC cell line. The insect cell line is useful in replicating baculoviruses,
 CC as a host substrate for baculovirus plaque assays, as a source of insect
 CC proteins, acts as a depot for cell transfection to produce recombinant
 CC baculoviruses, and in expressing viral recombinant proteins.
 CC Extracellular and intracellular viral recombinant proteins and virus-like
 CC particles expressed from the cell line are useful as pharmaceutical
 CC compositions, vaccines or diagnostic reagents. The present sequence
 CC represents a human papillomavirus type 16 (HPV-16) L2/E7/E2 fusion
 CC protein, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 805 AA;
 Query Match 99.2%; Score 513; DB 6; Length 805;
 Best Local Similarity 96.9%; Pred. No. 2.4e-56;
 Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPLHEHYMLDLOPETTDLYXXQJLNDSSBEDEIDGPAQAEPRRAHYNIIVTFCCK 60
 DB 471 MHGDTPLHEHYMLDLOPETTDLYGYEQJLNDSSBEDEIDGPAQAEPRRAHYNIIVTFCCK 530
 QY 61 CDSTLRLCVQSTHVDIRTLLEDLMGTIGIYKPICSQKP 98
 DB 531 CDSTLRLCVQSTHVDIRTLLEDLMGTIGIYKPICSQKP 568
 RESULT 8
 ADA92544
 ID ADA92544 standard; protein; 805 AA.
 XX
 AC ADA92544;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 XX HPV-16 L2/E7/E2 fusion amino acid sequence SEQ ID NO:9.
 DE
 XX
 XX codon optimised; viral capsid protein; virus-like particle; VLP;
 KM antigenic; human papillomavirus infection; virucide; vaccine;
 KM gene therapy; human papillomavirus type 16; dysplasia; infection; HPV-16;
 XX fusion protein.
 XX
 OS Synthetic.
 OS Human papillomavirus type 16.
 XX
 PN WO2003068933-A2.

XX 21-AUG-2003.
 PD
 XX
 XX 14-FEB-2003; 2003WO-US004480.
 PP
 XX
 PR 14-FEB-2002; 2002US-0356113P.
 PR 14-FEB-2002; 2002US-0356118P.
 PR 14-FEB-2002; 2002US-0356119P.
 PR 14-FEB-2002; 2002US-0356123P.
 PR 14-FEB-2002; 2002US-0356126P.
 PR 14-FEB-2002; 2002US-0356133P.
 PR 14-FEB-2002; 2002US-0356135P.
 PR 14-FEB-2002; 2002US-0356150P.
 PR 14-FEB-2002; 2002US-0356151P.
 PR 14-FEB-2002; 2002US-0356152P.
 PR 14-FEB-2002; 2002US-0356154P.
 PR 14-FEB-2002; 2002US-0356156P.
 PR 14-FEB-2002; 2002US-0356157P.
 PR 14-FEB-2002; 2002US-0356161P.
 PR 14-FEB-2002; 2002US-0356162P.
 XX
 PA (NOVA-) NOVAVAX INC.
 XX
 PI Robinson RA;
 DR WPI; 2003-689664/65.
 DR N-PSDB; ADA92552.
 XX
 XX New codon optimised polynucleotide encoding a viral capsid protein that
 PT self assembles into a virus-like particle, useful for diagnosing,
 PT preventing or treating human papillomavirus infections or associated
 PT disorders.
 XX
 PS Disclosure; Page 119-120; 123pp; English.
 XX
 CC The present invention describes a codon optimised polynucleotide encoding
 CC a viral capsid protein that self assembles into a virus-like particle
 CC (VLP) that exhibits conformational antigenic epitopes capable of raising
 CC neutralising antibodies, where the VLP is expressed from a host cell
 CC extracellularly. Also described: (1) a vector comprising the above codon
 CC optimised polynucleotide operably linked to a eukaryotic or prokaryotic
 CC regulatory control element, capable of replication in prokaryotic and/or
 CC eukaryotic host; (2) a host cell comprising the vector; (3) a
 CC pharmaceutical or vaccine composition for treating, ameliorating or
 CC preventing a papillomavirus related disease or disorder, comprising a
 CC multiplicity of VLPs that exhibit conformational antigenic epitopes, and
 CC a carrier, diluent or adjuvant; (4) a diagnostic kit for detecting a
 CC papillomavirus infection, comprising a multiplicity of VLPs that exhibit
 CC conformational antigenic epitopes, and a detection agent comprising a
 CC detectable label; (5) a method for preparing the above codon optimised
 CC polynucleotide, comprising replacing codons that are underutilised in
 CC insect cells with codons that are utilised at high levels in insect
 CC cells, to create an initially-modified nucleotide sequence, and modifying
 CC the initially-modified nucleotide sequence by choosing a preferred codon
 CC for the initially-modified sequence, where the ratio of GC nucleotide
 CC pairs to AT nucleotide pairs in the further-modified nucleotide sequence
 CC trends towards about 1:1, where the number of palindromic and stem-loop
 CC DNA structures in the further-modified nucleotide sequence is minimised,
 CC and where the number of transcription and post-transcription repressor
 CC elements are minimised; and (6) methods for treating, ameliorating or
 CC preventing a papillomavirus related disease or disorder, or for
 CC protecting an individual against a papillomavirus infection, comprising
 CC administering to an individual an amount of the composition or vaccine
 CC cited above. The VLP has virucide activity and can be used in vaccines
 CC and in gene therapy. The composition and methods of the present invention
 CC are useful in diagnosing, preventing or treating human papillomavirus
 CC infections or associated disorders, such as dysplasia. The present
 CC sequence represents an HPV-16 codon optimised L2/E7/E2 fusion amino acid
 CC sequence from the present invention.
 XX
 SQ Sequence 805 AA;
 Query Match 99.2%; Score 513; DB 7; Length 805;

Best Local Similarity 96.9%; Pred. No. 2.4e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDTPTLHEYMLDLPETTDLYXXYYQLNDSSBEEDEIDPAGQAEPRRAHNIIVTFECK 60
Db 471 MHGDTPTLHEYMLDLPETTDLYGYEQLNDSSBEEDEIDPAGQAEPRRAHNIIVTFECK 530			

Db 471 MHGDTPTLHEYM L D Q P E T T D L Y G Y E Q L N D S S E E D E I D G P A G A E P D R A H Y N I V T F C C K 530

QY 61 CDSTLRLCVQSTHVDIRLTLEDLLMGTLGIVXPCISQKP 98
 |||
DB 531 CDSTLRLCVQSTHVDIRLTLEDLLMGTLGIVCPICISQKP 568

RESULT 9
ADA14293
ID ADA14293 standard; protein; 805 AA

HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.

KM purification; recombinant extracellular virus-like particle;
KM recombinant intracellular virus-like particle; virus-like particle; VLP;
KM virucide; vaccine; gene therapy; human papillomavirus; HPV, infection;
KM dysplasia; HPV-16; fusion protein.

OS	Synthetic.
OS	Human papillomavirus type 16.

PD 21-AUG-2003.

14-FEB-2003; 2003WO-US004474.

PR 14-FEB-2002; 2002US-0356113P.

PR 14-FEB-2002; 2002US-0356119P.

PR 14-FEB-2002; 2002US-0356126P.

PR 14-FEB-2002; 2002US-0356135P.

PR 14-FEB-2002; 2002US-0356151P.
FR 14 FEB - 2003
FR 14 FEB - 2003TTC-03E6153D

PR 14-FEB-2002; 2002US-0356154P.
 PR 14-FEB-2002; 2002US-0356156P.

PR 14-FEB-2002; 2002US-0356161P

14-FEB-2002; 200203-032010Z
XX
XX

XX :
: C
: /
: C
: C
: C
: C

XX

DR N-PSDB; ADA14301.

PT Purifying a recombinant human

PT concentrating and diafiltering

PS Disclosure; Page 103-104; 111
xx

cc The present invention describes
cc extracellular or intracellular

CC comprises harvesting a cell
CC plurality of VLPs to produce

CC disrupting the harvested cell
CC
CC VLP, clarifying the harvested
CC

the purified recombinant VLP.

Local Similarity	96.9%	Pred. No. 2.4e-56;	Indels	0;	Gaps	0;
Conservative	0;	Mismatches	3;			
1	MHGDPTLHEHYMLDLOPETTDLYXXQUNDSSEDEIDGPAGQAEPPRAHYNIVTFCK	60				
471	MHGDPTLHEHYMLDLOPETTDLYXGEQUNDSSEDEIDGPAGQAEPPRAHYNIVTFCK	530				
61	CDSTLRLCVOSTHYDRIETDLMLGTGLGIVPICQKP	98				
531	CDSTLRLCVOSTHYDRIETDLMLGTGLGIVPICQKP	568				
ADA14293	standard; protein; 805 AA.					
06-NOV-2003	(first entry)					
HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.						
purification; recombinant extracellular virus-like particle; recombinant intracellular virus-like particle; virus-like particle; VLP; virucide; vaccine; gene therapy; human papillomavirus; HPV; infection; dysplasia; HPV-16; fusion protein.						
Synthetic.						
Human papillomavirus type 16.						
WO2003068993-A1.						
21-AUG-2003.						
14-FEB-2003; 2003WO-US004474.						
14-FEB-2002; 2002US-0356113P.						
14-FEB-2002; 2002US-0356118P.						
14-FEB-2002; 2002US-0356119P.						
14-FEB-2002; 2002US-0356123P.						
14-FEB-2002; 2002US-0356126P.						
14-FEB-2002; 2002US-0356133P.						
14-FEB-2002; 2002US-0356135P.						
14-FEB-2002; 2002US-0356150P.						
14-FEB-2002; 2002US-0356152P.						
14-FEB-2002; 2002US-0356154P.						
14-FEB-2002; 2002US-0356156P.						
14-FEB-2002; 2002US-0356157P.						
14-FEB-2002; 2002US-0356161P.						
14-FEB-2002; 2002US-0356162P.						
(NOVA-) NOVAVAX INC.						
Robinson RA, Thompson MW;						
WPI; 2003-679645/64.						
N-PSDB; ADA14301.						
Purifying a recombinant human papillomavirus (HPV) L1, useful for diagnosing, preventing or treating HPV infections, comprises clarifying, concentrating and diafiltering cells containing HPV particles.						
disclosure; Page 103-104; 111P; English.						

The present invention describes a method for purifying a recombinant extracellular or intracellular virus-like particle (VLP). The method comprises harvesting a cell suspension comprising cells containing a plurality of VLPs to produce a harvested supernatant, optionally disrupting the harvested cells to produce cell lysates containing the VLP, clarifying the harvested supernatant, concentrating the clarified supernatant, dialysing the concentrated supernatant, and recovering the purified recombinant VLP. Also described: (1) a cell line designated

DR N-PSDB; AADS8574.
 XX
 XX New chimeric virus-like particles comprising a recombinant viral capsid
 PT protein encapsulating a recombinant viral protein, useful for inducing
 PT humoral and/or cell-mediated immunity against papillomavirus infection.
 XX
 PS Disclosure; Page 122-123; 126pp; English.
 XX
 CC The present invention relates to chimeric virus-like particle comprising
 CC a recombinant viral capsid protein that encapsulates a recombinant viral
 CC protein during self assembly into a chimeric virus-like particle and
 CC exhibiting conformational antigenic epitopes capable of eliciting
 CC neutralizing antibodies. The vaccine comprising the chimeric virus-like
 CC particles are useful for inducing immunity (humoral and/or cell-mediated
 CC immunity) against papillomavirus infection. The invention is also useful
 CC in gene therapy. The present sequence is HPV (human papillomavirus)-16
 CC L2/E7/E2 fusion protein
 XX
 SQ Sequence 805 AA;
 Query Match 99.2%; Score 513; DB 7; Length 805;
 Best Local Similarity 96.9%; Pred. No. 2.4e-56;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MGGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDIDGPAQAEPDRAHYNIVTFCK 60
 DB 471 MGGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDIDGPAQAEPDRAHYNIVTFCK 530
 QY 61 CDSTLRLCVOSTHYDRTLEDLMGTLGIYXPCISQKP 98
 DB 531 CDSTLRLCVOSTHYDRTLEDLMGTLGIYXPCISQKP 568
 RESULT 11
 AAR22767
 ID AAR22767 standard; peptide; 98 AA.
 XX
 AC AAR22767;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-SEP-1992 (first entry)
 XX
 DE HPV E7 peptide.
 XX
 KW Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN W09205248-A.
 XX
 PD 02-APR-1992.
 XX
 PF 26-SEP-1991; 91WO-US007081.
 XX
 PR 26-SEP-1990; 90US-00588384.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL;
 XX WPI; 1992-132119/16.
 DR
 XX
 XX Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and
 PT recombinant cells encoding them, useful in treatment and prophylaxis of
 PT cervical warts or cancer resulting from HPV infection.
 XX
 PS Disclosure; Fig 7; 81pp; English.
 XX
 CC The peptide is the sequence of the human papillomavirus HPV 16 E7
 CC nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)
 CC of HPV 16 E7 were synthesised by standard Merrifield synthesis. Examples
 CC of such peptides are E7 1-10, 29-50 or 70-81. Compositions contg. these

CC peptides, antibodies against the peptides, or recombinant cells contg.
 CC the gene encoding the immunogenic peptides may be utilised in methods for
 CC inhibiting and treating HPV infection and tumour initiation and
 CC progression e.g. in the prevention or retardation of cervical warts and
 CC cervical carcinoma resulting from HPV infection. See also AAR22766.
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX
 SQ Sequence 98 AA;
 Query Match 99.0%; Score 512; DB 2; Length 98;
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MGGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDIDGPAQAEPDRAHYNIVTFCK 60
 DB 1 MGGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDIDGPAQAEPDRAHYNIVTFCK 60
 QY 61 CDSTLRLCVOSTHYDRTLEDLMGTLGIYXPCISQKP 98
 DB 61 CDSTLRLCVOSTHYDRTLEDLMGTLGIYXPCISQKP 98
 RESULT 12
 AAR42361
 ID AAR42361 standard; protein; 98 AA.
 XX
 AC AAR42361;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-MAY-1994 (first entry)
 XX
 DE Human papillomavirus 16 E7 protein and fragments.
 XX
 KW Tumours; cows; horses; donkeys; regression; udder warts; HPV16.
 XX
 OS Synthetic.
 XX
 FN W09320844-A1.
 XX
 PD 28-OCT-1993.
 XX
 PF 01-APR-1993; 93WO-GB000679.
 XX
 PR 08-APR-1992; 92GB-00007701.
 XX
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI Camp MS;
 XX
 DR WPI; 1993-351368/44.
 DR
 XX
 XX Use of papilloma-virus E7 protein or fragments for the therapy of
 PT papilloma-virus disease - for the regression of tumours e.g. removal of
 PT warts from udders or mouth of milking cows or for treatment of horses or
 PT donkeys.
 XX
 PS Disclosure; Fig 2; 31pp; English.
 XX
 CC The sequence is that of the human papillomavirus type 16 E7 protein. The
 CC protein sequence was aligned with that of bovine papillomavirus type 4.
 CC See also AAR42360. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 98 AA;
 Query Match 99.0%; Score 512; DB 2; Length 98;
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MGGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDIDGPAQAEPDRAHYNIVTFCK 60
 DB 1 MGGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDIDGPAQAEPDRAHYNIVTFCK 60

Qy 61 CDSTLRCLCVGOSTHVDIRLTEDLLMGTLGIYXPICSQKP 98
 Db 61 CDSTLRCLCVGOSTHVDIRLTEDLLMGTLGIYXPICSQKP 98

RESULT 13

AAW46886
 ID AAW46886 standard; protein; 98 AA.

XX AAW46886;

DT 25-MAR-2003 (revised)
 DT 15-JUN-1998 (first entry)

DE Amino acid sequence of the HPV-16 E7 oncoprotein.

XX E7 oncoprotein; proliferative state; HPV; kinase activity;
 KM cyclin/cyclin-dependent kinase; p21CIP1; interaction; inactivation;
 KM cyclin/cyclin-dependent kinase inhibitor.

XX Human papillomavirus.

XX US5736318-A.

XX 07-APR-1998.

XX 17-MAR-1995; 95US-00406248.

XX 17-MAR-1995; 95US-00406248.

XX (HARD) UNIV HARVARD.

XX (HARD) HARVARD COLLEGE.

XX Muenger K, Jones DL;

XX WPI; 1998-239202/21.

XX N-PSDB; AAV16717.

PT Evaluation of proliferative state of cells transformed with human
 PT papilloma virus - by determining cyclin-dependent kinase activity induced
 PT by E7 onco-protein.

XX Disclosure; Col 19-20; 14pp; English.

XX The present sequence represents Human papillomavirus (HPV), strain 16, E7
 CC oncoprotein. The proliferative state of a cell transformed with HPV can
 CC be evaluated in the following manner. Cyclin/cyclin-dependent kinase
 CC complexes containing protein p21CIP1 (AAW46887-88) are isolated from the
 CC transformed cell, and the HPV E7 oncoprotein added to the isolated
 CC protein. Cyclin/cyclin-dependent kinase complexes are isolated from an
 CC untransformed cell that is substantially homogenic with the transformed
 CC cell, and the HPV E7 oncoprotein added. The kinase activities of the 2
 CC samples are measured, where a proliferating transformed cell has a
 CC greater kinase activity than the untransformed cell. The method is used
 CC for determining the extent of interaction and/or inactivation between a
 CC cyclin/cyclin-dependent kinase inhibitor and the HPV E7 oncoprotein and
 CC thus evaluating the proliferative state of a transformed cell. (Updated
 CC on 25-MAR-2003 to correct PI field.)

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 2; Length 98;
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPTTDLXXYXQUNDSSSEDEIDDPAGQAEPRRAHYNIYTFCK 60
 Db 1 MHGDTPLHEHYMDLQPTTDLXXYXQUNDSSSEDEIDDPAGQAEPRRAHYNIYTFCK 60

Qy 61 CDSTLRCLCVGOSTHVDIRLTEDLLMGTLGIYXPICSQKP 98
 Db 61 CDSTLRCLCVGOSTHVDIRLTEDLLMGTLGIYXPICSQKP 98

RESULT 14
 ID AAY58474 standard; protein; 98 AA.

XX AAY58474;

DT 10-APR-2000 (first entry)

DE Human papillomavirus (HPV) E7 oncoprotein.

XX HPV E7 oncoprotein; proteasome activity; degradation; virus component;
 KM viral infection; inflammatory disease; anti-inflammatory; anti-HIV;
 KM virucide.

XX Human papillomavirus.

XX W09966065-A2.

XX 23-DEC-1999.

XX 10-JUN-1999; 99WO-GB001840.

XX 13-JUN-1998; 98GB-00012756.

XX 13-JUN-1998; 98GB-00012757.

XX 13-JUN-1998; 98GB-00012758.

XX 13-JUN-1998; 98GB-00012759.

XX 13-JUN-1998; 98GB-00012760.

XX (BRID-) BRIDGEHEAD TECHNOLOGIES LTD.

XX Schmid H, Petic F, Klotzel P, Jarrousse A, Gautier K, Badaoui S;
 PI Mouzevar S, Nicolas P;

XX WPI; 2000-106109/09.

XX Novel assay methods for identifying compounds which modulate and/or
 XX regulate proteosomal activity.

XX Disclosure; Page 8; 35pp; English.

XX The invention relates to a novel assay for identifying compounds which
 CC inhibit viral replication and pathogenesis by increasing proteosomal
 CC degradation of viral components or molecules induced by viral infection.
 CC The method comprises reacting a compound with proteosomal protein (20S
 CC proteasomes separately with or without 19S and 11S complexes), viral gene
 CC product, and protein or peptide substrates; measuring protease activity;
 CC and identifying the compound as an inhibitor if the protease activity of
 CC the assay system is increased. The assays of the invention can be used to
 CC identify compounds which inhibit viral replication and pathogenesis, and
 CC modulate and/or regulate proteasome activity. Compounds which increase
 CC proteosomal degradation of viral components or molecules induced by viral
 CC infection are of value in the treatment of viral disease. Compounds which
 CC modulate proteosomal nuclease activity have use in the treatment of
 CC inflammatory disease, and AIDS in HIV infected patients. The methods may
 CC also be used to generate resistance to bacterial or viral damage.
 CC Sequences AAY58472-Y58474 represent examples of viral proteins which
 CC affect proteosomal function

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 3; Length 98;
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPTTDLXXYXQUNDSSSEDEIDDPAGQAEPRRAHYNIYTFCK 60
 Db 1 MHGDTPLHEHYMDLQPTTDLXXYXQUNDSSSEDEIDDPAGQAEPRRAHYNIYTFCK 60

Qy 61 CDSTLRCLCVGOSTHVDIRLTEDLLMGTLGIYXPICSQKP 98
 Db 61 CDSTLRCLCVGOSTHVDIRLTEDLLMGTLGIYXPICSQKP 98

RESULT 15

AAV57721 standard; protein; 98 AA.

AAV57721;

14-MAR-2000 (first entry)

Human papillomavirus 16 E7 protein SEQ ID NO:4.

Human papillomavirus; HPV; L1 fusion protein; vaccine; cytostatic;
 KM viral capsomere; virucide; dermatological; malignant tumour formation;
 KM cervical cancer; cervical intraepithelial neoplasia; genital wart;
 KM condylomata acuminata.

Human papillomavirus.

CA2229955-A1.

20-AUG-1999.

20-FEB-1998; 98CA-02229955.

20-FEB-1998; 98CA-02229955.

(MED1-) MEDIGENE GMBH.

Burger A, Hallek M;

WPI; 2000-063092/06.

N-PSDB; AA248175.

Fusion proteins comprising papillomavirus specific proteins useful for
 PT vaccinating against malignant tumors of the anogenital tract such as
 PT cervical carcinomas.

Example 1; Page 34; 46pp; English.

The present invention describes a fusion protein comprising 2 amino acids
 CC sequences from 2 different papillomavirus specific (PVS) proteins. The
 CC fusion protein may be administered for preventing and treating
 CC papillomavirus infections in humans and animals. Papillomaviruses are
 CC implicated in the pathology of malignant tumour formation in the
 CC anogenital tract (of these tumours, cervical cancer is the most frequent
 CC (500000 cases/year) and in the formation of precursor lesions of cervical
 CC intraepithelial neoplasia (CIN). Papillomaviruses also cause benign
 CC genital warts such as condylomata acuminata. However, the type and
 CC severity of disease caused by the papillomavirus is dependent on the
 CC strain causing the infection. The present sequence represents the human
 CC papillomavirus 16 E7 protein

Sequence 98 AA;

Query Match 99.0%; Score 512; DB 3; Length 98;

Best Local Similarity 96.9%; Pred. No. 2.2e-57; Mismatches 3; Indels 0; Gaps 0;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEMYMDLOPETTDLYXXQXNDSSSEDEIDDPAGQAEPPRAHYNIVTFCK 60
 DB 1 MHGDTPLHEMYMDLOPETTDLYCYEQUNSSSEDEIDDPAGQAEPPRAHYNIVTFCK 60

QY 61 CDSTLRCLVQSTHVDIRTLIEDLLMGTLGIYXPCISQRP 98
 DB 61 CDSTLRCLVQSTHVDIRTLIEDLLMGTLGIYXPCISQRP 98

RESULT 16

AAB98421 standard; protein; 98 AA.

AAB98421;

22-AUG-2001 (first entry)

Human papillomavirus protein HPV16 E7.

Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
 KM epitope; T cell; identification; vaccine; infection; genital wart;
 KM neoplastic growth; antiviral.

Human papillomavirus.

WO200141799-A1.

14-JUN-2001.

11-DEC-2000; 2000MO-US033549.

10-DEC-1999; 99US-0172705P.

15-AUG-2000; 2000US-00641528.

(EPIM-) EPIMMUNE INC.

Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;

WPI; 2001-381497/40.

An isolated human papilloma virus (HPV) epitope, useful in vaccines for

treating HPV infections.

Disclosure; Page 21; 756pp; English.

The present invention describes an isolated prepared human papillomavirus
 CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine
 CC production. Peptides and corresponding nucleic acid compositions from the
 CC present invention are useful for stimulating an immune response to HPV by
 CC stimulating the production of CTL or HTL responses, specifically in the
 CC treatment or prophylaxis of HPV infection, in persons who have not
 CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
 CC can also be used in a tetramer staining assay to assess peripheral blood
 CC mononuclear cells for the presence of antigen-specific CTLs following
 CC exposure to a pathogen or immunogen, and as reagents to evaluate immune
 CC recall responses or evaluate the efficacy of a vaccine. The vaccine
 CC compositions are useful for removing warts or treating HPV infections.
 CC The epitopes for inclusion in an epitope-base vaccine may be selected
 CC from conserved regions of viral or tumour-associated antigens, which
 CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
 CC that may be present in whole antigens can be avoided with the use of
 CC epitope-base vaccines. An additional advantage is the ability to combine
 CC selected epitopes (CTL and HTL) and to modify the composition of the
 CC epitopes achieving enhanced immunogenicity, the major benefit of the
 CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
 CC polypeptide sequences used in the exemplification of the present
 CC invention

Sequence 98 AA;

Query Match 99.0%; Score 512; DB 4; Length 98;

Best Local Similarity 96.9%; Pred. No. 2.2e-57; Mismatches 3; Indels 0; Gaps 0;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEMYMDLOPETTDLYXXQXNDSSSEDEIDDPAGQAEPPRAHYNIVTFCK 60
 DB 1 MHGDTPLHEMYMDLOPETTDLYCYEQUNSSSEDEIDDPAGQAEPPRAHYNIVTFCK 60

QY 61 CDSTLRCLVQSTHVDIRTLIEDLLMGTLGIYXPCISQRP 98
 DB 61 CDSTLRCLVQSTHVDIRTLIEDLLMGTLGIYXPCISQRP 98

RESULT 17

AAU01718 standard; protein; 98 AA.

AAU01718;

XX 29-AUG-2001 (first entry)
DT Human papilloma virus-16 (HPV-16) E7 antigen.
XX
DE Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF;
XX chimeric; heat shock protein; HSP; Flt-3 ligand; Flt-3 ligand A; ERA d11;
XX antigenic; immunogenic; cytotoxic T cell response; tumour; vaccine;
XX immunotherapy; HPV-16; E7 antigen.
XX
OS Human papillomavirus.
XX
PN WO200129233-A2.
XX
PD 26-APR-2001.
XX
PP 20-OCT-2000; 2000WO-US041422.
XX
XX 20-OCT-1999; 99US-00421608.
PR 09-FEB-2000; 2000US-00501097.
XX
XX (UJJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Wu T, Hung C;
XX WPI; 2001-290921/30.
DR N-PSDB; AAS02608.
XX
XX New chimeric polypeptide, useful as anti-tumor vaccines, comprises
PT carboxy terminal fragment of heat shock protein, Flt-3 ligand or
PT cytoplasmic translocation domain of Pseudomonas exotoxin A and antigenic
PT polypeptide.
XX
XX Example 1; Page 39; 110pp; English.
PS
XX The sequence represents the amino acid sequence of human papilloma virus-
CC 16 (HPV-16) E7 antigen used in construction of a chimeric polypeptide
CC comprising: (a) a first polypeptide domain containing a carboxy terminal
CC fragment of a heat shock protein (HSP), an Flt-3 ligand (FL), a
CC cytoplasmic translocation domain of a Pseudomonas exotoxin A (ETA d11),
CC or a granulocyte-macrophage colony stimulating factor (GM-CSF); and (b) a
CC second polypeptide domain containing an antigenic polypeptide. A
CC composition comprising the chimeric polypeptide is useful for inducing an
CC immune response such as a cytotoxic T cell response. The nucleic acid or
CC vector encoding the chimeric polypeptide present in the composition is
CC administered as naked DNA by gene gun or equivalent, or by liposomal
CC formulation. These are thus useful for vaccinating a mammal against
CC infection by inducing an immune response to a pathogen. Preferably they
CC are useful for vaccinating a mammal against a tumour antigen. The
CC compositions and methods are useful for stimulating or enhancing the
CC immunogenicity of a selected antigen or stimulating or enhancing a
CC cellular immune response specific for that antigen. The chimeric nucleic
CC acid molecules and vaccination methods, yield potent antigen-specific
CC immunotherapy. The polynucleotides and DNA vaccines can induce a cellular
CC immune response that is at least 40 fold more potent than conventional
CC DNA vaccines. The vaccines are safe and useful for administration to
CC domesticated or agricultural animals, as well as humans, and have low
CC immunogenicity
XX
SQ Sequence 98 AA;
Query Match 99.0%; Score 512; DB 4; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 18
AAU72607
ID AAU72607 standard; protein; 98 AA.
XX
XX AAU72607;
AC
XX
XX 06-AUG-2003 (revised)
DT 26-FEB-2002 (first entry)
XX
XX Human papilloma virus (HPV) E7 fragment.
DE
XX
XX Human papillomavirus; HPV; E7; cyclin B; cyclin A; viruside;
XX E7-induced cyclin-dependent kinase-2; CDK2 kinase; HPV infection;
XX adenoviral infection; simian virus 40 infection; SV40.
XX
XX Human papillomavirus.
OS
XX
XX US2001029022-A1.
PN
XX
XX 11-OCT-2001.
PD
XX
XX 01-DEC-2000; 2000US-00728466.
PF
XX
XX 25-AUG-1999; 99US-00382616.
PR 25-AUG-2000; 2000US-00648215.
XX
XX (FISH/) FISHER C.
PA (HEMW/) HE W.
XX
XX Fisher C, He W;
PI
XX
XX WPI; 2001-647983/74.
DR
XX
XX Identifying E7-induced cyclin-dependent kinase-2 activity inhibitor,
PT comprises identifying test compounds which reduce cyclin-dependent kinase
PT 2-substrate phosphorylation in presence of human papillomavirus E7 or
PT its fragment.
XX
XX
XX Claim 1; Page 12-13; 21pp; English.
PS
XX The invention relates to identifying inhibitor of E7-induced cyclin-
CC dependent kinase-2 (CDK2) kinase (I) activity, comprising measuring (1)
CC activity on CDK2 substrate in the presence of human papillomavirus (HPV)
CC E7 or its fragment, and in the presence and absence of test compound. The
CC test compound is identified as inhibitor of E7-induced (I) activity when
CC decreased phosphorylation of CDK2 substrate is detected. The method is
CC used for identifying inhibitor of E7-induced CDK2 kinase activity. This
CC method is useful for identifying an antiviral agent which involves
CC identifying an inhibitor of E7-induced increase in CDK2 kinase activity,
CC measuring viral proliferation in the presence and absence of identified
CC inhibitor and identifying the inhibitor as an antiviral agent when
CC decreased proliferation is detected in the presence of the inhibitor
CC compared to viral proliferation in the absence of the inhibitor. The
CC identified inhibitors are useful for reducing HPV E7-induced kinase
CC activity or for ameliorating HPV proliferation by inhibiting E7-induced
CC proliferation in a HPV infected cell by inhibiting E7-binding to CDK2
CC kinase complex. The inhibitors identified by the above method are useful
CC for produced medicament for ameliorating viral infection e.g. HPV
CC infection, adenoviral infection or simian virus 40 (SV40) infection. The
CC present sequence represents the amino acid sequence of HPV E7 fragment as
CC described in the method of the invention. (Updated on 06-AUG-2003 to
CC correct OS field.)
XX
XX
SQ Sequence 98 AA;
Query Match 99.0%; Score 512; DB 4; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98
 DB 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98

RESULT 19

AAB67546 standard; peptide; 98 AA.

AC AAB67546;

DT 11-SEP-2003 (revised)

DT 29-MAY-2001 (first entry)

DE Amino acid sequence of a E7 fragment that activates CDK2.

KM E7-induced CDK2 kinase; CDK2 substrate; papillomavirus; E7;

KW viral infection.

OS Cottoncotton rabbit papillomavirus.

PN W0200114584-A2.

PD 01-MAR-2001.

PF 25-AUG-2000; 2000WO-US023487.

PR 25-AUG-1999; 99US-00382616.

PA (PHAA) PHARMACIA & UPJOHN.

PI Fisher C, He W;

PS WPI; 2001-226622/23.

PT Identifying inhibitors of human papilloma virus E7 protein-induced

PT increase in CDK2 kinase activity for use as antiviral agent, by measuring

PT kinase activity on CDK2 substrate in presence of E7 protein, test

PS compound.

PS Claim 2; Page 40; 49pp; English.

CC The specification describes a method for identifying inhibitors of E7-

CC induced CDK2 kinase activity. The method comprises measuring CDK2 kinase

CC activity on a CDK2 substrate in presence of human papillomavirus (HPV) E7

CC (or fragment), in presence and absence of a test compound and measuring

CC phosphorylation of substrate. The method is useful for identifying an

CC inhibitor of E7-induced CDK2 kinase activity. The identified inhibitor is

CC useful for reducing or inhibiting HPV proliferation in an individual.

CC Inhibitors of E7 binding to the CDK2 complex are useful in preparing

CC adenoviral or SV40 infection. The present sequence represents a

CC papillomavirus E7 fragment, which is used in the method of the invention.

CC (updated on 11-SEP-2003 to standardise OS field)

CC Sequence 98 AA;

QY 1 MHGDTPLHEHYMDLOPETTDLYXXYXOLNDSSEDEIDGPAGAEPRAHYNIIVTFCK 60

DB 1 MHGDTPLHEHYMDLOPETTDLYXXYXOLNDSSEDEIDGPAGAEPRAHYNIIVTFCK 60

QY 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98

DB 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98

RESULT 20

AAB6332

ID AAB6332 standard; protein; 98 AA.

AC AAB6332;

DT 18-SEP-2001 (first entry)

DE HPV 16 E7 peptide fragment.

KM Fusion protein; VP22; E7; cell import signal; cell export signal;

KW antigen; immunization; infection-induced auto-immune disease;

KW tumor disease.

OS Human papillomavirus.

PN W0200151516-A2.

PD 19-JUL-2001.

PF 15-JAN-2001; 2001WO-DE000134.

PR 13-JAN-2000; 2000DE-01001230.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Mueller M, Michel N, Osen W, Giesmann L, Zentgraf H;

PS WPI; 2001-442135/47.

PT Identifying inhibitors and activators of eukaryotic potassium channels,

PT for use as therapeutic agents, comprises using a transformed yeast cell

PT that does not express endogenous channels.

PS Disclosure; Fig 4; 23pp; German.

CC This invention describes a fusion protein comprising cell import and/or

CC export signal sequences and an antigen which is suitable for immunizing

CC an individual against a disease, together with a DNA that codes for said

CC protein. The invention also relates to the use of the protein (II) and

CC its encoding DNA (I) for immunizing an individual against disease, in

CC particular against infection-induced auto-immune and tumor disease. This

CC sequence represents a fragment of the human papillomavirus E7 protein

CC used in the preparation of the fusion constructs described in the method

CC of the invention

CC Sequence 98 AA;

QY 1 MHGDTPLHEHYMDLOPETTDLYXXYXOLNDSSEDEIDGPAGAEPRAHYNIIVTFCK 60

DB 1 MHGDTPLHEHYMDLOPETTDLYXXYXOLNDSSEDEIDGPAGAEPRAHYNIIVTFCK 60

QY 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98

DB 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98

QY 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98

DB 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98

QY 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98

DB 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98

QY 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98

DB 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPICSQKP 98

RESULT 21

AAU77713 standard; protein; 98 AA.

AC AAU77713;

DT 05-JUN-2002 (first entry)

DE Human papillomavirus 16 (HPV16), E7 protein.

KM Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;

KW cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;

KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;

KW tumour; cancer; cervical cancer.

```
XX OS Human papillomavirus type 16.
XX PN WO200212281-A2.
XX PD 14-FEB-2002.
XX PF 02-AUG-2001; 2001WO-US024134.
XX PR 03-AUG-2000; 2000US-0222902P.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Wu T, Hung C;
XX DR WPI; 2002-257463/30.
XX PT New nucleic acids encoding a fusion polypeptide comprising an endoplasmic
XX PT reticulum chaperone polypeptide linked to an antigenic polypeptide,
XX PS useful as a vaccine for inducing antigen-specific immune responses.
XX PS Example 1; Page 32; 71pp; English.
XX CC The invention describes a nucleic acid molecule (I) encoding a fusion
XX CC polypeptide comprising a first polypeptide domain comprising an
XX CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and a
XX CC second polypeptide domain comprising at least one antigenic peptide e.g.
XX CC Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a
XX CC vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
XX CC responses, particularly those mediated by cytotoxic T lymphocytes. The
XX CC nucleic acid and compositions comprising the nucleic acid is also useful
XX CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.
XX CC This is the amino acid sequence of the human papillomavirus type 16 (HPV
XX CC 16) early gene 7 (E7) used in the creation of a DNA vaccine
XX SQ Sequence 98 AA;
XX Query Match 99.0%; Score 512; DB 5; Length 98;
XX Best Local Similarity 96.9%; Pred. No. 2.2e-57;
XX Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDPPTLHEMYMDLPQETTDLYXXYXQINDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
DB 1 MHGDPPTLHEMYMDLPQETTDLYCYEQINDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
QY 61 CDSFRLCVOSTHVDIRTLBLLMGTLGIVPICSQRP 98
DB 61 CDSFRLCVOSTHVDIRTLBLLMGTLGIVPICSQRP 98
RESULT 22
AAU10810
ID AAU10810 standard; protein; 98 AA.
XX AC AAU10810;
XX XX
XX DT 29-AUG-2003 (revised)
XX DT 14-FEB-2002 (first entry)
XX XX
XX DE Human papillomavirus (HPV) 16, E7 coding region.
XX XX
XX XX Human papillomavirus 16; HPV 16; cancer; squamous cell carcinoma;
XX KM adenocarcinoma; kolloidcyosis; hyperkerotosis; intraepithelial neoplasia;
XX KM intraepithelial lesion; dysplasia; head cancer; neck cancer;
XX KM small cell lung cancer; melanoma; oncogene.
XX XX
XX OS Human papillomavirus type 16.
XX XX
XX FH Key Location/Qualifiers
XX FT 6..35
XX FT Peptide /label= E7_peptide_epitope_1
XX FT /note= "This region is specifically referred to in claim
XX FT 2"
```

```
FT FT Peptide 60..80
FT FT /label= E7_peptide_epitope_2
FT FT /note= "This region is specifically referred to in claim
FT FT 2"
XX XX WO200177142-A1.
XX XX 18-OCT-2001.
XX PD
XX PF 05-APR-2001; 2001WO-US011233.
XX PR 05-APR-2000; 2000US-0194796P.
XX PA (IMPA-) IMPACT DIAGNOSTICS INC.
XX XX
XX PI Hu YX;
XX PT
XX DR WPI; 2002-010888/01.
XX XX
XX PT New peptides derived from E2, E6 or E7 early coding regions of human
XX PT papillomavirus 16 and 18, useful in diagnosis of human papillomavirus
XX PT infection and associated malignancy e.g. cervical carcinoma.
XX PS Disclosure; Fig 3; 28pp; English.
XX XX
XX CC The invention describes a novel peptide derived from the E2, E6 or E7
XX CC early coding region of human papillomavirus (HPV) 16 and 18, which is
XX CC soluble in aqueous solution and has a lysine or cysteine residue near the
XX CC amino terminus, very few tryptophan, methionine and cysteine residues,
XX CC and/or many glycine and asparagine residues. The peptides and diagnostic
XX CC method are used to diagnose HPV infection, especially infection with
XX CC oncogenic HPV by using peptides derived from the E2 region, since HPV 16
XX CC and 18 are the main HPV genetic types associated with cancers, and
XX CC presence of antibodies to E2 protein is known to provide evidence of HPV
XX CC infection. They are also useful to diagnose HPV associated malignancy or
XX CC premalignancy, especially carcinoma by using peptides derived from the E6
XX CC or E7 regions, since E6 and E7 are thought to be tumour-specific
XX CC antigens. The peptides and diagnostic method are especially useful to
XX CC diagnose cervical carcinoma (e.g. adenocarcinoma of the uterine cervix)
XX CC and any HPV associated epithelial cell abnormality including high grade
XX CC dysplasias, kolloidcyosis, hyperkerotosis, precancerous conditions
XX CC encompassing intraepithelial neoplasias or intraepithelial lesions, and
XX CC invasive or malignant cancers. They are also used to detect head and neck
XX CC cancers, small cell lung cancers, penai and anal squamous cell carcinomas
XX CC and melanoma. This is the amino acid sequence of the E7 early coding
XX CC region of HPV 16, an oncoprotein that destabilises cell cycle control
XX CC through its interaction with the cyclin-dependent kinase inhibitor
XX CC protein, p21, described in the method of the invention. (Updated on 29-
XX CC AUG-2003 to standardise OS field)
XX SQ Sequence 98 AA;
XX Query Match 99.0%; Score 512; DB 5; Length 98;
XX Best Local Similarity 96.9%; Pred. No. 2.2e-57;
XX Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDPPTLHEMYMDLPQETTDLYXXYXQINDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
DB 1 MHGDPPTLHEMYMDLPQETTDLYCYEQINDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
QY 61 CDSFRLCVOSTHVDIRTLBLLMGTLGIVPICSQRP 98
DB 61 CDSFRLCVOSTHVDIRTLBLLMGTLGIVPICSQRP 98
RESULT 23
ABB82375
ID ABB82375 standard; protein; 98 AA.
XX AC ABB82375;
XX XX
XX DT 08-JAN-2003 (first entry)
XX FT
```

[illegible]

KW		uterine cancer lesion.
XX		
OS		Human papillomavirus type 16.
XX		
PN		WO2002100889-A1.
XX		
PD		19-DEC-2002.
XX		
XX		
PB		10-JUN-2002; 2002WO-JP005747.
PF		Cda-positive T cells specific to (pre-)uterine cancer lesion, applicable
PT		in drug compositions for preventing and treating uterine cancer.
PS		
CC		Disclosure; Page 34; 40pp; Japanese.
CC		The invention comprises an epitope of the human papillomavirus E7 antigen
CC		that is capable of activating Cda-positive T cells that are specific to
CC		uterine cancer lesions. The epitope of the invention is useful for
CC		preventing and treating uterine cancer. The present amino acid sequence
CC		represents the human papillomavirus E7 antigen
XX		
SQ		Sequence 98 AA;
Query Match	99.0%; Score 512; DB 6; Length 98;	
Best Local Similarity	96.9%; Pred.No. 2.2e-57;	
Matches	95; Conservative 0; Mismatches 3; Indels 0; Gaps 0,	
OY	1 MHGDTPTLHEHYMLDLPETTDLYXIXQLNDSSSEDEIDGPAGQAEPRAHYNIVTFCKK 60	
DB	1 MHGDTPTLHEHYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPRAHYNIVTFCKK 60	
OY	61 CDSTLRCLCVOSTHVDIRTLIEDLLMGTGLGVXPICSOQP 98	
DB	61 CDSTLRCLCVOSTHVDIRTLIEDLLMGTSIGVPCISOQP 98	
RESULT 25		
ADFO9516		
ID	ADFO9516 standard; protein, 98 AA.	
XX		
AC	ADF09516;	
XX		
DT	12-FEB-2004 (first entry)	
XX		
DE	Human papillomavirus 16 E7 SEQ ID NO.17.	
XX		
KW	human; protein-protein interaction; virucide; cytostatic; vaccine;	
KX	human papilloma virus; HPV; cancer.	
OS	Human papillomavirus.	
XX		
PN	WO2003068940-A2.	
XX		
PD	21-AUG-2003.	
XX		
PF	14-FEB-2003; 2003WO-US004594.	
XX		
PR	14-FEB-2002; 2002US-0356911P.	
XX		
PA	(CURA -) CURAGEN CORP.	
PA	(HOFF) HOFFMANN LA ROCHE INC.	
PI	Jackson A, Ooi CE, Lewin DA, Cutchall S;	
XX		

DR WPI: 2003-689668/65.
DR N-PSDB; ADF09608.
XX
PT New purified complex comprising a first polypeptide and a second
PT polypeptide, useful for identifying agents for treating/preventing a
PT condition involving altered level of the complex e.g. human papilloma
PT virus infection, or cancer.
XX
PS Example 3; SEQ ID NO 17; 156pp; English.
CC
CC The invention relates to a novel purified complex comprising a first
CC polypeptide and a second polypeptide, where the polypeptides comprise
CC defined amino acid sequences listed in the specification, and where the
CC first polypeptide binds to the second polypeptide. A complex of the
CC invention has virucide and cytostatic activity, and may have a use as a
CC vaccine. The complex is useful for identifying agents for treating or
CC preventing a conditions involving altered level of the complex, e.g.
CC human papilloma virus (HPV) infection, or cancer. The compositions,
CC antibodies, vectors and methods are useful for treating such diseases.
CC The sequences shown in ADF09500-ADF09583 represent proteins of the
CC invention.
XX
SQ Sequence 98 AA;
Query Match 99.0%; Score 512; DB 7; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGAEPPRAHNYITFCCK 60
Db 1 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGAEPPRAHNYITFCCK 60
Qy 61 CDSTLRICVOSTHVDIRLTEDLMLGTIGIVXPCISQKP 98
Db 61 CDSTLRICVOSTHVDIRLTEDLMLGTIGIVPCISQKP 98
RESULT 26
ADFI8632
ID ADFI8632 standard; protein; 98 AA.
XX
AC ADFI8632;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human papilloma virus E7 oncoprotein.
XX
KW HPV; oncoprotein E7; cytosolic; gene therapy; kinase; enzyme.
XX
OS Human papillomavirus.
XX
PN WO2003088922-A2.
XX
PD 30-OCT-2003.
XX
PF 21-APR-2003; 2003WO-US012667.
XX
PR 19-APR-2002; 2002US-0374245P.
XX
PA (UTRP) UNIV ROCHESTER.
XX
PI Mccance D, Westbrook TF;
XX
DR WPI: 2003-845498/78.
DR N-PSDB; ADFI8633; ADFI8634.
XX
PT Identifying a compound that inhibits E7 cellular proliferation activity
PT by administering a compound to a system, where the system maintains Akt
PT activity and selecting a compound that decreases the amount of Akt
PT activity.
XX
PS Disclosure; SEQ ID NO 8; 119pp; English.

CC The present sequence is the protein sequence of human papillomavirus E7
CC oncoprotein. E7 promotes oncogenesis through an inhibition of p21cip1
CC transport into the nucleus. E7 abrogates Raf-associated arrest and
CC prevents inhibition of cyclin E-CDK2 activity without disrupting Raf
CC induction of p21cip1. E7 neither interacts with p21cip1 nor derepresses
CC p21cip1-associated CDK2 activity, but instead reduces the association
CC between p21cip1 and cyclin E-CDK2 complexes. Raf down-regulates steady-
CC state levels of Akt, a regulator of p21cip1 localisation, leading to loss
CC of p21cip1 phosphorylation and accumulation of p21cip1. E7 disrupts the
CC effects of Raf on Akt activity and prevents p21cip1 nuclear accumulation.
CC Maintenance of Akt activity is necessary and sufficient to bypass Raf
CC arrest. The invention provides methods for identifying and
CC inhibitors of E7 cell proliferation activity, and for identifying and
CC using compounds capable of promoting the nuclear localisation of p21cip1.
CC The methods can be used to inhibit aberrant cellular proliferation for
CC treatment of cancer.
XX
SQ Sequence 98 AA;
Query Match 99.0%; Score 512; DB 7; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGAEPPRAHNYITFCCK 60
Db 1 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGAEPPRAHNYITFCCK 60
Qy 61 CDSTLRICVOSTHVDIRLTEDLMLGTIGIVXPCISQKP 98
Db 61 CDSTLRICVOSTHVDIRLTEDLMLGTIGIVPCISQKP 98
RESULT 27
ADL90076
ID ADL90076 standard; protein; 98 AA.
XX
AC ADL90076;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human papillomavirus 16-E7 protein, SEQ ID 16.
XX
KW Immune response; immunoglobulin; Ig; E7.
XX
OS Human papillomavirus.
XX
PN WO2004027049-A2.
XX
PD 01-APR-2004.
XX
PF 18-SEP-2003; 2003WO-US030188.
XX
PR 20-SEP-2002; 2002US-0412219P.
XX
PR 14-MAR-2003; 2003WO-US007995.
XX
PA (ASTR-) ASTRAL INC.
XX
PI Bot A, Wang L, Smith D, Phillips B;
XX
DR WPI: 2004-295415/27.
XX
PT Generating an immune response to an antigen, useful for generating
PT desired T cell responses comprises administering an immunoglobulin having
PT one peptide epitope of the antigen attached to the immunoglobulin.
XX
PS Disclosure; Fig 1G; 154pp; English.
XX
CC The present invention relates to a method for generating an immune
CC response to an antigen in a patient. The method comprises administering
CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at
CC least one peptide epitope of the antigen attached to the Ig or its
CC portion and administering the immunoglobulin or its portion in
CC conjunction with a RNA segment. The present sequence is an antigen

CC sequence, used to illustrate the invention.

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 8; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEHYMLDLOPETTDLYXXYXQNDSSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60
DB 1 MHGDTPTLHEHYMLDLOPETTDLYCYEQNDSSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60
QY 61 CDSTLRLCVQSTHYDRTTLEDLMGTGIXPICSQKP 98
DB 61 CDSTLRLCVQSTHYDRTTLEDLMGTGIXPICSQKP 98

RESULT 28

ID ADM32916 standard; protein; 98 AA.

AC ADM32916;

DT 17-JUN-2004 (first entry)

DE Amino acid sequence of HPV16 E7 protein.

XX synonymous codon; translation efficiency; HPV16; E7 protein.

OS Human papillomavirus type 16.

XX WO2004024915-A1.

XX 25-MAR-2004.

PF 15-SEP-2003; 2003WO-AU001200.

PR 13-SEP-2002; 2002US-0410410P.

PA (UYQU) UNIV QUEENSLAND.

PI Frazer IH;

XX WPI; 2004-270043/25.

DR N-PSDB; ADM32915, ADM32917.

PT Constructing a synthetic polynucleotide, useful for producing a
PT polypeptide at a higher level in a Chinese Hamster Ovary cell, comprises
PT selecting a first codon of the parent polynucleotide for replacement with
PT a synonymous codon.

XX Example 2; Fig 2; 82pp; English.

XX The specification describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible at a different
CC level in a Chinese Hamster Ovary (CHO) cell compared to when using a
CC parent polynucleotide encoding the same polypeptide. The method comprises
CC selecting a first codon of the parent polynucleotide for replacement with
CC a synonymous codon, where the synonymous codon is selected on the basis
CC that it exhibits a different translational efficiency in the CHO cell
CC than the first codon in a comparison of translational efficiencies of
CC codons in test CHO cells. The method is useful for constructing synthetic
CC polynucleotides which are translated more efficiently, compared to the
CC parent polynucleotide. The present sequence represents Human
CC papillomavirus type 16 (HPV16) E7 protein. The E7 polynucleotide was
CC codon-modified, to demonstrate the method of the invention.

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 8; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEHYMLDLOPETTDLYXXYXQNDSSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60
DB 1 MHGDTPTLHEHYMLDLOPETTDLYCYEQNDSSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60

QY 61 CDSTLRLCVQSTHYDRTTLEDLMGTGIXPICSQKP 98
DB 61 CDSTLRLCVQSTHYDRTTLEDLMGTGIXPICSQKP 98

RESULT 29

ID ADO44073 standard; protein; 98 AA.

AC ADO44073;

DT 15-JUL-2004 (first entry)

DE Amino acid sequence of a wild type HPV16 E7 protein.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
XX cervical cancer; immune response; lower gastrointestinal tract cancer;
XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

OS Human papillomavirus type 16.

XX Synthetic.

XX WO2004030636-A2.

PD 15-APR-2004.

PF 02-OCT-2003; 2003WO-US031726.

PR 03-OCT-2002; 2002US-0415929P.

PA (AMHP) WYETH HOLDINGS CORP.

PI Smith L, Cassetti MC;

XX WPI; 2004-316328/29.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.

XX Claim 1; Page 77; 101pp; English.

CC The present sequence represents a wild type E7 protein from human
CC papillomavirus type 16 (HPV16), which is used to produce fusion proteins
CC of the invention. The specification describes human papillomavirus E6 and
CC E7 polypeptides, where the E7 polypeptide has mutations at any one or
CC more of the amino acids corresponding to amino acids 24, 26 or 91 of the
CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
CC mutations at any one or more of the amino acids corresponding to amino
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
CC the invention are useful for treating or preventing human papillomavirus
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC and nucleic acids encoding the fusion proteins are useful for generating
CC immune responses against HPV. They are also useful for treating lower
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
CC the reproductive system, including penile and vulvar cancer.

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 8; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEHYMLDLOPETTDLYXXYXQNDSSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60
DB 1 MHGDTPTLHEHYMLDLOPETTDLYCYEQNDSSSEEDIDBPAGQAEPRRAHYNIIVTFCK 60
QY 61 CDSTLRLCVQSTHYDRTTLEDLMGTGIXPICSQKP 98

D6 61 CDSTLRLCVQSTHVDIRTLIEDLLMGTLGIVCPICSQKP 98

RESULT 30

ADN49005

ADN49005 standard; protein; 98 AA.

AC ADN49005;

DT 15-JUL-2004 (first entry)

XX Human papilloma virus (HPV) strain HPV16 E7 protein.

DE Papilloma-virus specific protein; PVS; vaccine; infection;

KW human papilloma virus; HPV; E7.

XX Human papillomavirus.

OS US2004081661-A1.

PN 29-APR-2004.

PD 04-SEP-2003; 2003US-00654129.

XX 20-FEB-1998; 98US-00026896.

PR 06-APR-1999; 99US-00284017.

XX (MEDI-) MEDIGENE AG.

PA Hallel M, Burger A;

XX WPI; 2004-340126/31.

DR N-PSDB; ADN49004.

XX

PT New fusion proteins comprising an amino acid sequence from a first and a second papilloma-virus specific protein, useful in vaccines for treating PT or preventing a papilloma virus infection in an animal, particularly humans.

PT

XX

PS Disclosure; SEQ ID NO 4; 20pp; English.

XX The invention relates to papilloma-virus specific (PVS) protein and CC fusion protein constructs. The invention also relates to vaccine CC formulations comprising viral capsomeres and methods for their CC production. The fusion protein is useful for treating or preventing a CC papilloma virus infection in an animal, particularly humans and is also CC useful in the production of vaccines. The present sequence is human CC papilloma virus (HPV) strain HPV16 E7 protein.

XX

SQ Sequence 98 AA;

Query Match 99.0%; Score 512; DB 8; Length 98;

Best Local Similarity 96.9%; Pred. No. 2.2e-57;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLPETTDLYXXYXQLNDSSEEDIEDGPAGQAEPPRAHYNIVTFCK 60

DB 1 MHGDTPTLHEYMLDLPETTDLYCYEQNDSSSEEDIEDGPAGQAEPPRAHYNIVTFCK 60

QY 61 CDSTLRLCVQSTHVDIRTLIEDLLMGTLGIVCPICSQKP 98

DB 61 CDSTLRLCVQSTHVDIRTLIEDLLMGTLGIVCPICSQKP 98

RESULT 31

ADU66362

ID ADU66362 standard; protein; 98 AA.

XX ADU66362;

DT 10-FEB-2005 (first entry)

XX Human papillomavirus type 16 (HPV16) E7 protein - SEQ ID 3.

XX vaccine; MHC class I pathway; antigen specific immune response; tumor;

KW E7 protein; E6 protein.

XX

OS Human papillomavirus type 16.

XX

PN WO2004098526-A2.

XX

PD 18-NOV-2004.

XX

PF 05-MAY-2004; 2004WO-US013756.

XX

PR 05-MAY-2003; 2003US-0467602P.

XX (UYJO) UNIV JOHNS HOPKINS.

PA

XX Wu T, Hung CF;

PI

XX WPI; 2004-813972/80.

DR

XX

PT New nucleic acid molecules encoding a fusion polypeptide comprising an PT antigen, a signal peptide, and a heat shock protein, useful as a vaccine PT for inducing or enhancing immune response or for inhibiting or preventing PT tumor growth.

PT

XX

PS Disclosure; SEQ ID NO 3; 67pp; English.

XX

CC The invention comprises a nucleic acid molecule (DNA vaccine) that CC encodes a fusion polypeptide which is useful as a vaccine composition. CC The nucleic acid of the invention contains: a first nucleic acid encoding CC a polypeptide that promotes processing via the MHC class I pathway; a CC second sequence encoding a signal peptide; and a third sequence encoding CC an antigenic polypeptide. The DNA vaccine of the invention is useful for CC inducing or enhancing an antigen specific immune response, or to inhibit CC growth or prevent re-growth of a tumor expressing Human papillomavirus CC (HPV) E7 or E6 protein. The present amino acid sequence represents a CC human papillomavirus type 16 (HPV16) E7 protein.

XX

SQ Sequence 98 AA;

Query Match 99.0%; Score 512; DB 8; Length 98;

Best Local Similarity 96.9%; Pred. No. 2.2e-57;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLPETTDLYXXYXQLNDSSEEDIEDGPAGQAEPPRAHYNIVTFCK 60

DB 1 MHGDTPTLHEYMLDLPETTDLYCYEQNDSSSEEDIEDGPAGQAEPPRAHYNIVTFCK 60

QY 61 CDSTLRLCVQSTHVDIRTLIEDLLMGTLGIVCPICSQKP 98

DB 61 CDSTLRLCVQSTHVDIRTLIEDLLMGTLGIVCPICSQKP 98

RESULT 32

ADX15532

ID ADX15532 standard; protein; 98 AA.

XX ADX15532;

AC

XX

DT 21-APR-2005 (first entry)

XX Human papillomavirus E7 fragment, SEQ ID NO: 1.

DE

XX

KW High throughput screening; pharmaceutical; antiviral.

XX

OS Human papillomavirus.

XX

PN US2005032038-A1.

XX

PD 10-FEB-2005.

XX

PF 08-SEP-2003; 2003US-00657399.

XX

PR 25-AUG-1999; 99US-00382616.
 PR 01-DEC-2000; 2000US-00728466.
 XX
 XX (FISH/) FISHER C.
 PA (HEMW/) HE W.
 XX
 PI Fisher C, He W;
 XX
 DR WPI; 2005-151661/16.
 XX
 XX Ameliorating human papillomavirus proliferation involves administering
 PT inhibitor of E7-induced cyclin-dependent kinases 2 phosphorylation or
 PT inhibitor of E7-binding cyclin-dependent kinases 2 kinase complex that
 PT reduces kinase activity.
 PS
 XX Disclosure; SEQ ID NO 1; 20pp; English.
 CC The present invention relates to a method of ameliorating human papilloma
 CC virus (HPV) proliferation. The method involves administering an inhibitor
 CC of E7-induced cyclin-dependent kinases (CDK2) phosphorylation or an
 CC inhibitor of E7-binding CDK2 kinase complex that reduces HPV E7-induced
 CC CDK2 kinase activity. The present sequence is the human papillomavirus E7
 CC fragment.
 XX
 SQ Sequence 98 AA;
 Query Match 99.0%; Score 512; DB 9; Length 98;
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPTLHRYMDLOPETTDLYXXQNDSSSEEDIDGPAQAEPRAHYNIIVTFCK 60
 DB 1 MHGDTPTLHRYMDLOPETTDLYCYEQNDSSSEEDIDGPAQAEPRAHYNIIVTFCK 60
 QY 61 CDSTLRACVOSTHYDRTLEDLMGTLGIYXPCSQKP 98
 DB 61 CDSTLRACVOSTHYDRTLEDLMGTLGIYXPCSQKP 98
 RESULT 33
 ID ADY69083 standard; protein; 98 AA.
 XX
 AC ADY69083;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE HPV 16 E7.
 XX
 KW Cytostatic; Gene Therapy; human papillomavirus; E7 protein;
 KW immunohistological detection; Pap-smear; cervical; carcinoma; biopsy;
 KW anogenital; head; neck; prostate; sexually transmitted disease;
 KW cancer.
 XX
 OS Human papillomavirus.
 XX
 PN WO2005026731-A1.
 XX
 PD 24-MAR-2005.
 XX
 PF 17-SEP-2004; 2004WO-EP010484.
 XX
 PR 17-SEP-2003; 2003EP-00020564.
 XX
 PA (AMYN-) AMYNON BIOTECH GMBH.
 XX
 PI Zwerschke WP, Jansen-Duerr P, Fiedler M, Latch A, Fitzky B;
 XX
 DR WPI; 2005-242459/25.
 DR N-PSDB; ADY69082.
 XX
 PT New combination of antibodies comprises an anti-HPV-16 E7 antibody and an
 PT anti-HPV-18 E7 antibody, useful for preparing a diagnostic composition

PT for the (immuno-) histological detection of high risk HPV E7 protein.
 XX
 XX Example 2; SEQ ID NO 2; 146pp; English.
 PS
 XX This sequence represents human papillomavirus-16 (HPV-16) E7 protein. An
 CC antibody raised against this protein may be used in a combination of
 CC antibodies which comprises an anti-HPV-16 E7 antibody obtainable by
 CC eliciting an in vivo humoral response against HPV-16 E7 protein or its
 CC fragment in a goat, and affinity-purifying antibodies as obtained in the
 CC eliciting step, and an anti-HPV-18 E7 antibody. The combination of
 CC antibodies is useful for the preparation of a diagnostic composition for
 CC the (immuno-) histological detection of high risk HPV E7 protein. The
 CC (immuno-) histological detection is carried out on Pap-smears, cervical
 CC (carcinoma) biopsies, anogenital biopsies, mamma biopsies, head- or neck
 CC biopsies, or prostate biopsies. The diagnostic composition is used for
 CC evaluating the risk of acquiring a sexually transmitted disease or
 CC cancer, for measuring the status of an existing sexually transmitted
 CC disease or cancer, or for screening therapy efficiency in the treatment
 CC of a sexually transmitted disease or cancer. The sexually transmitted
 CC disease is a high risk HPV infection or where the cancer is cervical
 CC cancer, breast cancer/mamma cancer, prostate cancer, head and neck
 CC cancer, penile cancer, and/or anogenital cancer/neoplasia (A1N). The
 CC combination of antibodies or the diagnostic composition are useful in an
 CC in vitro method for the detection of high risk HPV E7 protein. The
 CC antibody is useful for detecting E7 protein of HPV-31, HPV-33, HPV-35,
 CC HPV-39, HPV-45, HPV-52, HPV-56, HPV-58, and/or HPV-59. It is also useful
 CC for the preparation of a diagnostic composition for detecting E7 protein
 CC of HPV-16, HPV-18, HPV-31, HPV-33, HPV-35, HPV-39, HPV-45, HPV-52, HPV-
 CC 56, HPV-58, and/or HPV-59.
 XX
 SQ Sequence 98 AA;
 Query Match 99.0%; Score 512; DB 9; Length 98;
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPTLHRYMDLOPETTDLYXXQNDSSSEEDIDGPAQAEPRAHYNIIVTFCK 60
 DB 1 MHGDTPTLHRYMDLOPETTDLYCYEQNDSSSEEDIDGPAQAEPRAHYNIIVTFCK 60
 QY 61 CDSTLRACVOSTHYDRTLEDLMGTLGIYXPCSQKP 98
 DB 61 CDSTLRACVOSTHYDRTLEDLMGTLGIYXPCSQKP 98
 RESULT 34
 ID AEA40816 standard; protein; 98 AA.
 XX
 AC AEA40816;
 XX
 DT 28-JUL-2005 (first entry)
 XX
 DE Anti-apoptotic vector HPV E7 antigenic protein, SEQ ID 6.
 XX
 KW immunogenicity; immunogenicity-potentiating polypeptide; ITP; T-cell;
 KW vaccine; immune stimulation; tumor; cytostatic.
 XX
 OS Human papillomavirus - 16.
 XX
 PN WO2005047501-A1.
 XX
 PD 26-MAY-2005.
 XX
 PF 24-FEB-2004; 2004WO-US005292.
 XX
 PR 24-FEB-2003; 2003US-0449429P.
 PR 18-JUL-2003; 2003US-0488527P.
 PR 31-DEC-2003; 2003US-0533792P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Wu T, Hung CF, Kim T;

XX WPI: 2005-367009/37.
DR GENBANK; NC_001526.
XX
PT New nucleic acid composition comprising a first nucleic acid vector
PT encoding an anti-apoptotic polypeptide and a second nucleic acid vector
PT inhibiting the growth of a tumor.
XX
PS Disclosure; SEQ ID NO 6; 158bp; English.
XX
XX The invention relates to a novel nucleic acid composition useful as an
CC immunogen. The composition comprises a combination of: a first nucleic
CC acid vector comprising a first sequence encoding an antigenic polypeptide
CC or peptide, and optionally, a second sequence linked to the first
CC sequence and encoding an immunogenicity-potentiating polypeptide (IPP);
CC and a second nucleic acid vector encoding an anti-apoptotic polypeptide.
CC When the second vector is administered with the first vector to a
CC subject, a T cell mediated immune response to the antigenic polypeptide
CC or peptide is induced that is greater in magnitude and/or duration than
CC an immune response induced by administration of the first vector alone.
CC The invention further includes: a particle comprising a material that is
CC suitable for introduction into a cell or an animal by particle
CC bombardment, bound to which is the first and second vectors or
CC composition; a pharmaceutical composition capable of inducing or
CC enhancing an antigen specific immune response, comprising the particle
CC and a carrier or an excipient; inducing or enhancing an antigen specific
CC immune response in a subject; increasing the numbers of CD8+ CTLs
CC specific for a selected desired antigen in a subject; and inhibiting the
CC growth of a tumor in a subject. The nucleic acid composition is useful as
CC an immunogen for inhibiting the growth of a tumor, hence it has
CC cytostatic activity. This sequence represents an anti-apoptotic vector HPV
CC E7 antigenic protein of the invention.
XX
SQ Sequence 98 AA;
Query Match 99.0%; Score 512; DB 9; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGPTLHEHYMLDQPTTDLXXYXQUNDSEEDIEDPAGQAEPPRAHYNIVTFCK 60
DB 1 MHGPTLHEHYMLDQPTTDLXXYXQUNDSEEDIEDPAGQAEPPRAHYNIVTFCK 60
QY 61 CDSTLRFCVOSTHVDIRLTEDLLMGTGIGVPCISQKP 98
DB 61 CDSTLRFCVOSTHVDIRLTEDLLMGTGIGVPCISQKP 98
RESULT 35
AEB11989
ID AEB11989 standard; protein; 98 AA.
XX
AC AEB11989;
XX
DT 08-SEP-2005 (first entry)
XX
DE HPV16 E7 protein.
XX
KW Tumor-associated antigen; vaccine; papilloma; cytostatic; neoplasm;
KW cancer; HPV16 E7.
XX
OS Human papillomavirus type 16.
XX
PN WO2005060993-A1.
XX
PD 07-JUL-2005.
XX
PF 24-DEC-2003; 2003WO-NL000929.
XX
PR 24-DEC-2003; 2003WO-NL000929.
XX
PA (UILE-) UNIV LEIDEN MEDICAL CENT.

XX
PI Van Der Burg SH, Driftout JW;
XX WPI: 2005-497704/50.
XX
XX Producing a synthetic protein of a pathogen or tumor comprises chemically
PT synthesizing two or more fragments of 2-80 continuous amino acids of
PT sequence, the sequence of two or more fragments are neighboring and non-
PT overlapping.
XX
PS Claim 11; SEQ ID NO 1; 53bp; English.
XX
XX The invention relates to a method of producing a synthetic protein
CC comprising an amino acid sequence that is at least 80% identical to a
CC naturally occurring antigenic protein of a pathogen or tumor comprising
CC chemically synthesizing two or more fragments, chemically ligating the C-
CC terminus of a fragment to the N-terminus of a neighboring fragment to
CC produce the synthetic protein or its part and optionally repeating the
CC second step to sequentially ligate a further neighboring fragment
CC obtained from the second step. The invention also relates to a
CC composition comprising the protein and a method for treating or
CC preventing human papillomavirus (HPV) associated disease by administering
CC to the subject the protein or composition in a therapeutically effective
CC amount. In producing a synthetic protein, the neighboring non-overlapping
CC fragments are selected to comprise N-terminal cysteine or glycine
CC residues. The naturally occurring protein is an HPV protein, e.g. E2, E6
CC or E7 protein from HPV16, HPV18, HPV31, HPV33 or HPV45. The composition
CC further comprises an anti-CD40 antibody. The composition is useful as a
CC vaccine for preventing or treating HPV associated disease, such as
CC cancer. This sequence represents an HPV16 E7 protein used in the method
CC of the invention.
XX
SQ Sequence 98 AA;
Query Match 99.0%; Score 512; DB 9; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGPTLHEHYMLDQPTTDLXXYXQUNDSEEDIEDPAGQAEPPRAHYNIVTFCK 60
DB 1 MHGPTLHEHYMLDQPTTDLXXYXQUNDSEEDIEDPAGQAEPPRAHYNIVTFCK 60
QY 61 CDSTLRFCVOSTHVDIRLTEDLLMGTGIGVPCISQKP 98
DB 61 CDSTLRFCVOSTHVDIRLTEDLLMGTGIGVPCISQKP 98
RESULT 36
AEC96392
ID AEC96392 standard; protein; 98 AA.
XX
AC AEC96392;
XX
DT 01-DEC-2005 (first entry)
XX
DE HPV protein E7 from HPV16.
XX
KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
XX
OS Human papillomavirus type 16.
XX
PN WO2005089164-A2.
XX
PD 29-SEP-2005.
XX
PF 03-JAN-2005; 2005WO-US000077.
XX
PR 31-DEC-2003; 2003US-0533211P.
XX
PR 02-JUL-2004; 2004US-0584652P.
XX
PA (EPIM-) EPIMUNE INC.
PA (INNO-) INNOGENETICS NV.

PA (CHES/) CHESNUT R.
 PA (NEWM/) NEWMAN M J.
 PA (MOTB/) MOTHE B.
 PA (BAKE/) BAKER D.
 PA (SOUT/) SOUTHWOOD S.
 PA (BABE/) BABE L M.
 PA (CHEN/) CHEN Y.
 PA (DEYO/) DEYOUNG L M.
 PA (HUAN/) HUANG M T F.
 PA (POWE/) POWER S D.
 PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;
 PI Chen Y, Deyoung LM, Huang MTF, Power SD;
 DR WPI: 2005-658982/67.
 XX New polynucleotide comprises a multi-epitope construct comprising nucleic
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.
 PS Disclosure; Page 56; 518pp; English.
 XX The invention relates to a new polynucleotide comprising a multi-epitope
 CC construct comprising nucleic acids encoding the human papillomavirus
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that
 CC are directly or indirectly joined to one another in the same reading
 CC frame, a vaccine minigene. Also included are a vector comprising the
 CC multi-epitope construct, a polypeptide comprising an amino acid sequence
 CC encoded by the polynucleotide, a composition (comprising the
 CC polynucleotide, vector and/or polypeptide and a carrier), a cell
 CC (comprising the polynucleotide, vector or polypeptide), inducing an
 CC immune response against human papillomavirus virus (HPV) and making the
 CC polynucleotide, vector or polypeptide. The epitopes are derived from
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the
 CC epitopes in the vaccine protein are disclosed in the tables referred to
 CC in the claims of the specification. The polynucleotide, vector or
 CC polypeptide is useful in preparing a composition for inducing an immune
 CC response against human papillomavirus virus (HPV) and thus providing a
 CC defense against HPV infection and HPV-related cancers. The present
 CC sequence is an HPV protein used to derive epitopes for the vaccine of the
 CC invention.
 XX
 SQ Sequence 98 AA;
 Query Match 99.0%; Score 512; DB 9; Length 98;
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPTLHEHYMDLQEPETDLYXXQUNDSSSEEDSIDPAGAEPPRAHYNIIVTFCK 60
 DB 1 MHGDTPTLHEHYMDLQEPETDLYCYEQUNDSSSEEDSIDPAGAEPPRAHYNIIVTFCK 60
 QY 61 CDSTLRLCVOSTHYDRTLEDLMGTGIVXPICSQKP 98
 DB 61 CDSTLRLCVOSTHYDRTLEDLMGTGIVXPICSQKP 98
 RESULT 37
 ID AEC98871 standard; protein; 98 AA.
 AC AEC98871;
 XX
 DT 01-DEC-2005 (first entry)
 DE HPV_16 Envelope protein E7.
 XX
 KM Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
 KM epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
 XX
 OS Human papillomavirus type 16.
 XX

PN WO2005089164-A2.
 XX
 XX 29-SEP-2005.
 PD
 XX
 XX 03-JAN-2005; 2005MO-US000077.
 XX
 XX
 PF 31-DEC-2003; 2003US-0533211P.
 PR 02-JUL-2004; 2004US-0584652P.
 XX
 XX (BEIM-) EPIMUNE INC.
 PA (INNO-) INNOGENETICS NV.
 PA (CHES/) CHESNUT R.
 PA (NEWM/) NEWMAN M J.
 PA (MOTB/) MOTHE B.
 PA (BAKE/) BAKER D.
 PA (SOUT/) SOUTHWOOD S.
 PA (BABE/) BABE L M.
 PA (CHEN/) CHEN Y.
 PA (DEYO/) DEYOUNG L M.
 PA (HUAN/) HUANG M T F.
 PA (POWE/) POWER S D.
 PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;
 PI Chen Y, Deyoung LM, Huang MTF, Power SD;
 DR WPI: 2005-658982/67.
 XX New polynucleotide comprises a multi-epitope construct comprising nucleic
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.
 XX
 XX Example 10; Page 350; 518pp; English.
 PS
 XX The invention relates to a new polynucleotide comprising a multi-epitope
 CC construct comprising nucleic acids encoding the human papillomavirus
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that
 CC are directly or indirectly joined to one another in the same reading
 CC frame, a vaccine minigene. Also included are a vector comprising the
 CC multi-epitope construct, a polypeptide comprising an amino acid sequence
 CC encoded by the polynucleotide, a composition (comprising the
 CC polynucleotide, vector and/or polypeptide and a carrier), a cell
 CC (comprising the polynucleotide, vector or polypeptide), inducing an
 CC immune response against human papillomavirus virus (HPV) and making the
 CC polynucleotide, vector or polypeptide. The epitopes are derived from
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the
 CC epitopes in the vaccine protein are disclosed in the tables referred to
 CC in the claims of the specification. The polynucleotide, vector or
 CC polypeptide is useful in preparing a composition for inducing an immune
 CC response against human papillomavirus virus (HPV) and thus providing a
 CC defense against HPV infection and HPV-related cancers. The present
 CC sequence is an HPV protein used to derive epitopes for the vaccine of the
 CC invention.
 XX
 SQ Sequence 98 AA;
 Query Match 99.0%; Score 512; DB 9; Length 98;
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPTLHEHYMDLQEPETDLYXXQUNDSSSEEDSIDPAGAEPPRAHYNIIVTFCK 60
 DB 1 MHGDTPTLHEHYMDLQEPETDLYCYEQUNDSSSEEDSIDPAGAEPPRAHYNIIVTFCK 60
 QY 61 CDSTLRLCVOSTHYDRTLEDLMGTGIVXPICSQKP 98
 DB 61 CDSTLRLCVOSTHYDRTLEDLMGTGIVXPICSQKP 98
 RESULT 38
 ID AED13078 standard; protein; 98 AA.
 XX

AC AED13078;
 XX
 DT 15-DEC-2005 (first entry)
 XX
 DE HPV16 E7 wild-type protein sequence.
 XX
 KW mutagen; vaccine; antigen; virucide; antibacterial.
 XX
 OS Human papillomavirus type 16.
 XX
 PN FR2868781-A1.
 PD 14-OCT-2005.
 XX
 PF 13-APR-2004; 2004FR-00003848.
 XX
 PR 13-APR-2004; 2004FR-00003848.
 XX
 PA (IMMU-) IMMUTEP.
 PI Triebel F;
 XX
 DR WPI: 2005-678227/70.
 XX
 DR N-PSDB; AED13076.
 XX
 PT Therapeutic vaccine, for viral and bacterial conditions, comprises an
 PT antigen protein and a viral or bacterial protein, coupled together by
 PT stable hydrogen or covalence bonds in biological media.
 XX
 PS Disclosure; Fig 1; 51pp; French.
 XX
 CC The invention relates to a novel vaccine composed of an antigen protein
 CC and a second protein as an s-(methyl mercury)-l-cysteine (CMH class II)
 CC ligand. The second protein is taken from a group including human
 CC lymphocyte Activation Gene (hLAG)-3. The first protein is a viral or
 CC bacterial antigen, a tumor antigen, parasitic antigen, or their mixtures.
 CC The viral antigens can be for hepatitis B (HBV), human papillomavirus
 CC (HPV), hepatitis C (HCV), human immunodeficiency virus (HIV), Epstein-
 CC Barr virus (EBV), cytomegalovirus (CMV), and their combinations. The
 CC bacterial antigens can be intracellular bacteria of tuberculosis, leprosy
 CC and listeria. A vaccine of the invention has virucide, and antibacterial
 CC activity. The present sequence represents the HPV16 wild-type E7 protein
 CC sequence.
 XX
 SQ Sequence 98 AA;
 Query Match 99.0%; Score 512; DB 9; Length 98;
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPTLHEYMLDLPETTDLYXXQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
 DB 1 MHGDTPTLHEYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
 QY 61 CDSTLRLCVOSTHYDIRTLDLMGTGLGIYXPICSOQP 98
 DB 61 CDSTLRLCVOSTHYDIRTLDLMGTGLGIYXPICSOQP 98
 RESULT 39
 AED64360
 ID AED64360 standard; protein: 98 AA.
 AC AED64360;
 XX
 DT 12-JAN-2006 (first entry)
 XX
 DE Human papillomavirus type 16 E7 protein.
 XX
 KW Vaccine; therapeutic; papillomavirus infection; virucide; infection;
 KW fusion protein; E7.
 XX
 OS Human papillomavirus type 16.

XX
 PN US2005249745-A1.
 XX
 PD 10-NOV-2005.
 XX
 PF 13-JUL-2005; 2005US-00179478.
 XX
 PR 20-FEB-1998; 98US-00026896.
 PR 03-APR-2001; 2001US-00824017.
 PR 04-SEP-2003; 2003US-00654129.
 XX
 PA (MED1-) MEDIGENE AG.
 XX
 PI Haliek M, Burger A;
 XX
 DR WPI: 2005-746775/76.
 XX
 DR N-PSDB; AED64359.
 XX
 PT New fusion protein comprising an amino acid sequence from a first or a
 PT second papilloma virus-specific (PVS) protein, useful in preparing a
 PT composition for treating or preventing papilloma virus infection.
 XX
 PS Example 1; SEQ ID NO 4; 20pp; English.
 XX
 CC The present invention relates to fusion protein comprising papilloma
 CC virus-specific (PVS) protein and their encoding polynucleotides. The
 CC invention is useful in preparing a composition for treating and
 CC preventing papilloma virus infection in humans. The present sequence is
 CC the Human papillomavirus type 16 E7 protein.
 XX
 SQ Sequence 98 AA;
 Query Match 99.0%; Score 512; DB 9; Length 98;
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPTLHEYMLDLPETTDLYXXQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
 DB 1 MHGDTPTLHEYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
 QY 61 CDSTLRLCVOSTHYDIRTLDLMGTGLGIYXPICSOQP 98
 DB 61 CDSTLRLCVOSTHYDIRTLDLMGTGLGIYXPICSOQP 98
 RESULT 40
 AEE94089
 ID AEE94089 standard; protein: 98 AA.
 AC AEE94089;
 XX
 DT 23-FEB-2006 (first entry)
 XX
 DE HPV16 E7 protein.
 XX
 KW Gene expression; therapeutic; immune stimulation; HIV infection;
 KW acquired immune deficiency syndrome; E7 protein; anti-HIV; virucide;
 KW infection; immune disorder.
 XX
 OS Human papillomavirus type 16.
 XX
 PN WO2005118874-A1.
 XX
 PD 15-DEC-2005.
 XX
 PF 06-JUN-2005; 2005MO-US019592.
 XX
 PR 04-JUN-2004; 2004US-0576819P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Smith LR, Shahabi V, Sidhu MK;

DR	WPI: 2006-047579/05.
DR	N-PSDB; AEE94088.
XX	
XX	Preparing a polynucleotide, useful for enhancing gene expression,
PT	comprises assembling oligonucleotides comprising surrogate codons to form
PT	a modified polynucleotide.
XX	
PS	Claim 149, SEQ ID NO 2, 131pp; English.
XX	
CC	The invention relates to a method of preparing a polynucleotide that
CC	provides enhanced expression of a gene, comprising assembling
CC	oligonucleotides comprising surrogate codons to form a modified
CC	polynucleotide, comprising a predetermined nucleic acid sequence encoding
CC	the same protein or polypeptide as a wild-type polynucleotide. The
CC	invention also relates to a method for enhancing expression of a gene, a
CC	method of preventing or treating a disease in a mammal, a composition
CC	comprising a modified polynucleotide describe above and a pharmaceutical
CC	vector. The method additionally comprises adding an immunoglobulin leader
CC	sequence, such as an IGE leader sequence, to the modified polynucleotide.
CC	The composition is useful for preparing a medicament for inducing an
CC	immune response in a mammal or for treating an infection or condition,
CC	e.g. HIV or AIDS in a mammal. The polynucleotide and methods are useful
CC	for enhancing gene expression. This sequence represents the HPV16 E7
CC	protein used in the scope of the invention.
XX	
SQ	Sequence 98 AA:
XX	
Query Match	99.0%; Score 512; DB 10; Length 98;
Best Local Similarity	96.9%; Pred. No. 2,2e-57;
Matches	95; Conservative 0; Mismatches 3; Indels 0; Gaps 0.
QY	1 MHGDPPTLHEWMLDQPERTDLYXXKXOLNDSESEDEIDGPAGQAEPPRAHNYITFPCK 60
DB	1 MHGDPPTLHEWMLDQPERTDLYCYEQUNDSESEDEIDGPAGQAEPPRAHNYITFPCK 60
QY	61 CDSTLRLCVGSTHVDIRLTEDLLMGTGIVXPICGQKP 98
DB	61 CDSTLRLCVGSTHVDIRLTEDLLMGTGIVCPICGQKP 98
XX	
RESULT 41	
ID	ADQ88451 standard; protein; 99 AA.
XX	ADQ88451
XX	ADQ88451;
XX	
DT	23-SEP-2004 (first entry)
XX	
DE	HPV16 E7 protein.
XX	
KW	HPV 16; E7 gene; cytostatic; vaccine; tumour.
XX	
OS	Human papillomavirus; HPV16.
XX	
FN	R02229307-C1.
XX	
PD	27-MAY-2004.
XX	
PF	22-OCT-2002; 2002RU-00128131.
XX	
PR	22-OCT-2002; 2002RU-00128131.
XX	
PA	(BIOM=) BIOMEDINVEST STOCK CO.
XX	
PI	Paltshev MA, Severin ES, Kiselev OI, Kiselev VI, Sveshnikov FG;
XX	
DR	WPI: 2004-446846/42.
XX	
DR	N-PSDB; ADQ88450.
XX	
PT	Recombinant protein composition, useful in immunotherapy and prophylactic
PT	vaccination of tumor diseases in anus-genital sphere.
XX	
PS	Disclosure: Page 7; 10pp; Russian

XX		The invention involves hybrid proteins consisting of amino acid sequences
CC		of oncprotein E7 of human papilloma virus of 16 and 18 types that are
CC		bound covalently with amino acid sequence of heat shock protein with
CC		molecular mass 70 kDa (Hsp70) from M. tuberculosis - E716-Hsp70 and E718-
CC	Hsp70,	respectively. The invention relates to composition of recombinant
CC		proteins, method for preparing the composition, pharmaceutical kit of
CC		reagents used in immunotherapy and prophylactic vaccination of tumour
CC		diseases in anal-genital region and methods for immunotherapy and
CC		prophylactic vaccination. The fusion proteins are used in immunotherapy
CC		and prophylactic vaccination of tumour diseases in anal-genital sphere.
CC		The present sequence is the HPV16 E7 protein.
XX		
SQ	Sequence 99 AA;	
Query Match	99.0%;	Score 512; DB 8; Length 99;
Best Local Similarity	96.9%;	Pred. No. 2.2e-57;
Matches	95; Conservative	0; Mismatches 3; Indels 0; Gaps 0
Oy	1 MHGDPPTLHEWMLDQPETTTDLVYXKXOLNDSSSEDEIDEIGPAGQAEPDBAHNYIVTFCK 60 2 MHGDPTLHEWMLDQPETTTDYCTEQLNDSSEEDIEDIPGAPEPDAAHNIVTFCK 61	
Db	61 CDSTLRLCVGOSTHVDIRTLTEDLLMGTLGIYPICSGKP 98 62 CDSTLRLCVGOSTHVDIRTLTEDLLMGTLGIVCPICSGKP 99	
RESULT 42		
ID	ADY92615	standard; protein; 99 AA.
XX	ADY92615;	
AC	ADY92615;	
XX	16-JUN-2005	(first entry)
DT		
XX		
XX	HPV16 E7 oncprotein protein sequence.	
DE		
KW		Antibody; monoclonal antibody; antibody production; hydridoma; screening;
KW	E7 oncprotein; immuno-diagnosis; diagnostic; immunoconjugate;	
KW	immunosassy; radiolimmunosassy; enzyme-linked immuosorbent assay;	
KW	transmissible spongiform encephalopathy; cerebroprotective;	
KW	cervical intraepithelial neoplasia; cytostatic; immunoglobulin.	
OS	Human papillomavirus type 16.	
XX		
PN	WO2005028510-A2.	
PD	31-MAR-2005.	
PF	24-SEP-2004; 2004WO-RU000373.	
PR	25-SEP-2003; 2003RU-00128660.	
PA	(KISE/) KISELEV V I. (SVES/) SVESHNIKOV P G.	
PI	Kiselev VI, Sveshnikov PG;	
DR	WI: 2005-273121/28.	
N-P	PSDB; ADY92614.	
PT	Producing monoclonal antibodies specific to an antigen of low	
PT	immunogenicity by immunizing an animal with the chemically conjugated	
PT	antigen, useful for detecting cervical intraepithelial neoplasia.	
XX		
BS	Disclosure; SEQ ID NO 2; 72pp; English.	
XX		
CC		The new invention relates to methods and compositions that allow
CC		production of antigen specific antibodies to antigens that have
CC		traditionally been unable to elicit an adequate and specific immune
CC		response. The method comprises producing monoclonal antibodies specific
CC		to an antigen of low immunogenicity by chemically conjugating the antigen

CC to a carrier molecule, immunizing an animal with the conjugated antigen,
 CC harvesting B cells from the animal, creating a hybridoma from the
 CC native antigen. The antigens can be E7 oncoprotein, P10n protein
 CC peptide, hyaluronic acid or matrix metalloproteinase 3. The carrier
 CC molecule is HSP70. The chemical conjugation comprises creating a plasmid
 CC with a nucleotide sequence encoding the antigen, such as E7 oncoprotein
 CC with the plasmid. The nucleotide sequence encoding E7 oncoprotein
 CC comprises ADY92614 or ADY92616. The nucleotide sequence encoding HSP70
 CC comprises ADY92618. Alternatively, the conjugating is performed
 CC chemically using glutaraldehyde. Screening for specificity is done by
 CC various assays such as radioimmunoassay, enzyme-linked immunosorbent
 CC assay, or sandwich immunoassay. The antibodies are useful for determining
 CC if a subject is at risk of developing spongiform encephalopathy. The P10n
 CC comprising an antibody that specifically detects Prion protein. The P10n
 CC protein peptide comprises ADY92619, ADY92620 or ADY92622. Antibodies
 CC specific to E7 oncoprotein are useful for detecting cervical
 CC intraepithelial neoplasia by obtaining a specimen of cervical epithelial
 CC cells and screening the specimen for the presence of E7 oncoprotein. The
 CC monoclonal antibodies comprise at least two immunoglobulin isotypes. The
 CC immunoglobulin isotype is IgG2a or IgG2b. The immunoglobulin isotype has
 CC specificity for a different antigenic determinant than the second
 CC immunoglobulin isotype. The present sequence HPV16 E7 oncoprotein
 CC sequence.

XX Sequence 99 AA;

Query Match 99.0%; Score 512; DB 9; Length 99;
 Best Local Similarity 96.9%; Pred. No. 2.2e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEXYMLDLPETTTDLXXYXQLNDSSEEDIDGPAQAEPDRAHNYIVTFCK 60
 Db 2 MHGDPPTLHEXYMLDLPETTTDLXXYXQLNDSSEEDIDGPAQAEPDRAHNYIVTFCK 61
 61 CDSTLRFCVQSTHVDIRLTEDLMTGLGIVXPCISQKP 98
 62 CDSTLRFCVQSTHVDIRLTEDLMTGLGIVCPCISQKP 99

RESULT 43

AAB31608
 ID AAB31608 standard; protein; 121 AA.

XX AAB31608;

XX 30-APR-2001 (first entry)

XX Amino acid sequence of a His-tagged HPV16 E7 protein.

XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;

XX lymphocyte; Hep5; Hep40; Hep10; Hep60; Hep71; microbial pathogen;

XX E7 protein.

XX Synthetic.

XX Human papillomavirus.

XX WO200104344-A2.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-US018828.

XX 08-JUL-1999; 99US-0143757P.

XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX Siegel M, Chu NR, Mitzzen LA;

XX WPI; 2001-138361/14.

XX N-PSDB; AAF25008.

XX

PT Screening for compounds that stimulate Th1-like responses in CD4+ T
 PT lymphocyte cells.

XX Example 4; Fig 3; 88pp; English.

XX The present sequence represents a HPV16 E7 protein. HPV16 E7 was fused to
 CC a heat shock protein (Hsp), and used used in the method of the invention.
 CC The specification describes a method of determining whether a compound
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
 CC lymphocyte cells. The method comprises contacting naive lymphocytes in
 CC vitro with a fusion protein comprising at least a fragment of Hsp, and
 CC then detecting the Th1-like response exhibited by the cell sample. The
 CC proteins which may be used in the method of the invention are Hep5,
 CC Hep40, Hep10, Hep60, and Hep71. The method may be used to identify
 CC compounds that stimulate Th1-like responses in response to microbial
 CC pathogens

XX Sequence 121 AA;

Query Match 99.0%; Score 512; DB 4; Length 121;
 Best Local Similarity 96.9%; Pred. No. 2.8e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEXYMLDLPETTTDLXXYXQLNDSSEEDIDGPAQAEPDRAHNYIVTFCK 60
 Db 24 MHGDPPTLHEXYMLDLPETTTDLXXYXQLNDSSEEDIDGPAQAEPDRAHNYIVTFCK 83
 61 CDSTLRFCVQSTHVDIRLTEDLMTGLGIVXPCISQKP 98
 84 CDSTLRFCVQSTHVDIRLTEDLMTGLGIVCPCISQKP 121

RESULT 44

AAB31616
 ID AAB31616 standard; protein; 198 AA.

XX AAB31616;

XX 30-APR-2001 (first entry)

XX Amino acid sequence of Hsp10-E7 fusion protein.

XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;

XX lymphocyte; Hep5; Hep40; Hep10; Hep60; Hep71; microbial pathogen;

XX E7 protein.

XX Synthetic.

XX Mycobacterium tuberculosis.

XX Human papillomavirus.

XX WO200104344-A2.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-US018828.

XX 08-JUL-1999; 99US-0143757P.

XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX Siegel M, Chu NR, Mitzzen LA;

XX WPI; 2001-138361/14.

XX N-PSDB; AAF25023.

XX Screening for compounds that stimulate Th1-like responses in CD4+ T
 PT lymphocyte cells.

XX Example 13; Fig 12; 88pp; English.

XX The present sequence represents a fusion protein comprising Mycobacterium
 CC tuberculosis heat shock protein (Hsp) 10 fused at its 3' end to HPV16 E7
 CC protein. The fusion protein is used in the method of the invention. The

CC specification describes a method of determining whether a compound
CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
CC lymphocyte cells. The method comprises contacting native lymphocytes in
CC vitro with a fusion protein comprising at least a fragment of Hsp, and
CC then detecting the Th1-like response exhibited by the cell sample. The
CC proteins which may be used in the method of the invention are Hsp65,
CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
CC compounds that stimulate Th1-like responses in response to microbial
CC pathogens
CC
XX Sequence 198 AA:
SQ
Query Match 99.0%; Score 512; DB 4; Length 198;
Best Local Similarity 96.9%; Pred. No. 5.3e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MHGDPPLHRYMDLOPETDLDYXXYQLNDSSEEDIDDPAGQAEPPRAHYNIVTFCK 60
Db 101 MHGDPPLHRYMDLOPETDLDYCYEQUNDSSSEEDIDDPAGQAEPPRAHYNIVTFCK 160
Qy 61 CDSTLRRCVOSTHVDIRTELDLMGTGIVXPICQKP 98
Db 161 CDSTLRRCVOSTHVDIRTELDLMGTGIVCPICQKP 198
RESULT 45
ADT75831
ID ADT75831 standard; protein; 212 AA.
XX
XX ADT75831:
XX
XX 13-JAN-2005 (first entry)
XX
XX Novel Fve fusion protein mutant sequence #48.
XX
XX Fve polypeptide; anti-allergic; anti-inflammatory; antiasthmatic;
XX cytostatic; respiratory-Gen; antiasthmatic; vaccine; immunomodulator;
XX immune response; atopic disease; allergy; seasonal respiratory allergy;
XX perennial respiratory allergy; allergic rhinitis; hayfever;
XX nonallergic rhinitis; vasomotor rhinitis; irritant rhinitis;
XX grass pollen allergy; weed pollen; tree pollen; animal danders;
XX allergic asthma; food allergy; house dust mite allergy; fungal spore;
XX cancer; tumour progression; T cell lymphoma; melanoma; lung cancer;
XX colon cancer; breast cancer; prostate cancer.
XX
XX Plasmulina velutipes.
XX Human Papillomavirus.
OS Chimeric.
OS
XX WO2004092210-A2.
XX
XX 28-OCT-2004.
XX
XX 16-APR-2004; 2004WO-SG000098.
XX
XX 17-APR-2003; 2003GB-00008988.
XX
XX (UYNA-) UNIV NAT SINGAPORE.
XX (SCTE-) AGENCY SCI TECHNOLOGY & RES.
XX
XX Chua KY, Seow SV, Kojalakar PR;
XX
XX WPI; 2004-758336/74.
XX N-PSDB; ADT75832.
XX
XX
XX New Fve polypeptide that is a fragment, homologue, variant or derivative
XX of Fve protein and that comprises a biological activity of native Fve
XX protein, useful for preventing and treating allergy or cancer.
XX
XX Claim 6; Page 166; 286pp; English.
XX
XX This invention relates to a novel Fve (Plasmulina velutipes) polypeptide
XX comprising at least one biological activity of native Fve protein, and

CC being its fragment, homologue, variant or derivative. The invention may
CC be useful for the production of compounds with an anti-allergic,
CC anti-inflammatory, antiasthmatic, cytostatic, respiratory-Gen or
CC antiasthmatic activity or for the development of a vaccine. The
CC composition (including the native Fve polypeptide, or an Fve polypeptide,
CC nucleic acid, vector, DNA vaccine, host cell or transgenic organism) is
CC useful as an immunomodulator or to enhance an immune response in a
CC mammal, as an adjuvant for a vaccine, in a method of treatment or
CC prophylaxis of a disease, for the preparation of a pharmaceutical
CC composition for the treatment of a disease, such as an atopic disease or
CC an allergy (for example seasonal respiratory allergy, perennial
CC respiratory allergy, allergic rhinitis, hayfever, nonallergic rhinitis,
CC vasomotor rhinitis, irritant rhinitis, an allergy against grass pollen,
CC weed pollen, tree pollen or animal danders, an allergy associated with
CC allergic asthma, food allergy or an allergy to a house dust mite from
CC Family Glyphagidae, preferably Blomia tropicalis or from Family
CC Pyroglyphidae, preferably Dermatophagoides pteronyssinus or
CC Dermatophagoides farinae, or to fungi or fungal spores, preferably
CC Aspergillus fumigatus). These may also be used for treating or preventing
CC cancer or in suppressing tumour progression, where the cancer comprises a
CC T cell lymphoma, melanoma, lung cancer, colon cancer, breast cancer or
CC prostate cancer. The present sequence is that of a gene which encodes a
CC novel Fve-derived protein of the invention.
XX
XX Sequence 212 AA:
SQ
Query Match 99.0%; Score 512; DB 8; Length 212;
Best Local Similarity 96.9%; Pred. No. 5.8e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MHGDPPLHRYMDLOPETDLDYXXYQLNDSSEEDIDDPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDPPLHRYMDLOPETDLDYCYEQUNDSSSEEDIDDPAGQAEPPRAHYNIVTFCK 60
Qy 61 CDSTLRRCVOSTHVDIRTELDLMGTGIVXPICQKP 98
Db 61 CDSTLRRCVOSTHVDIRTELDLMGTGIVCPICQKP 98
RESULT 46
AAV25375
ID AAV25375 standard; protein; 220 AA.
XX
XX AAV25375:
XX
XX 06-SEP-1999 (first entry)
XX
XX HPV fusion protein D1/3-E7-His (HPV16).
XX
XX
XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
XX immunological fusion partner; CpG oligonucleotide; immune response;
XX HPV antigen; prevention; treatment.
XX
XX Synthetic.
XX Human Papillomavirus.
OS
XX WO9933868-A2.
XX
XX 08-JUL-1999.
XX
XX 18-DEC-1998; 98WO-EP008563.
XX
XX 24-DEC-1997; 97GB-00027262.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Dalemans WJ, Gerard CMG;
XX
XX WPI; 1999-405485/34.
XX N-PSDB; AAV28791.
XX
XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
XX induce immune response to HPV.
XX
XX

XX Example 1; Page 46-47; 62pp; English.

XX
PS
CC AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAY25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours

XX
SQ Sequence 220 AA;

Query Match 99.0%; Score 512; DB 2; Length 220;
Best Local Similarity 96.9%; Pred. No. 6.1e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEYMLDLPETTDLYXXYQLNDSSEDEIDGPAGQAEPPRAHYNIITFCCK 60
114 MGGDPTLHEYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIITFCCK 173

Qy 61 CDSTLRLCVOSTHYDIRTLDLMGTGIVXPICSQKP 98
174 CDSTLRLCVOSTHYDIRTLDLMGTGIVCPICSQKP 211

Db

RESULT 47
AAY02631
ID AAY02631 standard; protein; 220 AA.

XX
AC AAY02631;

XX
DT 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)

XX
DE ProtdChx126-E7-His tail protein.

XX
KW Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KW tumour; lesion; benign; malignant; virus; infection.

XX
OS Human papillomavirus.
OS Haemophilus influenzae.
OS Chimeric.

XX
PN MO9910375-A2.

XX
PD 04-MAR-1999.

XX
PF 17-AUG-1998; 98WO-EP005285.

XX
PR 22-AUG-1997; 97GB-00017953.

XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX
PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
PI Lombardo-Bencheikh A;

XX
DR WPI: 1999-190587/16.
DR N-PSDB: AAX29780.

XX
PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT treatment or prophylaxis of HPV induced lesions.

XX
PS Disclosure; Fig 1; 95pp; English.

XX
CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B protein
CC D. The sequence also contains a histidine tag at the C-terminus of the
CC encoded protein. The protein can be used in a vaccine, for immuno-
CC therapeutically treating HPV induced tumour lesions (benign or malignant)
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to
CC standardise OS field)

XX
SQ Sequence 220 AA;

Query Match 99.0%; Score 512; DB 2; Length 220;
Best Local Similarity 96.9%; Pred. No. 6.1e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEYMLDLPETTDLYXXYQLNDSSEDEIDGPAGQAEPPRAHYNIITFCCK 60
114 MGGDPTLHEYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIITFCCK 173

Qy 61 CDSTLRLCVOSTHYDIRTLDLMGTGIVXPICSQKP 98
174 CDSTLRLCVOSTHYDIRTLDLMGTGIVCPICSQKP 211

Db

RESULT 48
AED52631
ID AED52631 standard; protein; 220 AA.

XX
AC AED52631;

XX
DT 29-DEC-2005 (first entry)

XX
DE Fusion protein D1/3-E7-His (HPV16).

XX
KW Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KW virucide; uterine cervix tumor; E7; D protein.

XX
OS Haemophilus influenzae; strain 772.
OS Human papillomavirus type 16.
OS Synthetic.
OS Chimeric.

XX
PN IN9801903-I4.

XX
PD 04-MAR-2005.

XX
PF 24-AUG-1998; 98IN-CH001903.

XX
PR 22-AUG-1997; 97EP-00179535.

XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX
PI Tyrrell AMR;

XX
DR WPI: 2005-557648/57.
DR N-PSDB: AED52632.

XX
PT Vaccine.

XX
PS Example 1; Fig 1; 96pp; English.

XX
CC The invention relates to human Papilloma virus (HPV) fusion proteins,
CC linked to an immunological fusion partner that provides T helper epitopes
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC are useful in the treatment or prophylaxis of HPV induced lesions
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
CC Haemophilus influenzae D protein (20-127), the C-terminus of
CC Streptococcus pneumoniae LytA protein (cLytA) or chloro-doxin. The present
CC sequence represents an HPV-H. influenzae D protein, fusion protein of the
CC invention.

XX
SQ Sequence 220 AA;

Query Match 99.0%; Score 512; DB 9; Length 220;
Best Local Similarity 96.9%; Pred. No. 6.1e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEYMLDLPETTDLYXXYQLNDSSEDEIDGPAGQAEPPRAHYNIITFCCK 60
114 MGGDPTLHEYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHYNIITFCCK 173

Db

QY 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSQRP 98
 DB 174 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSQRP 211

RESULT 49

AAV25380
 ID AAV25380 standard; protein; 239 AA.

AAV25380;

06-SEP-1999 (first entry)

HPV fusion protein CLYTA-E7-His/HPV16.

Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
 immunological fusion partner; Cpg oligonucleotide; immune response;
 HPV antigen; prevention; treatment.

Synthetic.

Human papillomavirus.

WO9933868-A2.

08-JUL-1999.

18-DEC-1998; 98WO-EP008563.

24-DEC-1997; 97GB-00027262.

(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

Dalemans WLJ, Gerard CMG;

WPI; 1999-405485/34.

N-PSDB; AAX78796.

Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
 induce immune response to HPV.

Example VII; Page 53; 62pp; English.

CC AAX78791-X78801 represent nucleic acid sequences which encode novel
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally
 CC linked to an immunological fusion partner and an immunomodulatory Cpg
 CC oligonucleotide. The products of the invention can be used to induce an
 CC immune response in a patient to an HPV antigen. They can also be used for
 CC preventing or treating HPV induced tumours

Sequence 239 AA;

Query Match 99.0%; Score 512; DB 2; Length 239;
 Best Local Similarity 96.9%; Pred. No. 6.8e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHXYMDLQPEETDLYXXYQNDSSSEDEIDGPAGAEPRRAHYNIVTFCK 60
 DB 133 MHGDTPTLHXYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPRRAHYNIVTFCK 192
 QY 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSQRP 98
 DB 193 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSQRP 230

RESULT 50

AAV02636
 ID AAV02636 standard; protein; 239 AA.

AAV02636;

17-OCT-2003 (revised)

DT 22-JUN-1999 (first entry)

CLYTA-E7-His protein.

Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;
 lesion; benign; malignant; virus; infection.

Human papillomavirus.

Streptococcus pneumoniae.

Chimeric.

WO9910375-A2.

04-MAR-1999.

17-AUG-1998; 98WO-EP005285.

22-AUG-1997; 97GB-00017953.

(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;

Lombardo-Bencheikh A;

WPI; 1999-190587/16.

N-PSDB; AAX29785.

Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
 treatment or prophylaxis of HPV induced lesions.

Disclosure; Fig 12; 95pp; English.

CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
 CC protein from Human papillomavirus (HPV) linked to an immunological fusion
 CC partner, in this case, a fragment of the Streptococcus pneumoniae CLYTA
 CC protein of the encoded protein. The protein can be used in a vaccine, for
 CC immuno-therapeutically treating HPV induced tumour lesions (benign or
 CC malignant) and preventing HPV viral infection. (updated on 17-OCT-2003 to
 CC standardise OS field)

Sequence 239 AA;

Query Match 99.0%; Score 512; DB 2; Length 239;
 Best Local Similarity 96.9%; Pred. No. 6.8e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHXYMDLQPEETDLYXXYQNDSSSEDEIDGPAGAEPRRAHYNIVTFCK 60
 DB 133 MHGDTPTLHXYMDLQPEETDLYCYEQNDSSSEDEIDGPAGAEPRRAHYNIVTFCK 192
 QY 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSQRP 98
 DB 193 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSQRP 230

RESULT 51

AED52644
 ID AED52644 standard; protein; 239 AA.

AED52644;

29-DEC-2005 (first entry)

Fusion protein cLYTA-E7-His/HPV16.

Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
 virucide; uterine cervix tumor; E7; LyTA.

Streptococcus pneumoniae.

Human papillomavirus type 16.

Synthetic.
 Chimeric.

PN IN9801903-14.
 XX
 PD 04-MAR-2005.
 XX
 PF 24-AUG-1998; 98IN-CH001903.
 XX
 PR 22-AUG-1997; 97EP-00179535.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Tyrrell AMR;
 XX
 DR WPI: 2005-557648/57.
 DR N-PSDB; AEDS2643.
 XX
 PT Vaccine.
 XX
 PS Example 11; Fig 12; 96pp; English.
 CC The invention relates to human Papilloma virus (HPV) fusion proteins,
 CC linked to an immunological fusion partner that provides T helper epitopes
 CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
 CC are useful in the treatment or prophylaxis of HPV induced lesions
 CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
 CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
 CC Haemophilus influenzae D protein (20-127), the C-terminus of
 CC Streptococcus pneumoniae Lyta protein (cLyta) or thioredoxin. The present
 CC sequence represents an HPV-Lyta, fusion protein of the invention.
 CC
 SQ Sequence 239 AA;

Query Match 99.0%; Score 512; DB 9; Length 239;
 Best Local Similarity 96.9%; Pred. No. 6.8e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDPPTLHEYMLDQPEPTDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 60
 DB 133 MHGDPPTLHEYMLDQPEPTDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 192
 QY 61 CDSTLRLCVOSTHVDIRTLBDMGLGIYXPCSQKP 98
 DB 193 CDSTLRLCVOSTHVDIRTLBDMGLGIYXPCSQKP 230

RESULT 52
 ADO44066 standard; protein; 248 AA.
 XX
 AC ADO44066;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Amino acid sequence of an E7E6 fusion protein.
 XX
 KM E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
 XX
 OS Human papillomavirus type 16.
 OS Synthetic.
 XX
 PN WO2004030636-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 02-OCT-2003; 2003WO-US031726.
 XX
 PR 03-OCT-2002; 2002US-0415929P.
 XX
 PA (AMHP) WYETH HOLDINGS CORP.
 XX
 PI Smith L, Caesetti MC;
 XX

DR WPI: 2004-316328/29.
 DR N-PSDB; ADO44067.
 XX
 PF New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PF useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.
 XX
 PS Example 1; Page 72-73; 101pp; English.
 XX
 CC The present sequence represents an E7E6 fusion protein, comprising wild
 CC type E7 and E6 polypeptides from human papillomavirus type 16 (HPV16).
 CC The specification describes human papillomavirus E6 and E7 polypeptides,
 CC where the E7 polypeptide has mutations at any one or more of the amino
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of
 CC there sequence given in ADO44072. The polypeptides of the invention are
 CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.
 CC
 SQ Sequence 248 AA;

Query Match 99.0%; Score 512; DB 8; Length 248;
 Best Local Similarity 96.9%; Pred. No. 7.1e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDPPTLHEYMLDQPEPTDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 60
 DB 1 MHGDPPTLHEYMLDQPEPTDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 60
 QY 61 CDSTLRLCVOSTHVDIRTLBDMGLGIYXPCSQKP 98
 DB 61 CDSTLRLCVOSTHVDIRTLBDMGLGIYXPCSQKP 98

RESULT 53
 AAY43480 standard; protein; 253 AA.
 XX
 AC AAY43480;
 XX
 DT 17-OCT-2003 (revised)
 DT 27-AUG-2003 (revised)
 DT 26-JAN-2000 (first entry)
 XX
 DE Amino acid sequence of a CTLA4-E7 fusion protein.
 XX
 KM CTLA4; E7; fusion protein; B7 receptor positive B cell;
 KM CTLA4 receptor positive T cell interaction; immune system; suppression;
 KM autoimmune disease; lupus erythematosus; host-graft;
 KM transplant rejection; chimera.
 XX
 OS Homo sapiens.
 OS Papillomavirus.
 OS Chimeric.
 XX
 FH Key
 FT Peptide 1..26 Location/Qualifiers
 FT /note="leader sequence"
 FT Protein 27..155
 FT /note="CTLA4 sequence"
 FT Protein 156..253
 FT /note="E7 sequence"
 XX
 PN US5968510-A.
 XX
 PD 19-OCT-1999.
 XX
 PF 04-OCT-1996; 96US-00725776.
 XX


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XX 27-JUN-1991; 91US-00723617.
PR 22-JAN-1993; 93US-00008898.
PR 15-APR-1994; 94US-00228208.
PR 18-JAN-1995; 95US-00375390.
PR 05-JUN-1995; 95US-00465078.
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX Ledbetter JA, Damle NK, Brady W, Kiener PA, Linsley PS;
XX WPI; 1999-600811/51.
XX
XX Regulating CTLA4 positive T cell interactions.
XX
XX Disclosure; Fig 37; 75pp; English.
XX
XX The present sequence represents a soluble CTLA4 fusion protein, for use
XX in the method of the invention. The specification describes a method for
XX regulating CTLA4 receptor positive T cell interactions with B7 receptor
XX positive B cells. The method comprises contacting the CTLA4-positive T
XX cells with monoclonal antibody fragments reacting with CTLA4. This
XX inhibits (and therefore regulates) interactions between CTLA4-positive T
XX cells and B7 positive B cells. The method may be used for regulating
XX CTLA4 receptor positive T cell interactions with B7 receptor positive B
XX cells. In this way the immune system of an individual can be manipulated
XX (especially lupus erythematosus) for the treatment of autoimmune diseases
XX (especially lupus erythematosus) and to prevent host-graft and transplant
XX rejection. (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-
XX OCT-2003 to standardize OS field)
XX
XX Sequence 253 AA:
XX
XX Query Match 99.0%; Score 512; DB 2; Length 253;
XX Best Local Similarity 96.9%; Pred. No. 7.3e-57;
XX Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 MHGDTPLHRYMLDLPQETTDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 60
XX 156 MHGDTPLHRYMLDLPQETTDLYCYEQNDSSSEDEIDGPAGAEPRRAHYNIVTFCK 215
XX
XX 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPCISQKP 98
XX 216 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPCISQKP 253
XX
XX
XX RESULT 54
XX ID AAY01502 standard; protein: 253 AA.
XX AC AAY01502;
XX
XX 26-MAY-1999 (first entry)
XX
XX Amino terminal CTLA4-carboxy terminal E7 fusion protein.
XX
XX CTLA4 receptor; immunoglobulin; Ig; fusion protein; B7 antigen;
XX soluble CTLA4; T cell interaction; B7 positive cell; immune disorder;
XX immune system disease; graft versus host disease; psoriasis;
XX graft transplant rejection; T cell lymphoma; benign lymphocytic angitis;
XX autoimmune disease; lupus erythematosus; Grave's disease;
XX Addison's disease; Crohn's disease; multiple sclerosis;
XX ulcerative colitis; Sjogren's syndrome; mixed connective tissue disease;
XX viral proliferation; T cell activation; AIDS; HTLV1.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX US5885579-A.
XX
XX 23-MAR-1999.
XX
XX 08-JUL-1997; 97US-00889666.

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XX 27-JUN-1991; 91US-00723617.
PR 22-JAN-1993; 93US-00008898.
PR 15-APR-1994; 94US-00228208.
PR 18-JAN-1995; 95US-00375390.
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX Damle NK, Kiener PA, Brady W, Ledbetter JA, Linsley PS;
XX WPI; 1999-228484/19.
XX
XX Human CTLA4 receptor protein - used to regulate T-cell interactions with
XX B7 positive cells.
XX
XX Disclosure; Fig 37; 75pp; English.
XX
XX The specification describes a CTLA4 receptor/immunoglobulin (Ig) fusion
XX protein which is reactive with the B7 antigen. DNA encoding the CTLA4
XX protein can be used in a vector in a host vector system for producing
XX soluble CTLA4. The CTLA4 fusion protein can be used for regulating T cell
XX interactions with B7 positive cells. The CTLA4 fusion protein can be
XX used for treating immune system diseases mediated by T cell interactions
XX with B7 positive cells. The immune system diseases include graft versus
XX host disease, psoriasis, immune disorders associated with graft
XX transplant rejection, T cell lymphoma, benign lymphocytic angitis, and
XX autoimmune diseases such as lupus erythematosus, Grave's disease,
XX Addison's disease, Crohn's disease, multiple sclerosis, ulcerative
XX colitis, Sjogren's syndrome, and mixed connective tissue disease. The
XX fusion protein may also be used to block the proliferation of viruses
XX dependent on T cell activation, such as the virus that causes AIDS,
XX HTLV1. The present sequence was created in the course of the invention
XX
XX Sequence 253 AA:
XX
XX Query Match 99.0%; Score 512; DB 2; Length 253;
XX Best Local Similarity 96.9%; Pred. No. 7.3e-57;
XX Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 MHGDTPLHRYMLDLPQETTDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 60
XX 156 MHGDTPLHRYMLDLPQETTDLYCYEQNDSSSEDEIDGPAGAEPRRAHYNIVTFCK 215
XX
XX 61 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPCISQKP 98
XX 216 CDSTLRLCVQSTHYDRTLEDLMLGTLGIYXPCISQKP 253
XX
XX
XX RESULT 55
XX ID AAW97612 standard; protein: 253 AA.
XX AC AAW97612;
XX
XX 26-MAY-1999 (first entry)
XX
XX Amino terminal CTLA4-carboxy terminal E7 fusion protein.
XX
XX CTLA4 receptor; immunoglobulin; Ig; fusion protein; B7 antigen;
XX soluble CTLA4; T cell interaction; B7 positive cell; immune disorder;
XX immune system disease; graft versus host disease; psoriasis;
XX graft transplant rejection; T cell lymphoma; benign lymphocytic angitis;
XX autoimmune disease; lupus erythematosus; Grave's disease;
XX Addison's disease; Crohn's disease; multiple sclerosis;
XX ulcerative colitis; Sjogren's syndrome; mixed connective tissue disease;
XX viral proliferation; T cell activation; AIDS; HTLV1.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX US5885796-A.
XX
XX 23-MAR-1999.

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XX 05-JUN-1995; 95US-00465078.
XX
XX 27-JUN-1991; 91US-00723617.
XX 22-JAN-1993; 93US-00008898.
XX 15-APR-1994; 94US-00228208.
XX 18-JAN-1995; 95US-00375390.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Damle NK, Brady W, Ledbetter JA, Linsley PS;
XX WPI; 1999-228535/19.
XX
XX CTLA4 receptor protein for use in treatment of immune system diseases.
XX
XX Disclousure; Fig 37; 75pp; English.
XX
XX The specification describes a CTLA4 receptor/immunoglobulin (Ig) fusion
XX protein which is reactive with the B7 antigen. DNA encoding the CTLA4
XX protein can be used in a vector in a host vector system for producing
XX soluble CTLA4. The CTLA4 fusion protein can be used for regulating T cell
XX interactions with B7 positive cells. The CTLA4Ig fusion protein can be
XX used for treating immune system diseases mediated by T cell interactions
XX with B7 positive cells. The immune system diseases include graft versus
XX host disease, psoriasis, immune disorders associated with graft
XX transplant rejection, T cell lymphoma, benign lymphocytic angitis, and
XX autoimmune diseases such as lupus erythematosus, Grave's disease,
XX Addison's disease, Crohn's disease, multiple sclerosis, ulcerative
XX colitis, Sjogren's syndrome, and mixed connective tissue disease. The
XX fusion protein may also be used to block the proliferation of viruses
XX dependent on T cell activation, such as the virus that causes AIDS,
XX HTLV1. The present sequence was created in the course of the invention
XX
XX
XX Sequence 253 AA;
XX
XX Query Match 99.0%; Score 512; DB 2; Length 253;
XX Best Local Similarity 96.9%; Pred. No. 7.3e-57;
XX Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 MHGDTPTLHEWMLDLPETTDLYXXOINDSSEEDRIDGAGQAEPRRAHYNIVTFCK 60
XX DB 156 MHGDTPTLHEWMLDLPETTDLYCYEQINDSSEEDRIDGAGQAEPRRAHYNIVTFCK 215
XX
XX QY 61 CDSTLRFCVOSTHVDIRTELDLMGTIGIVXPICQKP 98
XX DB 216 CDSTLRFCVOSTHVDIRTELDLMGTIGIVCPIQSKP 253
XX
XX RESULT 56
XX ID AAY41132 standard; protein; 253 AA.
XX AC AAY41132;
XX DT 24-JAN-2000 (first entry)
XX DE CTLA4/E7 fusion protein.
XX
XX Monoclonal antibody; Mab; extracellular domain; CTLA4; B7 antigen;
XX T cell interaction; inflammation; autoimmunity; transplantation; GCHD;
XX neoplasia; infectious disease; graft versus host disease; psoriasis;
XX immune disorder; lymphoma; leukemia; autoimmune disease; arthritis;
XX diabetes mellitus; oncostatin M; fusion protein; E7.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX US977318-A.
XX
XX 02-NOV-1999.
XX
XX 07-JUN-1995; 95US-00488062.

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XX 27-JUN-1991; 91US-00723617.
XX 22-JAN-1993; 93US-00008898.
XX 15-APR-1994; 94US-00228208.
XX 18-JAN-1995; 95US-00375390.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Kiener PA, Brady W, Damle NK, Linsley PS, Ledbetter JA;
XX WPI; 1999-619712/53.
XX
XX New anti-CTLA4 monoclonal antibodies, used for treating e.g.
XX inflammation, autoimmunity, transplant rejection, infectious diseases or
XX neoplasia.
XX
XX Example; Fig 37; 74pp; English.
XX
XX The invention provides new monoclonal antibodies (Mabs) which bind the
XX extracellular domain of CTLA4 and prevent the binding of CTLA4 to B7
XX antigen. The Mabs can be used for regulating T cell interactions with B7
XX positive cells. They can also be used for preventing or reversing
XX inflammation and for treating autoimmunity, transplantation, infectious
XX diseases and neoplasia. They can be used for treating diseases e.g. graft
XX versus host disease (GCHD), psoriasis, immune disorders associated with
XX graft transplantation rejection, T cell lymphoma, T cell acute
XX lymphoblastic leukemia, testicular angiocentric R cell lymphoma, benign
XX lymphocytic angitis, autoimmune diseases such as lupus erythematosus,
XX Hashimoto's thyroiditis, primary myxedema, Graves disease, pernicious
XX anemia, autoimmune atrophic gastritis, Addison's disease, insulin
XX dependent diabetes mellitus, Goodpasture's syndrome, myasthenia gravis,
XX pemphigus, Crohn's disease, sympathetic ophthalmia, autoimmune uveitis,
XX multiple sclerosis, autoimmune hemolytic anemia, primary biliary
XX cirrhosis, idiopathic thrombocytopenia, chronic action hepatitis,
XX ulcerative colitis, Sjogren's syndrome, rheumatoid arthritis,
XX CC polymyositis, scleroderma, and mixed connective tissue disease. They can
XX also be used for detection, diagnosis, prognosis and monitoring of
XX diseases. The present sequence represents the CTLA4/E7 fusion protein
XX containing an amino terminal CTLA4 domain and a E7 carboxy-terminal
XX domain
XX
XX
XX Sequence 253 AA;
XX
XX Query Match 99.0%; Score 512; DB 2; Length 253;
XX Best Local Similarity 96.9%; Pred. No. 7.3e-57;
XX Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 MHGDTPTLHEWMLDLPETTDLYXXOINDSSEEDRIDGAGQAEPRRAHYNIVTFCK 60
XX DB 156 MHGDTPTLHEWMLDLPETTDLYCYEQINDSSEEDRIDGAGQAEPRRAHYNIVTFCK 215
XX
XX QY 61 CDSTLRFCVOSTHVDIRTELDLMGTIGIVXPICQKP 98
XX DB 216 CDSTLRFCVOSTHVDIRTELDLMGTIGIVCPIQSKP 253
XX
XX RESULT 57
XX ID AAW81586 standard; protein; 253 AA.
XX AC AAW81586;
XX DT 05-FEB-1999 (first entry)
XX DE CTLA4/E7 fusion protein sequence.
XX
XX CTLA4 receptor; CTLA4-Ig; fusion protein; B7 antigen; hinge; CH2; CH3;
XX extracellular domain; human; immunoglobulin; T cell; immune system;
XX autoimmune disease; cancer; viral infection; E7.
XX
XX Homo sapiens.
XX
XX Human papillomavirus.
XX

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FH Key Location/Qualifiers
FT Peptide 1..26
FT /note= "leader sequence"
FT Protein 27..154
FT /note= "CTLA4 partial sequence"
FT Domain 27..154
FT /note= "CTLA4 amino terminal domain"
FT Protein 155..253
FT /note= "E7 partial sequence"
FT Domain 155..253
FT /note= "E7 carboxy terminal domain"
XX
XX US5844095-A.
XX
XX 01-DEC-1998.
XX
XX 18-JAN-1995; 95US-00375390.
XX
XX 27-JUN-1991; 91US-00723617.
XX 22-JAN-1993; 93US-00008898.
XX 28-MAY-1993; 93US-00069693.
XX 15-APR-1994; 94US-00228208.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Brady W, Linsley PS, Dample NK, Ledbetter JA;
XX WPI; 1999-044666/04.
XX
XX Fusion protein of CTLA4 and immunoglobulin fragment - for treating immune
XX system disorders.
XX
XX Example 8; Fig 37; 75pp; English.
XX
XX This represents a CTLA4/E7 fusion protein. The invention provides a CTLA4
XX -Ig fusion protein that binds the B7 antigen and has a first amino acid
XX sequence consisting of the extracellular domain of CTLA4 and a second
XX amino acid sequence consisting of the hinge, CH2 and CH3 regions of a
XX human immunoglobulin molecule. The fusion protein inhibits interaction of
XX T cells with B7-positive cells and may be useful for treating immune
XX system diseases, e.g. autoimmune diseases, cancer or viral infections.
XX The present sequence is an example of such a fusion protein and contains
XX an amino-terminal CTLA4 domain and an E7 carboxy-terminal domain
XX
XX Sequence 253 AA:
SQ
Query Match 99.0%; Score 512; DB 2; Length 253;
Best Local Similarity 96.9%; Pred. No. 7.3e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPTLHRYMDLQPEETDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
DB 156 MHGDTPTLHRYMDLQPEETDLYCYEQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 215
QY 61 CDSTLRLCVOSTHYDITRLDLMGTIGIYPCISQKP 98
DB 216 CDSTLRLCVOSTHYDITRLDLMGTIGIYPCISQKP 253

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OS Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..15
XX /note= "signal peptide"
XX Protein 16..155
XX /note= "CTLA4 protein"
XX Protein 155..253
XX /note= "E7 protein"
XX
XX US5851795-A.
XX
XX 22-DEC-1998.
XX
XX 02-JUN-1995; 95US-00459818.
XX
XX 27-JUN-1991; 91US-00723617.
XX 22-JAN-1993; 93US-00008898.
XX 15-APR-1994; 94US-00228208.
XX 18-JAN-1995; 95US-00375390.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Ledbetter JA, Brady W, Dample NK, Kiener PA, Linsley PS;
XX WPI; 1999-080402/07.
XX
XX Soluble CTLA4 protein that binds B7 antigen of activated B cells - and
XX fusion proteins useful for regulating T-cell interactions with B cells.
XX
XX Claim 18; Fig 37; 75pp; English.
XX
XX The present sequence represents a CTLA4-E7 fusion protein. CTLA4 is a
XX receptor protein having a high degree of homology with CD28. The CTLA4
XX receptor is identified as a ligand for the B7 antigen. The CTLA4 protein
XX can also be used to construct a fusion protein of CTLA4 and human
XX immunoglobulin (Ig-gamma1). The CTLA4 protein was fused to the hinge CH2
XX and CH3 regions of human IgG-gamma1. Soluble CTLA4-Ig fusion proteins can
XX be used to regulate T-cell interactions with B7-positive cells and to
XX treat immune system diseases mediated by such interactions
XX
XX Sequence 253 AA:
SQ
Query Match 99.0%; Score 512; DB 2; Length 253;
Best Local Similarity 96.9%; Pred. No. 7.3e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPTLHRYMDLQPEETDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
DB 156 MHGDTPTLHRYMDLQPEETDLYCYEQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 215
QY 61 CDSTLRLCVOSTHYDITRLDLMGTIGIYPCISQKP 98
DB 216 CDSTLRLCVOSTHYDITRLDLMGTIGIYPCISQKP 253

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RESULT 58
AAW87562
ID AAW87562 standard; protein; 253 AA.
XX
XX AAW87562;
XX
XX 01-MAR-1999 (first entry)
XX
XX CTLA4-E7 fusion protein.
XX
XX CD28; B7; fusion protein; hinge CH2; CH3; human IgG-gamma1; CTLA4;
XX CTLA4 receptor; ligand; regulation; T-cell interaction; B7-positive cell;
XX immune system disease.
XX
XX

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RESULT 59
ADRA7005
ID ADRA7005 standard; protein; 256 AA.
XX
XX ADRA7005;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human papillomavirus type 16 E7 protein for Dengue virus vaccine.
XX
XX cytostatic; virucide; dengue virus; recombinant replicon; deletion;
XX piem protein; C protein; NS1 protein signal; vaccine; cervical cancer;
XX viral disease; antigen; dendritic cell; immune response;
XX human papillomavirus.
XX
XX Human papillomavirus type 16.
XX

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XX      WO2004072274-A1.
PN      26-AUG-2004.
XX      30-JAN-2004; 2004WO-CN000088.
XX      30-JAN-2003; 2003CN-00115272.
XX      30-JAN-2003; 2003CN-00115273.
XX      (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
XX      (TENG-) TENGGEN BIOMEDICAL CO.
XX      (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX      Pang X;
XX      WPI; 2004-625870/60.
XX      N-PSDB; ADRA7004.
XX      Virus-like particle vaccines containing dengue virus recombinant replicon
PT      as core for carrier, applicable in preventives or/and remedies for tumors
PT      like cervical cancer and viral diseases.
XX      Example 2; SEQ ID NO 2; 38bp; Chinese.
XX      A dengue virus recombinant replicon has a deletion of the complete coding
CC      sequence for prem protein of dengue virus and also includes elements of
CC      e.g. the non-coding region in the whole of the 5'-end, the coding region
CC      of the front 20 amino acids in the C protein, and the coding region of
CC      NS1 protein signal; coding regions of all non-structural proteins. The
CC      obtained vaccines are useful in producing preventives or/and remedies for
CC      cancer like cervical cancer and viral diseases. Such vaccines can
CC      efficiently express antigen in infected cells, which is because dengue
CC      virus can infect dendritic cells, and can effectively present antigen to
CC      provide immunity effect. Different types of dengue virus can be used to
CC      repeatedly produce efficient immune response thereby strengthening the
CC      body's immune system against the pathogen that contains such antigen.
CC      Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC      expressing system using of the full-length dengue virus cDNA clone
CC      (pBS/FLU2). The recombinant virus vectors were transfected into baby
CC      hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC      lines. This sequence corresponds to the HPV type 16 E7 protein whose
CC      encoding gene is used as the gene of interest in the recombinant replicon
CC      of the invention.
XX      SQ      Sequence 256 AA;
XX      Query Match      99.0%; Score 512; DB 8; Length 256;
XX      Best Local Similarity 96.9%; Pred. No. 7.4e-57;
XX      Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 MHGDPPTLHEXYMLDLPETTDLYXXYXQUNDSSSEDEIDGPAGQAEPPRAHNYIVTFCK 60
AC      1 MHGDPPTLHEXYMLDLPETTDLYCYEQUNDSSSEDEIDGPAGQAEPPRAHNYIVTFCK 60
DB      1 MHGDPPTLHEXYMLDLPETTDLYCYEQUNDSSSEDEIDGPAGQAEPPRAHNYIVTFCK 60
QY      61 CDSTLRLCVOSTHVDIRTELDLMTGLGIVXPICSQKP 98
DB      61 CDSTLRLCVOSTHVDIRTELDLMTGLGIVCPICSQKP 98
XX      RESULT 60
XX      AEF40157
XX      ID      AEF40157 standard; protein; 256 AA.
XX      AC      AEF40157;
XX      DT      23-MAR-2006 (first entry)
XX      DE      Human papillomavirus 16 (HPV-16) E7-E6 oncoprotein.
XX      KW      Vaccine; virus-like particle; replicon; therapeutic; cancer; cytostatic;
XX      neoplasm; viral infection; virucide; infection; oncoprotein.
XX

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OS      Human papillomavirus type 16.
XX      US2006018928-A1.
XX      26-JAN-2006.
XX      29-JUL-2005; 2005US-00192923.
XX      30-JAN-2003; 2003CN-00115272.
XX      30-JAN-2003; 2003CN-00115273.
XX      30-JAN-2004; 2004WO-00072274.
XX      (PANG/) PANG X.
XX      Pang X;
XX      WPI; 2006-109169/11.
XX      N-PSDB; AEF40156.
XX      New recombinant DEN replicons with a deletion of prem, useful for
PT      producing a drug for the prophylaxis and treatment of cancer or viral
PT      infection.
XX      Example 2; SEQ ID NO 2; 24bp; English.
XX      The present invention provides a virus-like particle (VLP) vaccine which
CC      contains dengue virus (DEN) recombinant replicon as its core. The DEN
CC      replicon contains exogenous nucleotide sequences such as human
CC      papillomavirus (HPV) antigen proteins, immune regulators or combination
CC      of HPV antigen and immune regulators. The invention is useful for
CC      producing a drug for the prophylaxis and treatment of cancer or viral
CC      infection. The present sequence is a human papillomavirus oncoprotein.
XX      SQ      Sequence 256 AA;
XX      Query Match      99.0%; Score 512; DB 10; Length 256;
XX      Best Local Similarity 96.9%; Pred. No. 7.4e-57;
XX      Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 MHGDPPTLHEXYMLDLPETTDLYXXYXQUNDSSSEDEIDGPAGQAEPPRAHNYIVTFCK 60
DB      1 MHGDPPTLHEXYMLDLPETTDLYCYEQUNDSSSEDEIDGPAGQAEPPRAHNYIVTFCK 60
QY      61 CDSTLRLCVOSTHVDIRTELDLMTGLGIVXPICSQKP 98
DB      61 CDSTLRLCVOSTHVDIRTELDLMTGLGIVCPICSQKP 98
XX      RESULT 61
XX      AAR97561
XX      ID      AAR97561 standard; protein; 266 AA.
XX      AC      AAR97561;
XX      DT      27-AUG-2003 (revised)
XX      DT      11-JAN-1997 (first entry)
XX      DE      Human papilloma virus E6/E7 protein variant.
XX      DE      Human papilloma virus E6/E7 protein variant.
XX      KW      Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;
XX      humoral immune response; cellular immune response; vaccine.
XX      OS      Human papillomavirus.
XX      PN      WO9619496-A1.
XX      PD      27-JUN-1996.
XX      PF      20-DEC-1995; 95WO-AU000868.
XX      PR      20-DEC-1994; 94AU-00000157.
XX      PA      (CSLC-) CSL LTD.

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PA (UYOU) UNIV QUEENSLAND.
 XX Edwards SJ, Cox J, Webb EA, Frazer I;
 PT WPI; 1996-309518/31.
 DR N-PSDB; AAT31833.
 XX
 PT Vaccine variants of human papilloma virus antigens - contain variants of
 PT E6 and/or E7 protein, pref. deletion mutants, and are used to treat or
 PT prevent HPV infection.
 XX
 PS Example 1; Page 15-16; 37pp; English.
 XX
 CC A variant of the human papilloma virus (HPV) E6 or E7 protein which
 CC elicits a humoral and/or cellular immune response against HPV can be used
 CC in vaccines against HPV or to treat HPV infection. The variant is
 CC preferably a deletion mutant comprising at least half, and preferably two
 CC thirds of full length E6 or E7 protein starting from the N- or C-
 CC terminal, or is a full length E6 moiety fused to a full length E7 moiety.
 CC The variant optionally has a linkage moiety and a foreign protein or
 CC peptide which facilitates the purification of, and enhances the
 CC immunogenicity of, the fusion protein. This sequence is a full length
 CC E6/E7 fusion protein. (Updated on 27-AUG-2003 to correct OS field.)
 CC
 XX Sequence 266 AA:
 SQ
 Query Match 99.0%; Score 512; DB 2; Length 266;
 Best Local Similarity 96.9%; Pred. No. 7.8e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPLHXYMLDLPETTDLYXXOLNDSSEEDRIDPAGAEPRAHYNIIVTFCK 60
 DB 161 MHGDTPLHXYMLDLPETTDLYCYEQLNDSSEEDRIDPAGAEPRAHYNIIVTFCK 220
 QY 61 CDSTLRLCVQSTHVDIRTLBDMGTIGIYXPICQKP 98
 DB 221 CDSTLRLCVQSTHVDIRTLBDMGTIGIYXPICQKP 258
 RESULT 62
 AAU02129
 ID AAU02129 standard; protein; 288 AA.
 XX
 AC AAU02129;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Flt-3 ligand (FL) used to make chimeric immunogenic polypeptide.
 XX
 KW Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF;
 KW chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotoxin A; ETA dII;
 KW antigenic; immunogenic; cytotoxic T cell response; tumour; vaccine;
 KW immunotherapy.
 XX
 OS Unidentified.
 XX
 FN WO200129233-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 20-OCT-2000; 2000WO-US041422.
 XX
 PR 20-OCT-1999; 99US-00421608.
 XX
 PR 09-FEB-2000; 2000US-00501097.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Wu T, Hung C;
 XX
 DR WPI; 2001-290921/30.
 XX
 PT New chimeric polypeptide, useful as anti-tumor vaccines, comprises
 PT carboxy terminal fragment of heat shock protein, Flt-3 ligand or

PT cytoplasmic translocation domain of Pseudomonas exotoxin A and antigenic
 PT polypeptide.
 XX
 XX Claim 9; Fig 19; 110pp; English.
 XX
 CC The sequence represents the amino acid sequence of Flt-3 ligand (FL) used
 CC in construction of a chimeric polypeptide comprising: (a) a first
 CC polypeptide domain containing a carboxy terminal fragment of a heat shock
 CC protein (HSP), an Flt-3 ligand (FL), a cytoplasmic translocation domain
 CC of a Pseudomonas exotoxin A (ETA dII), or a granulocyte-macrophage
 CC stimulating factor (GM-CSF); and (b) a second polypeptide domain
 CC containing an antigenic polypeptide. A composition comprising the
 CC chimeric polypeptide is useful for inducing an immune response such as a
 CC cytotoxic T cell response. The nucleic acid or vector encoding the
 CC chimeric polypeptide present in the composition is administered as naked
 CC DNA by gene gun or equivalent, or by liposomal formulation. These are
 CC thus useful for vaccinating a mammal against infection by inducing an
 CC immune response to a pathogen. Preferably they are useful for vaccinating
 CC a mammal against a tumour antigen. The compositions and methods are
 CC useful for stimulating or enhancing the immunogenicity of a selected
 CC antigen or stimulating or enhancing a cellular immune response specific
 CC for that antigen. The chimeric nucleic acid molecules and vaccination
 CC methods, yield potent antigen-specific immunotherapy. The polynucleotides
 CC and DNA vaccines can induce a cellular immune response that is at least
 CC 40 fold more potent than conventional DNA vaccines. The vaccines are safe
 CC and useful for administration to domesticated or agricultural animals, as
 CC well as humans, and have low immunogenicity
 CC
 XX Sequence 288 AA:
 SQ
 Query Match 99.0%; Score 512; DB 4; Length 288;
 Best Local Similarity 96.9%; Pred. No. 8.7e-57;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPLHXYMLDLPETTDLYXXOLNDSSEEDRIDPAGAEPRAHYNIIVTFCK 60
 DB 190 MHGDTPLHXYMLDLPETTDLYCYEQLNDSSEEDRIDPAGAEPRAHYNIIVTFCK 249
 QY 61 CDSTLRLCVQSTHVDIRTLBDMGTIGIYXPICQKP 98
 DB 250 CDSTLRLCVQSTHVDIRTLBDMGTIGIYXPICQKP 287
 RESULT 63
 AAB31615
 ID AAB31615 standard; protein; 295 AA.
 XX
 AC AAB31615;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Amino acid sequence of Hsp65-E7 fusion protein.
 XX
 KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
 KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
 KW E7 protein.
 XX
 OS Synthetic.
 OS Mycobacterium bovis.
 OS Human papillomavirus.
 XX
 FN WO200104344-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 10-JUL-2000; 2000WO-US018828.
 XX
 PR 08-JUL-1999; 99US-0143757P.
 XX
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 XX
 PI Siegel M, Chu NR, Mitzzen LA;
 XX

DR WPI: 2001-138361/14.
DR N-PSDB: AAF25022.
XX Screening for compounds that stimulate Th1-like responses in CD4+ T
PT lymphocyte cells.
XX
PS Example 12; Fig 11; 88pp; English.
XX
CC The present sequence represents a fusion protein comprising Mycobacterium
CC bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7
CC protein. The fusion protein is used in the method of the invention. The
CC specification describes a method of determining whether a compound
CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
CC lymphocyte cells. The method comprises contacting naive lymphocytes in
CC vitro with a fusion protein comprising at least a fragment of Hsp, and
CC then detecting the Th1-like response exhibited by the cell sample. The
CC proteins which may be used in the method of the invention are Hsp65,
CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
CC compounds that stimulate Th1-like responses in response to microbial
CC pathogens
XX
SQ Sequence 295 AA;
Query Match 99.0%; Score 512; DB 4; Length 295;
Best Local Similarity 96.9%; Pred. No. 8.9e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEEDIDGPAQAEPDRAHYNIVTFCK 60
DB 198 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEEDIDGPAQAEPDRAHYNIVTFCK 257
OY 61 CDSTLRFCVOSTHYDIRTLEDLMGTGIGVXPICSQKP 98
DB 258 CDSTLRFCVOSTHYDIRTLEDLMGTGIGVXPICSQKP 295
RESULT 64
ID AAB31613 standard; protein; 324 AA.
XX
AC AAB31613;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of glutathion-S-transferase (GST) -E7 protein.
XX
KM Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
KM glutathion-S-transferase; GST; E7 protein.
XX
XX Synthetic.
OS Human papillomavirus.
OS Unidentified.
XX
XX MO200104344-A2.
XX
XX 18-JAN-2001.
XX
XX 10-JUL-2000; 2000WO-US018828.
XX
XX 08-JUL-1999; 99US-0143757P.
XX
PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
PI Siegel M, Chu NR, Mizzzen LA;
XX
XX WPI: 2001-138361/14.
DR N-PSDB: AAF25016.
XX
XX Screening for compounds that stimulate Th1-like responses in CD4+ T
PT lymphocyte cells.
XX
PS Example 10; Fig 9; 88pp; English.

XX
CC The present sequence represents a glutathion-S-transferase (GST) linked
CC to HPV16 E7 protein, for purification purposes. The E7 protein was used
CC to construct a fusion protein with Mycobacterium bovis heat shock
CC proteins (Hsp). The fusion proteins are used in the method of the
CC invention. The specification describes a method of determining whether a
CC compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
CC lymphocyte cells. The method comprises contacting naive lymphocytes in
CC vitro with a fusion protein comprising at least a fragment of Hsp, and
CC then detecting the Th1-like response exhibited by the cell sample. The
CC proteins which may be used in the method of the invention are Hsp65,
CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
CC compounds that stimulate Th1-like responses in response to microbial
CC pathogens
XX
SQ Sequence 324 AA;
Query Match 99.0%; Score 512; DB 4; Length 324;
Best Local Similarity 96.9%; Pred. No. 1e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEEDIDGPAQAEPDRAHYNIVTFCK 60
DB 227 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEEDIDGPAQAEPDRAHYNIVTFCK 286
OY 61 CDSTLRFCVOSTHYDIRTLEDLMGTGIGVXPICSQKP 98
DB 287 CDSTLRFCVOSTHYDIRTLEDLMGTGIGVXPICSQKP 324
RESULT 65
ID AAO22926 standard; protein; 334 AA.
XX
XX AAO22926;
XX
XX 12-DEC-2002 (first entry)
XX
DE HbsAg-EB7 fusion protein sequence.
XX
KM Virucide; cyrostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;
KM fusion partner; immunogenicity; HPV infection; neoplasm; HbsAg-EB7;
KM chimeric.
XX
XX Unidentified.
OS Chimeric.
XX
XX EPI243655-A1.
XX
XX 25-SBP-2002.
XX
XX 23-MAR-2001; 2001EP-00107271.
XX
XX 23-MAR-2001; 2001EP-00107271.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Cid-Arregui A, Zur Hausen H;
XX
XX WPI: 2002-724952/79.
DR N-PSDB: AAL53424.
XX
XX A new DNA sequence encoding a fusion protein comprising a mutagenized HPV
XX (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a
XX highly immunogenic fusion partner is useful to vaccinate against HPV
XX infection.
XX
XX Dieclozure; Fig 5; 34pp; English.
XX
XX The invention relates to a new DNA sequence encodes an E6 or E7 fusion
XX protein of HPV, where at least 20% of the original codons are replaced by
XX codons which lead to enhanced translation in a mammalian cell, containing
XX a mutation which results in production of a truncated non-functional

CC protein, and encoding a highly immunogenic polypeptide fusion partner
CC capable of enhancing immunogenicity of the B6 or E7 protein in the
CC mammalian host. The invention is used as a vaccine for the prevention or
CC treatment of an HPV infection or a neoplasm associated with HPV
CC infection. This sequence represents the HbsAg-E67 fusion protein
CC sequence of the invention
XX

SO Sequence 334 AA;

Query Match 99.0%; Score 512; DB 5; Length 334;

Best Local Similarity 96.9%; Pred. No. 1e-56;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGPTPLHEMLDLOPETTDLYXXQLNDSSEEDIDGAGQAEPRRAHYNIVTFCCK 60

Db 229 MGGPTPLHEMLDLOPETTDLYCYEQLNDSSEEDIDGAGQAEPRRAHYNIVTFCCK 288

Qy 61 CDSTLRFCVOSTHVDIRTEEDLMGTGIVXPICSOXP 98

Db 289 CDSTLRFCVOSTHVDIRTEEDLMGTGIVXPICSOXP 326

RESULT 66

AEA40828

ID AEA40828 standard; protein; 349 AA.

AC AEA40828;

DT 28-JUL-2005 (first entry)

DE Anti-apoptotic vector E7-BCL-XL protein.

XX immunogenicity; immunogenicity-potentiating polypeptide; IPP; T-cell;

KM vaccine; immune stimulation; tumor; cytostatic.

XX Human Papillomavirus.

OS Synthetic.

OS Undifferentiated.

XX WO2005047501-A1.

XX 26-MAY-2005.

PF 24-FEB-2004; 2004WO-US005292.

XX 24-FEB-2003; 2003US-0449429P.

PR 18-JUL-2003; 2003US-0488527P.

PR 31-DEC-2003; 2003US-0533792P.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Wu T, Hung CF, Klm T;

XX WPI; 2005-367009/37.

DR N-PSDB; AEA40827.

XX New nucleic acid composition comprising a first nucleic acid vector

PT encoding an anti-apoptotic polypeptide and a second nucleic acid vector

PT inhibiting the growth of a tumor.

XX Dielosure; SEQ ID NO 18; 158pp; English.

XX The invention relates to a novel nucleic acid composition useful as an

CC immunogen. The composition comprises a combination of: a first nucleic

CC acid vector comprising a first sequence encoding an antigenic polypeptide

CC or peptide, and optionally, a second sequence linked to the first (IPP);

CC and a second nucleic acid vector encoding an anti-apoptotic polypeptide.

CC When the second vector is administered with the first vector to a

CC subject, a T cell mediated immune response to the antigenic polypeptide

CC or peptide is induced that is greater in magnitude and/or duration than

CC an immune response induced by administration of the first vector alone.

CC The invention further includes: a particle comprising a material that is
CC suitable for introduction into a cell or an animal by particle
CC bombardment, bound to which is the first and second vectors or
CC composition; a pharmaceutical composition capable of inducing or
CC enhancing an antigen specific immune response, comprising the particle
CC and a carrier or an excipient; inducing or enhancing an antigen specific
CC immune response in a subject; increasing the numbers of CD8+ CTLs
CC specific for a selected desired antigen in a subject; and inhibiting the
CC growth of a tumor in a subject. The nucleic acid composition is useful as
CC an immunogen for inhibiting the growth of a tumor, hence it has
CC cytostatic activity. This sequence represents an anti-apoptotic vector E7-
CC BCL-XL protein of the invention.

SO Sequence 349 AA;

Query Match 99.0%; Score 512; DB 9; Length 349;

Best Local Similarity 96.9%; Pred. No. 1.e-56;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGPTPLHEMLDLOPETTDLYXXQLNDSSEEDIDGAGQAEPRRAHYNIVTFCCK 60

Db 1 MGGPTPLHEMLDLOPETTDLYCYEQLNDSSEEDIDGAGQAEPRRAHYNIVTFCCK 60

Qy 61 CDSTLRFCVOSTHVDIRTEEDLMGTGIVXPICSOXP 98

Db 61 CDSTLRFCVOSTHVDIRTEEDLMGTGIVXPICSOXP 98

RESULT 67

AEA40831

ID AEA40831 standard; protein; 349 AA.

AC AEA40831;

DT 28-JUL-2005 (first entry)

DE Anti-apoptotic vector E7-mtBCL-XL fusion protein.

XX immunogenicity; immunogenicity-potentiating polypeptide; IPP; T-cell;

KM vaccine; immune stimulation; tumor; cytostatic.

XX Human Papillomavirus.

OS Synthetic.

OS Undifferentiated.

XX WO2005047501-A1.

XX 26-MAY-2005.

PF 24-FEB-2004; 2004WO-US005292.

XX 24-FEB-2003; 2003US-0449429P.

PR 18-JUL-2003; 2003US-0488527P.

PR 31-DEC-2003; 2003US-0533792P.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Wu T, Hung CF, Klm T;

XX WPI; 2005-367009/37.

XX New nucleic acid composition comprising a first nucleic acid vector

PT encoding an anti-apoptotic polypeptide and a second nucleic acid vector

PT inhibiting the growth of a tumor.

XX Dielosure; SEQ ID NO 21; 158pp; English.

XX The invention relates to a novel nucleic acid composition useful as an

CC immunogen. The composition comprises a combination of: a first nucleic

CC acid vector comprising a first sequence encoding an antigenic polypeptide

CC or peptide, and optionally, a second sequence linked to the first

CC sequence and encoding an immunogenicity-potentiating polypeptide (IPP);

QY 1 MHGDTPTLHEHYMDLQEPETDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
 DB 265 MHGDTPTLHEHYMDLQEPETDLYCYEQNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 324
 QY 61 CDSTLRLCVOSTHVDIRLTEDLDMGTGIVXPICSOXP 98
 DB 325 CDSTLRLCVOSTHVDIRLTEDLDMGTGIVXPICSOXP 362

RESULT 70

AED52638
 ID AED52638 standard; protein: 371 AA.

AC AED52638;

DT 29-DEC-2005 (first entry)

DE Fusion protein D1/3-E6-E7-His/HPV16.

KM Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;

OS virucide; uterine cervix tumor; E7; D protein.

OS Haemophilus influenzae; strain 772.

OS Synthetic.

OS Chimeric.

PN IN9801903-14.

PD 04-MAR-2005.

PP 24-AUG-1998; 98IN-CH001903.

PR 22-AUG-1997; 97EP-00179535.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Tyrell AMR;

DR WPI; 2005-557648/57.

DR N-PSDB; AED52637.

XX Vaccine.

XX Example 6; Fig 6; 96pp; English.

XX The invention relates to human Papilloma virus (HPV) fusion proteins, CC linked to an immunological fusion partner that provides T helper epitopes CC to the HPV antigen. Vaccine formulations comprising the fusion proteins CC are useful in the treatment or prophylaxis of HPV induced lesions CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either CC Haemophilus influenzae D protein (20-127), the C-terminus of CC Streptococcus pneumoniae Lyta protein (cLYTA) or thioridoxin. The present CC sequence represents an HPV-H. influenzae D protein, fusion protein of the CC invention.

XX Sequence 371 AA;

Query Match 99.0%; Score 512; DB 9; Length 371;
 Best Local Similarity 96.9%; Pred. No. 1.2e-56;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEHYMDLQEPETDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
 DB 265 MHGDTPTLHEHYMDLQEPETDLYCYEQNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 324
 QY 61 CDSTLRLCVOSTHVDIRLTEDLDMGTGIVXPICSOXP 98
 DB 325 CDSTLRLCVOSTHVDIRLTEDLDMGTGIVXPICSOXP 362

RESULT 71

AAV25381
 ID AAV25381 standard; protein: 390 AA.

AC AAV25381;

DT 06-SEP-1999 (first entry)

DE HPV fusion protein CLYTA-E6E7-His/HPV16.

XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;

KM immunological fusion partner; CpG oligonucleotide; immune response;

KW HPV antigen; prevention; treatment.

XX Synthetic.

OS Human papillomavirus.

PN WO9933868-A2.

PD 08-JUL-1999.

PP 18-DEC-1998; 98WO-EP008563.

PR 24-DEC-1997; 97GB-00027262.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Dalemans WLJ, Gerard CMG;

DR WPI; 1999-405485/34.

DR N-PSDB; AAX78797.

XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to

PT induce immune response to HPV.

XX Example VIII; Page 55-56; 62pp; English.

XX AA78791-X78801 represent nucleic acid sequences which encode novel CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from CC HPV (represented in AAV25375-125386). These constructs are optionally CC linked to an immunological fusion partner and an immunomodulatory CpG CC oligonucleotide. The products of the invention can be used to induce an CC immune response in a patient to an HPV antigen. They can also be used for CC preventing or treating HPV induced tumours

XX Sequence 390 AA;

Query Match 99.0%; Score 512; DB 2; Length 390;
 Best Local Similarity 96.9%; Pred. No. 1.3e-56;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEHYMDLQEPETDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
 DB 284 MHGDTPTLHEHYMDLQEPETDLYCYEQNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 343
 QY 61 CDSTLRLCVOSTHVDIRLTEDLDMGTGIVXPICSOXP 98
 DB 344 CDSTLRLCVOSTHVDIRLTEDLDMGTGIVXPICSOXP 381

RESULT 72

AAV02637
 ID AAV02637 standard; protein: 390 AA.

AC AAV02637;

DT 17-OCT-2003 (revised)

DT 22-JUN-1999 (first entry)

DE CLYTA-E6E7-His protein.

KW Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;

XX lesion; benign; malignant; virus; infection.

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XX OS Human Papillomavirus.
XX OS Streptococcus pneumoniae.
XX OS Chimeric.
XX PN MO9910375-A2.
XX PD 04-MAR-1999.
XX PF 17-AUG-1998; 98WO-EP005285.
XX PR 22-AUG-1997; 97GB-00017953.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Bruck C, Cabezon Silva T, Delisse ABF, Gerard CMG,
XX P1 Lombardo-Benichalk A;
XX DR WPI; 1999-190587/16.
XX DR N-PSDB; AAX29786.
XX PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX treatment or prophylaxis of HPV induced lesions.
XX PS Disclosure: Fig 14; 95pp; English.
XX CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
XX CC protein from Human papillomavirus (HPV) linked to an immunological fusion
XX CC partner, in this case, a fragment of the Streptococcus pneumoniae CLYTA
XX CC protein of the encoded protein. The protein can be used in a vaccine, for
XX CC immuno-therapeutically treating HPV induced tumour lesions (benign or
XX CC malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 390 AA;

Query Match 99.0%; Score 512; DB 2; Length 390;
Best Local Similarity 96.9%; Pred. No. 1.3e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEEDSIDGPAQAEPDRAHNYITFCCK 60
DB 284 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEEDSIDGPAQAEPDRAHNYITFCCK 343
QY 61 CDSTLRLCVOSTHVDIRTLBDMGTIGIVXPICSOXP 98
DB 344 CDSTLRLCVOSTHVDIRTLBDMGTIGIVCPICSOXP 381

RESULT 73
AED52646
ID AED52646 standard; protein; 390 AA.
XX AC AED52646;
XX DT 29-DEC-2005 (first entry)
XX DE Fusion protein clytA-E6-E7-His/HPV16.
XX KM Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
XX KW virucide; uterine cervix tumor; E7; LytA.
XX OS Streptococcus pneumoniae.
XX OS Human Papillomavirus type 16.
XX OS Synthetic.
XX OS Chimeric.
XX PN IN9801903-14.
XX PD 04-MAR-2005.
XX PF 24-AUG-1998; 98IN-CH001903.
XX

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PR 22-AUG-1997; 97EP-00179535.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Tyrell AMR;
XX DR WPI; 2005-557648/57.
XX DR N-PSDB; AED52645.
XX PF Vaccine.
XX PS Example 12; Fig 14; 96pp; English.
XX CC The invention relates to human Papilloma virus (HPV) fusion proteins,
XX CC linked to an immunological fusion partner that provides T helper epitopes
XX CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
XX CC are useful in the treatment or prophylaxis of HPV induced lesions
XX CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
XX CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
XX CC Haemophilus influenzae D protein (20-127), the C-terminus of
XX CC Streptococcus pneumoniae LytA protein (clytA) or thioredoxin. The present
XX CC sequence represents an HPV-LytA, fusion protein of the invention.
XX SQ Sequence 390 AA;

Query Match 99.0%; Score 512; DB 9; Length 390;
Best Local Similarity 96.9%; Pred. No. 1.3e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEEDSIDGPAQAEPDRAHNYITFCCK 60
DB 284 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEEDSIDGPAQAEPDRAHNYITFCCK 343
QY 61 CDSTLRLCVOSTHVDIRTLBDMGTIGIVXPICSOXP 98
DB 344 CDSTLRLCVOSTHVDIRTLBDMGTIGIVCPICSOXP 381

RESULT 74
AAM50663
ID AAM50663 standard; protein; 421 AA.
XX AC AAM50663;
XX DT 29-AUG-2003 (revised)
XX DT 08-APR-2002 (first entry)
XX DE Thioredoxin-ubiquitin-ProteinD1/3 E7-His triple fusion protein.
XX KM Thioredoxin; ubiquitin; proteinD1/3 E7; tumour; antigen; cancer; vaccine;
XX KW therapy; human.
XX OS Homo sapiens.
XX OS Escherichia coli.
XX OS Chimeric.
XX FH Key
XX FT 1..109 Location/Qualifiers
XX FT /label= Thioredoxin
XX FT /label= Ubiquitin
XX FT /label= linker
XX FT 126..199
XX FT /label= Ubiquitin
XX FT 201..202
XX FT Cleavage-site
XX FT /label= UbP1_cleavage_site
XX FT Protein
XX FT 203..412
XX FT /label= ProteinD1/3-E7
XX FT 413..421
XX FT Peptide
XX FT /label= Histidine_tail
XX PN MO200200892-A1.
XX PD 03-JAN-2002.
XX

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XX PF 19-JUN-2001; 2001WO-EP006952.
XX PR 26-JUN-2000; 2000GB-00015619.
XX PR 30-OCT-2000; 2000GB-00026484.
XX XX
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Cabezón Silva TEV, Delisse AEF;
XX DR WPI; 2002-147888/19.
XX DR N-PSDB; ABA91285.
XX PT Novel DNA sequence encoding triple fusion protein comprising ubiquitin
XX PT fused between thiorodoxin and polypeptide of interest, useful for
XX PT producing recombinant polypeptide of interest suitable for medicinal use.
XX PS Example 12; Fig 19a; 87pp; English.
XX CC The present sequence is that of a triple fusion protein comprising, from
XX CC the N-terminal end, Escherichia coli thiorodoxin, human ubiquitin and
XX CC human papillomavirus Protein1/3 E7, followed by a histidine affinity
XX CC tail. The triple fusion protein was produced in E. coli G1724 host cells
XX CC transformed by an expression vector comprising DNA (see ABA91285)
XX CC encoding the fusion. This is an example of the production of triple
XX CC fusion proteins of the invention that comprise ubiquitin fused between
XX CC thiorodoxin and a protein of interest, in this case Protein1/3 E7. A
XX CC claimed method of producing a recombinant protein of interest involves:
XX CC culturing a host cell (preferably E. coli) under conditions which allow
XX CC co-expression of the triple fusion and a ubiquitin-specific endoprotease
XX CC (especially UBP1 from Saccharomyces cerevisiae); and recovering the
XX CC recombinant protein directly from the bacterial cells after it has been
XX CC subjected to the action of the ubiquitin-specific endoprotease in vivo.
XX CC In the present case, expression is controlled by the addition of
XX CC tryptophan. The recombinant protein can be used as a vaccine for cancer
XX CC therapy. (Updated on 29-AUG-2003 to standardise OS field)
XX SQ
SQ Sequence 421 AA;
Query Match 99.0%; Score 512; DB 5; Length 421;
Best Local Similarity 96.9%; Pred. No. 1.4e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDPPTLHEHYMDLOPBTDDLYXXYXQNDSSSEEDIDPAGQAEPRRAHYNIIVTFCK 60
DB 315 MHGDPPTLHEHYMDLOPBTDDLYCYEQNDSSSEEDIDPAGQAEPRRAHYNIIVTFCK 374
QY 61 CDSTLRLCVOSTHYDRTLEDLMGTIGIYXPICQKP 98
DB 375 CDSTLRLCVOSTHYDRTLEDLMGTIGIYCPICQKP 412
RESULT 75
AAB31610
ID AAB31610 standard; protein; 493 AA.
XX AC AAB31610;
XX DT 30-APR-2001 (first entry)
XX DE Amino acid sequence of Hsp40-E7 fusion protein.
XX KM Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
XX KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
XX KM E7 protein.
XX OS Synthetic.
XX OS Mycobacterium tuberculosis.
XX OS Human papillomavirus.
XX PN WO200104344-A2.
XX PD 18-JAN-2001.

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XX PF 10-JUL-2000; 2000WO-US018828.
XX PR 08-JUL-1999; 99US-0143757P.
XX XX
XX PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX PI Siegel M, Chu NR, Mäzen LA;
XX DR WPI; 2001-138361/14.
XX DR N-PSDB; AAF25013.
XX PT Screening for compounds that stimulate Th1-like responses in CD4+ T
XX PT lymphocyte cells.
XX PS Example 6; Fig 5A-B; 88pp; English.
XX CC The present sequence represents a fusion protein comprising a
XX CC Mycobacterium tuberculosis heat shock protein (Hsp) 40 fused at its 3'
XX CC end to a Hsp16 E7 protein. The fusion protein is used in the method of
XX CC the invention. The specification describes a method of determining
XX CC whether a compound stimulates a Th1-like response. Th1 cells are a subset
XX CC of CD4+ T lymphocyte cells. The method comprises contacting native
XX CC lymphocytes in vitro with a fusion protein comprising at least a fragment
XX CC of Hsp, and then detecting the Th1-like response exhibited by the cell
XX CC sample. The proteins which may be used in the method of the invention are
XX CC Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
XX CC compounds that stimulate Th1-like responses in response to microbial
XX CC pathogens
XX SQ
SQ Sequence 493 AA;
Query Match 99.0%; Score 512; DB 4; Length 493;
Best Local Similarity 96.9%; Pred. No. 1.7e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDPPTLHEHYMDLOPBTDDLYXXYXQNDSSSEEDIDPAGQAEPRRAHYNIIVTFCK 60
DB 396 MHGDPPTLHEHYMDLOPBTDDLYCYEQNDSSSEEDIDPAGQAEPRRAHYNIIVTFCK 455
QY 61 CDSTLRLCVOSTHYDRTLEDLMGTIGIYXPICQKP 98
DB 456 CDSTLRLCVOSTHYDRTLEDLMGTIGIYCPICQKP 493
RESULT 76
AAB03790
ID AAB03790 standard; protein; 638 AA.
XX AC AAB03790;
XX DT 12-SEP-2003 (revised)
XX DT 06-AUG-2003 (revised)
XX DT 13-OCT-2000 (first entry)
XX DE Heat shock protein and tumour specific antigen fusion protein sequence.
XX KM Heat shock protein; tumour specific antigen; colibacillus; microzyme;
XX KM plant; immune response; tumour; cancer; human papillomavirus;
XX KM pointed condyloma.
XX OS Mycobacterium bovis.
XX OS Human papillomavirus.
XX OS Chimeric.
XX PN CN1248631-A.
XX PD 29-MAR-2000.
XX PF 24-SEP-1998; 98CN-00112264.
XX PR 24-SEP-1998; 98CN-00112264.
XX PD 24-SEP-1998; 98CN-00112264.

```

PA (ZHOU/) ZHOU G.
 XX
 PI Zhou G;
 XX
 DR WPI: 2000-431995/38.
 XX
 PT New fusion protein for immunotherapy of venereal disease and cancer - is
 XX a heat shock protein of Mycobacterium bovis.
 PS Claim 9; Fig 1; 5pp; Chinese.
 XX
 CC The present sequence represents a fusion protein, consisting of a heat
 CC shock protein of mycobacterium bovis (var. BCG) fused to a tumour
 CC specific antigen of human papillomavirus (HPV). The fusion protein can be
 CC expressed in colibacillus, microzymes and plants. The fusion protein is
 CC used to make immunostimulant injections, as it can produce specific cell
 CC immune and humoral immune responses. It possesses prophylaxis and
 CC therapeutic capacity for preventing human papillomavirus (HPV) infection,
 CC but also can be used for immunotherapy of pointed condyloma, tumours and
 CC cancer caused by HPV. (Updated on 06-AUG-2003 to correct OS field.)
 CC (Updated on 12-SEP-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 638 AA;
 Query Match 99.0%; Score 512; DB 3; Length 638;
 Best Local Similarity 96.9%; Pred. No. 2.4e-56;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGPTLHEVMDLPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60
 DB 541 MHGPTLHEVMDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 600
 QY 61 CDSTLRLCVOSTHVDIRTLIEDLMGTGIVXPICSQKP 98
 DB 601 CDSTLRLCVOSTHVDIRTLIEDLMGTGIVCPICSQKP 638
 RESULT 77
 AAB31609
 ID AAB31609 standard; protein; 639 AA.
 AC AAB31609;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Amino acid sequence of Hsp65-E7 fusion protein.
 XX
 KM Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
 KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
 KM E7 protein.
 XX
 OS Synthetic.
 OS Mycobacterium bovis.
 OS Human papillomavirus.
 XX
 PN WO200104344-A2.
 PD 18-JAN-2001.
 XX
 PF 10-JUL-2000; 2000WO-US018828.
 XX
 PR 08-JUL-1999; 99US-0143757P.
 XX
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 XX
 PI Siegel M, Chu NR, Mizzen LA;
 XX
 DR WPI: 2001-138361/14.
 DR N-PSDB; AAF25012.
 XX
 PT Screening for compounds that stimulate Th1-like responses in CD4+ T
 PT lymphocyte cells.
 XX

PS Example 5; Fig 4A-B; 8pp; English.
 XX
 CC The present sequence represents a fusion protein comprising a
 CC Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal
 CC to a HPV16 E7 protein. The fusion protein is used in the method of the
 CC invention. The specification describes a method of determining whether a
 CC compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
 CC lymphocyte cells. The method comprises contacting native lymphocytes in
 CC vitro with a fusion protein comprising at least a fragment of Hsp, and
 CC then detecting the Th1-like response exhibited by the cell sample. The
 CC proteins which may be used in the method of the invention are Hsp65,
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
 CC compounds that stimulate Th1-like responses in response to microbial
 CC pathogens
 CC
 XX
 SQ Sequence 639 AA;
 Query Match 99.0%; Score 512; DB 4; Length 639;
 Best Local Similarity 96.9%; Pred. No. 2.4e-56;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGPTLHEVMDLPETTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 60
 DB 542 MHGPTLHEVMDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPRAHYNIYTFCK 601
 QY 61 CDSTLRLCVOSTHVDIRTLIEDLMGTGIVXPICSQKP 98
 DB 602 CDSTLRLCVOSTHVDIRTLIEDLMGTGIVCPICSQKP 639
 RESULT 78
 AAB31619
 ID AAB31619 standard; protein; 641 AA.
 AC AAB31619;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Amino acid sequence of Hsp65-E7 fusion protein.
 XX
 KM Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
 KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
 KM E7 protein.
 XX
 OS Synthetic.
 OS Streptococcus pneumoniae.
 OS Human papillomavirus.
 XX
 PN WO200104344-A2.
 PD 18-JAN-2001.
 XX
 PF 10-JUL-2000; 2000WO-US018828.
 XX
 PR 08-JUL-1999; 99US-0143757P.
 XX
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 XX
 PI Siegel M, Chu NR, Mizzen LA;
 XX
 DR WPI: 2001-138361/14.
 DR N-PSDB; AAF25036.
 XX
 PT Screening for compounds that stimulate Th1-like responses in CD4+ T
 PT lymphocyte cells.
 XX
 PS Example 15; Fig 15A-B; 8pp; English.
 XX
 CC The present sequence represents a fusion protein comprising a
 CC Streptococcus pneumoniae heat shock protein (Hsp) 65 fused to a HPV16 E7
 CC protein. The fusion protein is used in the method of the invention. The
 CC specification describes a method of determining whether a compound
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T

CC lymphocyte cells. The method comprises contacting naive lymphocytes in
CC vitro with a fusion protein comprising at least a fragment of Hsp, and
CC then detecting the Th1-like response exhibited by the cell sample. The
CC proteins which may be used in the method of the invention are Hsp65,
CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
CC compounds that stimulate Th1-like responses in response to microbial
CC pathogens
CC
SQ Sequence 641 AA;
Query Match 99.0%; Score 512; DB 4; Length 641;
Best Local Similarity 96.9%; Pred. No. 2.4e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPLHEHYMDLQPEETDLYXXYQNDSSSEDEIDDPAGQAEPRAHYNIIVTFCK 60
DB 544 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDDPAGQAEPRAHYNIIVTFCK 603
QY 61 CDSTLRFCVOSTHYDIRTELDLMGTIGIYCPICSOQR 98
DB 604 CDSTLRFCVOSTHYDIRTELDLMGTIGIYCPICSOQR 641
RESULT 79
AAB31620
ID AAB31620 standard; protein: 647 AA.
XX
AC AAB31620;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of Hsp60-E7 fusion protein.
XX
KM Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
KM E7 protein.
XX
OS Synthetic.
OS Aspergillus fumigatus.
OS Human papillomavirus.
XX
PN WO200104344-A2.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-US018828.
XX
PR 08-JUL-1999; 99US-0143757P.
XX
PS (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
PI Siegel M, Chu NR, Mlazen LA;
XX
DR WPI; 2001-138361/14.
DR N-PSDB; AAF25037.
XX
PT Screening for compounds that stimulate Th1-like responses in CD4+ T
PT lymphocyte cells.
XX
PS Example 16; Fig 16A-B; 88pp; English.
XX
CC The present sequence represents a fusion protein comprising a Aspergillus
CC fumigatus heat shock protein (Hsp) 60 fused to a HPV16 E7 protein. The
CC fusion protein is used in the method of the invention. The specification
CC describes a method of determining whether a compound stimulates a Th1-
CC like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The
CC method comprises contacting naive lymphocytes in vitro with a fusion
CC protein comprising at least a fragment of Hsp, and then detecting the Th1
CC like response exhibited by the cell sample. The proteins which may be
CC used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and
CC Hsp71. The method may be used to identify compounds that stimulate Th1-
CC like responses in response to microbial pathogens

SQ Sequence 647 AA;
Query Match 99.0%; Score 512; DB 4; Length 647;
Best Local Similarity 96.9%; Pred. No. 2.5e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPLHEHYMDLQPEETDLYXXYQNDSSSEDEIDDPAGQAEPRAHYNIIVTFCK 60
DB 550 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSSEDEIDDPAGQAEPRAHYNIIVTFCK 609
QY 61 CDSTLRFCVOSTHYDIRTELDLMGTIGIYCPICSOQR 98
DB 610 CDSTLRFCVOSTHYDIRTELDLMGTIGIYCPICSOQR 647
RESULT 80
ADP18635
ID ADP18635 standard; protein: 98 AA.
XX
AC ADP18635;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human papilloma virus E7 oncoprotein.
XX
KM HPV; oncoprotein E7; cytostatic; gene therapy; kinase; enzyme.
XX
OS Human papillomavirus.
OS
PN WO2003088922-A2.
XX
PD 30-OCT-2003.
XX
PF 21-APR-2003; 2003WO-US012667.
XX
PR 19-APR-2002; 2002US-0374245P.
XX
PS (UTR) UNIV ROCHESTER.
XX
PI Mccance D, Westbrook TF;
XX
DR WPI; 2003-845498/78.
DR N-PSDB; ADP18636, ADP18637.
XX
PT Identifying a compound that inhibits E7 cellular proliferation activity
PT by administering a compound to a system, where the system maintains Akt
PT activity and selecting a compound that decreases the amount of Akt
XX activity.
PS Disclosure; SEQ ID NO 11; 119pp; English.
XX
XX
CC The present sequence is the protein sequence of human papillomavirus E7
CC oncoprotein. E7 promotes oncogenesis through an inhibition of p21cip21
CC transport into the nucleus. E7 abrogates Raf-associated arrest and
CC prevents inhibition of cyclin E-CDK2 activity without disrupting Raf
CC induction of p21cip21. E7 neither interacts with p21cip21 nor degrades
CC p21cip21-associated CDK2 activity, but instead reduces the association
CC between p21cip21 and cyclin E-CDK2 complexes. Raf down-regulates steady-
CC state levels of Akt, a regulator of p21cip21 localisation, leading to loss
CC of p21cip21 phosphorylation and accumulation of p21cip21. E7 disrupts the
CC effects of Raf on Akt activity and prevents p21cip21 nuclear accumulation.
CC Maintenance of Akt activity is necessary and sufficient to bypass Raf
CC arrest. The invention provides methods for identifying and using
CC inhibitors of E7 cell proliferation activity, and for identifying and
CC using compounds capable of promoting the nuclear localisation of p21cip21.
CC The methods can be used to inhibit aberrant cellular proliferation for
CC treatment of cancer.
XX
SQ Sequence 98 AA;
Query Match 98.8%; Score 511; DB 7; Length 98;
Best Local Similarity 95.9%; Pred. No. 2.9e-57;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEXYMLDLOPETTTDLYXXYXQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDTPTLHEXYMLDLOPETTTDLYCYEQUNDSESEDEVDGRGQAEPPRAHYNIVTFCK 60
Qy 61 CDSTLRCLCVGSTHVDIRLTEDLMGTIGIYXPICSQRP 98
Db 61 CDSTLRCLCVGSTHVDIRLTEDLMGTIGIYVCPICSQRP 98

RESULT 81

ADO44064
ID ADO44064 standard; protein: 248 AA.

AC ADO44064;

DT 15-JUL-2004 (first entry)

DE Amino acid sequence of a fusion protein designated E6E7Pentm.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KW cervical cancer; immune response; lower gastrointestinal tract cancer;
KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

XX Human papillomavirus type 16.
OS Synthetic.

XX MO2004030636-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-US0311726.

XX 03-OCT-2002; 2002US-0415929P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Smith L, Caesetti MC;

XX WPI; 2004-316328/29.

DR N-PSDB; ADO44065.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.

PS Claim 22; Page 70-71; 101pp; English.

XX The present sequence represents a fusion protein, comprising E6 and E7
CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
CC protein is designated E6E7Pentm, and comprises an E6 amino terminus
CC (where residues 63 and 106 have been replaced with glycine) and an E7
CC carboxy terminus (where residues 24, 26 and 91 have been replaced with
CC glycine). E6E7Pentm is representative of fusion proteins of the
CC invention. The specification describes human papillomavirus E6 and E7
CC polypeptides, where the E7 polypeptide has mutations at any one or more
CC of the amino acids corresponding to amino acids 24, 26 or 91 of the
CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
CC mutations at any one or more of the amino acids corresponding to amino
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
CC the invention are useful for treating or preventing human papillomavirus
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC and nucleic acids encoding the fusion proteins are useful for generating
CC immune responses against HPV. They are also useful for treating lower
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
CC the reproductive system, including penile and vulvar cancer.

XX Sequence 248 AA;

Query Match 98.8%; Score 511; DB 8; Length 248;
Best Local Similarity 95.9%; Pred. No. 9.6e-57;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEXYMLDLOPETTTDLYXXYXQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 151 LHGDTPTLHEXYMLDLOPETTTDLYCYEQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 210
Qy 61 CDSTLRCLCVGSTHVDIRLTEDLMGTIGIYXPICSQRP 98
Db 211 CDSTLRCLCVGSTHVDIRLTEDLMGTIGIYVCPICSQRP 248

RESULT 82

ADO44062
ID ADO44062 standard; protein: 248 AA.

AC ADO44062;

DT 15-JUL-2004 (first entry)

DE Amino acid sequence of a fusion protein designated E6E7Tetm.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KW cervical cancer; immune response; lower gastrointestinal tract cancer;
KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

XX Human papillomavirus type 16.
OS Synthetic.

XX MO2004030636-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-US0311726.

XX 03-OCT-2002; 2002US-0415929P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Smith L, Caesetti MC;

XX WPI; 2004-316328/29.

DR N-PSDB; ADO44063.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.

PS Claim 22; Page 68-69; 101pp; English.

XX The present sequence represents a fusion protein, comprising E6 and E7
CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
CC protein is designated E6E7Tetm, and comprises an E6 amino terminus (where
CC residues 63 and 106 have been replaced with glycine) and an E7 carboxy
CC terminus (where residues 24 and 26 have been replaced with glycine).
CC E6E7Tetm is representative of fusion proteins of the invention. The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.

XX Sequence 248 AA;

Query Match 98.6%; Score 510; DB 8; Length 248;
Best Local Similarity 95.9%; Pred. No. 1.3e-56;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEXYMLDLOPETTTDLYXXYXQLNDSSEDEIDGPAGQAEPPRAHYNIVTFCK 60

```
Db 151 LHGGPTLHEHYMDLQPEPTDLYGYGQINDSSSEEDIDGPAGAEPPRAHYNIVTFCK 210
Oy 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPICSQKP 98
Db 211 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPICSQKP 248

RESULT 83
ADO44060
ID ADO44060 standard; protein; 248 AA.
XX
AC ADO44060;
XX
DT 15-JUL-2004 (first entry)
XX
DE Amino acid sequence of an E6E7 fusion protein.
XX
KM E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
XX
OS Human papillomavirus type 16.
XX
OS Synthetic.
XX
PN WO2004030636-A2.
XX
PD 15-APR-2004.
XX
PF 02-OCT-2003; 2003WO-US031726.
XX
PR 03-OCT-2002; 2002US-0415929P.
XX
PA (AMHP ) WYETH HOLDINGS CORP.
XX
PI Smith L, Caesetti MC;
XX
DR WPI; 2004-316328/29.
XX
DR N-PSDB; ADO44061.
XX
PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.
XX
PS Example 1; Page 67-68; 101pp; English.
XX
XX
CC The present sequence represents an E6E7 fusion protein, comprising wild
CC type E6 and E7 polypeptides from human papillomavirus type 16 (HPV16).
CC The specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC there sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancer, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.
XX
SQ Sequence 248 AA;

Query Match 98.5%; Score 509; DB 8; Length 248;
Best Local Similarity 95.9%; Pred. No. 1.7e-56;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDTPLHEHYMDLQPEPTDLYXXQINDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Db 151 LHGGPTLHEHYMDLQPEPTDLYCYEQINDSSSEEDIDGPAGAEPPRAHYNIVTFCK 210
Oy 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPICSQKP 98
```

```
Db 211 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPICSQKP 248
RESULT 84
AAV50703
ID AAV50703 standard; protein; 98 AA.
XX
AC AAV50703;
XX
DT 04-FEB-2000 (first entry)
XX
DE HPV16 E7 protein.
XX
KM E7 protein; immunogenic; active immunization.
XX
OS Human papillomavirus.
XX
PN WO955876-A2.
XX
PD 04-NOV-1999.
XX
PF 30-APR-1999; 99WO-DE001331.
XX
PR 30-APR-1998; 98DE-01019476.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Gissmann L, Jochmus I;
XX
DR WPI; 2000-023362/02.
XX
DR N-PSDB; AA224129.
XX
PT Immunogenic protein with altered biological function, useful for active
PT immunization.
XX
PS Example 1; Page 25; 33pp; German.
XX
XX
CC This invention describes the construction of a novel polypeptide with
CC immunogenic and altered biological function of a protein, where the
CC polypeptide has regions of the protein of about 10-40 amino acids in a
CC different order. The polypeptide, or its DNA, is useful for active
CC immunization without cross-reactivity and problems associated with the
CC biological function of the protein. This sequence represents the human
CC papillomavirus type 16 E7 protein which is used to illustrate the method
CC of the invention
XX
SQ Sequence 98 AA;

Query Match 98.1%; Score 507; DB 3; Length 98;
Best Local Similarity 95.9%; Pred. No. 9.5e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 MHGDTPLHEHYMDLQPEPTDLYXXQINDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEHYMDLQPEPTDLYCYEQINDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Oy 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPICSQKP 98
Db 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPICSQKP 98

RESULT 85
AAB49453
ID AAB49453 standard; protein; 98 AA.
XX
AC AAB49453;
XX
DT 06-AUG-2003 (revised)
DT 07-MAR-2001 (first entry)
XX
DE HPV 16E7.
XX
KM Immune response; gene therapy; antigen presentation; vaccine; cancer;
```

KW infection; autoimmune disease.
XX
OS Hepatitis B virus.
XX
PN MO200067761-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000MO-US012177.
XX
PR 06-MAY-1999; 99US-0132750P.
XX
PR 06-MAY-1999; 99US-0132752P.
XX
PA (UTWA-) UNIV WAKE FOREST.
XX
PI Chen S, You Z;
XX
DR WPI; 2001-007312/01.
XX
PT Novel vector expressing secreted antigen fused to cell binding element,
PT useful in vaccines for treatment of e.g. cancer and infection, also
PT identification of epitopes.
XX
PS Disclosure; Fig 17; 163pp; English.
XX
PS
XX
CC The present invention relates to an expression vector comprising a
CC promoter, signal sequences, an antigen, a cell-binding element, and a
CC polyadenylation sequence. The expression vector can be used directly or
CC after transduction of antigen-presenting cells, in vaccines for treatment
CC and prevention of cancer, infections and autoimmune diseases. Vectors
CC similar to the expression vector of the present invention, but expressing
CC a test sequence rather than an antigen, are used to identify polypeptides
CC that contain MHC-II restricted epitopes for activation of CD4+ cells or
CC elicitation of an immune response in vivo. The identified polypeptides
CC (in APC) or vector containing DNA that expresses the polypeptides are
CC useful for treating the above conditions. The present sequence is HPV
CC 1657. E7 is a cytosolic protein, which has a string of charged residues
CC which hamper the secretion of the protein. Elimination of these residues
CC to result in the present protein, stabilises the protein and facilitates
CC secretion. The coding sequence for the present protein was used to
CC construct the expression vector of the present invention. (Updated on 06-
CC AUG-2003 to correct OS field.)
XX
SQ Sequence 98 AA;
XX
Query Match 98.1%; Score 507; DB 4; Length 98;
Best Local Similarity 95.9%; Pred. No. 9.5e-57;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 MHGDPPTLHEYMLDQPEPTDLYXXYXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
Db 1 MHGDPPTLHEYMLDQPEPTDLYCYEQSLDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
XX
QY 61 CDSTLRLCVOSTHVDIRLTEDLMGTIGIYXPCSQKP 98
Db 61 CDSTLRLCVOSTHVDIRLTEDLMGTIGIYXPCSQKP 98
XX
RESULT 86
AAO22639 standard; protein; 98 AA.
XX
AC AAO22639;
XX
DT 15-MAY-2003 (first entry)
XX
DE HPV-16 protein sequence, SEQ ID No 26.
XX
KW Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;
KW cancer; human papilloma virus; cervix; cell-mediated immune response;
KW HPV; HPV-16.
XX
OS Human papilloma virus.

XX
PN MO2003008649-A1.
XX
PD 30-JAN-2003.
XX
PF 19-JUN-2002; 2002MO-US023198.
XX
PR 20-JUL-2001; 2001US-0306809P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Sastry KU, Tortolero-Luna G, Follen M,
XX
DR WPI; 2003-239363/23.
XX
PT Determining a possible recurrence of a (pre-)cancerous growth in a
PT patient infected with human papilloma virus (HPV), comprises incubating
PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
PT immune response.
XX
PS Disclosure; Page 129-130; 132pp; English.
XX
PS
XX
CC The invention relates to a novel method for determining the possibility
CC of recurrence of a (pre-)cancerous growth in a patient infected with
CC human papilloma virus (HPV) or suspected of being infected with HPV, and
CC has or had a (pre-)cancerous growth on or around the cervix. The novel
CC method comprises incubating an E6 or E7 peptide of HPV with a sample from
CC the patient, and assaying the sample for a cell-mediated immune response
CC against the peptide. The method is useful for determining the possibility
CC and preventing the recurrence of a (pre-)cancerous growth in a patient
CC infected with HPV or suspected of being infected with HPV. The HPV E6 or
CC E7 peptides are useful in immunotherapy for the preventing or reducing
CC the risk of development of (pre-)cancerous growths. This sequence
XX
SQ Sequence 98 AA;
XX
Query Match 98.1%; Score 507; DB 6; Length 98;
Best Local Similarity 95.9%; Pred. No. 9.5e-57;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 MHGDPPTLHEYMLDQPEPTDLYXXYXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
Db 1 MHGDPPTLHEYMLDQPEPTDLYCYEQSLDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
XX
QY 61 CDSTLRLCVOSTHVDIRLTEDLMGTIGIYXPCSQKP 98
Db 61 CDSTLRLCVOSTHVDIRLTEDLMGTIGIYXPCSQKP 98
XX
RESULT 87
AAO22923 standard; protein; 111 AA.
XX
AC AAO22923;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human papillomavirus-16 (HPV16) E67-protein sequence.
XX
KW Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;
KW fusion partner; immunogenicity; HPV infection; neoplasm; HPV16;
KW human papillomavirus-16; E67-sequence.
XX
OS Human papillomavirus.
XX
PN EPI243655-A1.
XX
PD 25-SEP-2002.
XX
PR 23-MAR-2001; 2001EP-00107271.
XX
PR 23-MAR-2001; 2001EP-00107271.


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XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX PI Cld-Arregui A, Zur Hausen H;
XX DR WPI; 2002-724952/79.
XX DR N-PSDB; AAL53421.
XX PT A new DNA sequence encoding a fusion protein comprising a mutagenized HPV
XX PT (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a
XX PT highly immunogenic fusion partner is useful to vaccinate against HPV
XX PT infection.
XX PS Disclosure; Fig 1; 34pp; English.
XX CC The invention relates to a new DNA sequence encodes an E6 or E7 fusion
XX CC protein of HPV, where at least 20% of the original codons are replaced by
XX CC codons which lead to enhanced translation in a mammalian cell, containing
XX CC a mutation which results in production of a truncated non-functional
XX CC protein, and encoding a highly immunogenic polypeptide fusion partner
XX CC capable of enhancing immunogenicity of the E6 or E7 protein in the
XX CC mammalian host. The invention is used as a vaccine for the prevention or
XX CC treatment of an HPV infection or a neoplasm associated with HPV
XX CC infection. This sequence represents the human papillomavirus-16 (HPV16)
XX CC E6/E7-protein sequence of the invention
XX SQ Sequence 111 AA;
XX Query Match 98.1%; Score 507; DB 5; Length 111;
XX Best Local Similarity 96.9%; Pred. No. 1.1e-56;
XX Matches 94; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 HGDPTLHEHYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGAPBRAHYNIVTFCKC 61
Db 7 HGDPTLHEHYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGAPBRAHYNIVTFCKC 66
Qy 62 DSTLRLCVOSTHYDRTLEDLMGTGIVXPCSQKP 98
Db 67 DSTLRLCVOSTHYDRTLEDLMGTGIVXPCSQKP 103
RESULT 88
AA27724
ID AA27724 standard; protein; 262 AA.
XX AC AA27724;
XX DT 24-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 09-MAR-1993 (first entry)
XX DE HPV 16 E7 protein fragment.
XX XX
XX KM Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;
XX KM immunotherapeutic.
XX OS Human papillomavirus type 16.
XX FH Key location/Qualifiers
XX FT Peptide 162..259
XX FT /note="start of HPV-16 E7 protein"
XX XX
XX PN WO9216636-A1.
XX PD 01-OCT-1992.
XX PR 10-MAR-1992; 92WO-GB000424.
XX PR 14-MAR-1991; 91GB-00005383.
XX PA (IMMU ) IMMUNOLOGY LTD.
XX PT Bournefell MEG, Inglis SC, Munro AJ;

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XX DR WPI; 1992-349219/42.
XX DR N-PSDB; AAQ29389.
XX PT Recombinant virus vectors encoding human papillomavirus proteins - for
XX PT treating and vaccinating against HPV infections and conditions caused by
XX PT them, such as cervical cancer.
XX PS Disclosure; Fig 1a; 83pp; English.
XX CC The fragment of DNA contg. the HPV-16 E6/E7 coding region was prep'd. by
XX CC PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: 3812 (1983)) using
XX CC oligonucleotides S05 and S06. The prod. of the second reading frame is
XX CC the HPV-16 E7 protein whereas the third reading frame encodes HPV-16 E6.
XX CC The E6 and E7 ORFs are fused together to form a single continuous ORF via
XX CC site directed mutagenesis and the immortalising potential of E7 is
XX CC removed by altering two key codons of the HPV E7 sequence. The single ORF
XX CC of HPV-16 E6/E7 may be inserted into vaccinia virus DNA at neutral sites
XX CC (pref. by inserting two sets of the DNA in opposite orientations to
XX CC overcome the problem of intertypic recombination) to make a recombinant
XX CC virus vector for use immunotherapeutically to activate cells of the
XX CC immune system against HPV. See also AA27723-43. (Updated on 25-MAR-2003
XX CC to correct PW field.) (Updated on 24-OCT-2003 to standardise OS field)
XX SQ Sequence 262 AA;
XX Query Match 97.7%; Score 505; DB 2; Length 262;
XX Best Local Similarity 95.9%; Pred. No. 6.1e-56;
XX Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MHGDPPLHEHYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGAPBRAHYNIVTFCKC 60
Db 162 MHGDPPLHEHYMLDLOPETTDLYXXYXQNDSSSEDEIDGPAGAPBRAHYNIVTFCKC 221
Qy 61 CDSTLRLCVOSTHYDRTLEDLMGTGIVXPCSQKP 98
Db 222 CDSTLRLCVOSTHYDRTLEDLMGTGIVXPCSQKP 259
RESULT 89
AA08020
ID AA08020 standard; protein; 98 AA.
XX AC AA08020;
XX DT 27-AUG-2003 (revised)
XX DT 08-JUL-1999 (first entry)
XX DE Human papilloma virus E7 protein.
XX XX
XX KM L1 protein; capsomer; virus; vaccine; infection; treatment; prevention;
XX KM cervical carcinoma; fusion protein; anti-capsid; antibody; E7 protein;
XX KM antigenicity.
XX OS Human papillomavirus.
XX XX
XX PN WO9918220-A1.
XX PD 15-APR-1999.
XX PR 06-OCT-1998; 98WO-US020965.
XX PR 06-OCT-1997; 97US-00944368.
XX PR (LOYO ) UNIV LOYOLA CHICAGO.
XX PI Giesmann L, Mueller M;
XX XX
XX WPI; 1999-264026/22.
XX DR N-PSDB; AAX37567.
XX PT Human papilloma virus (HPV) L1 fusion protein capsomers, used in vaccines
XX PT against HPV infection.

```

XX Disclosure; Page 33; 48pp; English.

PS This invention describes novel vaccines comprising a human papilloma

XX virus (HPV) capsomer, composed of a HPV L1 fusion protein or a HPV L1

CC truncated protein. The vaccines can prevent or treat human papilloma

CC virus infection. Such therapeutic vaccinations can be used for relief

CC against, e.g. cervical carcinoma. Construction of chimeric proteins

CC comprising amino acid residues from L1 protein, and e.g. E6 or E7

CC protein, which give rise to chimeric capsomers, combines prophylactic and

CC therapeutic functions of a vaccine. Capsomers can promote elimination of

CC persistently infected cells. Capsomers can also escape neutralization by

CC pre-existing anti-capsid antibodies and hence possess longer circulating

CC half-life as compared to chimeric virus-like particles. The fusion

CC protein, which forms the capsomer, provides increased antigenicity.

CC (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 98 AA;

SQ

Query Match 97.5%; Score 504; DB 2; Length 98;

Best Local Similarity 95.9%; Pred. No. 2.3e-56;

Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEXYMLDQPEPTTDLVYXXQLNDSSEDEIDPAGQAEPRAHYNIIVTFCK 60

Db 1 MHGDTPTLHEXYMLDQPEPTTDLVYEQQLNDSSEDEIDPAGQAEPRAHYNIIVTFCK 60

Qy 61 CDSTLRLCVOSTHYDITRLTDLMTGLTGIYXPICSQKP 98

Db 61 CDSTLRLCVOSTHYDITRLTDLMTGLTGIYXPICSQKP 98

RESULT 90

ADJ32548

ID ADJ32548 standard; protein; 98 AA.

XX

AC ADJ32548;

XX

DT 22-APR-2004 (first entry)

XX

DE Human papillomavirus (HPV) type 16 E7 protein.

XX

KW Integrin; cell proliferation; cancer; melanoma; adenoma; lymphoma;

KW myeloma; carcinoma; glioma; plasmocytoma; sarcoma; thymoma; leukaemia;

KW brain tumour; cytosratic.

XX

OS Human papillomavirus.

XX

PN US2003224993-A1.

XX

PD 04-DEC-2003.

XX

PF 17-MAR-2003; 2003US-00392113.

XX

PR 12-OCT-2000; 2000US-0239705P.

XX

PR 24-OCT-2000; 2000US-024812P.

XX

PR 12-OCT-2001; 2001WO-US032127.

XX

PR 15-MAR-2002; 2002US-0365078P.

XX

PA (LAND/) LAND H.

PA (DELE/) DELEU L.

XX

PI Land H, Deleu L;

XX

DR WPI: 2004-154528/15.

XX

DR N-PSDB; ADJ32547.

XX

PT Reducing the proliferation of a cancer cell involves inhibiting ligand

XX binding to an integrin receptor on the cancer cell, where the integrin

XX receptor comprises an integrin.

XX

PS Disclosure; SEQ ID NO 29; 161pp; English.

XX

CC The present invention relates to compositions and methods for reducing

CC the proliferation of cancer cells through interaction with integrins. The

CC invention is useful for reducing the proliferation of cancer cells e.g.

CC melanoma, adenoma, lymphoma, myeloma, carcinoma, glioma, plasmocytoma,

CC sarcoma, thymoma, leukaemia, skin cancer, retinal cancer, breast cancer,

CC prostate cancer, colon cancer, esophageal cancer, stomach cancer,

CC pancreas cancer, brain tumours, lung cancer, ovarian cancer, cervical

CC cancer, hepatic cancer, gastrointestinal cancer, and head and neck cancer

CC cells. The invention is also useful for identifying a therapeutic target

CC which involves assaying potential reagent for activity. The present

CC sequence is human papillomavirus (HPV) type 16 E7 protein.

XX

XX Sequence 98 AA;

SQ

Query Match 97.5%; Score 504; DB 8; Length 98;

Best Local Similarity 95.9%; Pred. No. 2.3e-56;

Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEXYMLDQPEPTTDLVYXXQLNDSSEDEIDPAGQAEPRAHYNIIVTFCK 60

Db 1 MHGDTPTLHEXYMLDQPEPTTDLVYEQQLNDSSEDEIDPAGQAEPRAHYNIIVTFCK 60

Qy 61 CDSTLRLCVOSTHYDITRLTDLMTGLTGIYXPICSQKP 98

Db 61 CDSTLRLCVOSTHYDITRLTDLMTGLTGIYXPICSQKP 98

RESULT 91

AAB31607

ID AAB31607 standard; protein; 98 AA.

XX

AC AAB31607;

XX

DT 30-APR-2001 (first entry)

XX

DE Amino acid sequence of the HPV16 E7 protein.

XX

XX

KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;

KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;

KW E7 protein.

XX

OS Human papillomavirus.

XX

PN WO200104344-A2.

XX

PD 18-JAN-2001.

XX

PF 10-JUL-2000; 2000WO-US018828.

XX

PR 08-JUL-1999; 99US-0143757P.

XX

PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX

PI Siegel M, Chu NR, Wizen LA;

XX

XX

DR WPI: 2001-138361/14.

XX

DR N-PSDB; AAF25005.

XX

PT Screening for compounds that stimulate Th1-like responses in CD4+ T

XX lymphocyte cells.

XX

PS Example 3; Fig 2; 88pp; English.

XX

CC The present sequence represents the HPV16 E7 protein. HPV16 E7 was fused

CC to a heat shock protein (hsp), and used used in the method of the

CC invention. The specification describes a method of determining whether a

CC compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T

CC lymphocyte cells. The method comprises contacting native lymphocytes in

CC vitro with a fusion protein comprising at least a fragment of Hsp, and

CC then detecting the Th1-like response exhibited by the cell sample. The

CC proteins which may be used in the method of the invention are Hsp65,

CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify

CC compounds that stimulate Th1-like responses in response to microbial

CC pathogens
 XX Sequence 98 AA;
 SQ

Query Match 97.3%; Score 503; DB 4; Length 98;
 Best Local Similarity 95.9%; Pred. No. 3.1e-56;
 Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEHYMDLQPTETDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIIVTFCK 60
 Db 1 MDGDTPTLHEHYMDLQPTETDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIIVTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTELDLMTGLGIVXPICSOXP 98
 Db 61 CDSTLRLCVOSTHVDIRTELDLMTGLGIVCPICSOXP 98

RESULT 92
 AD242209
 ID AD242209 standard; protein; 490 AA.
 XX
 AC AD242209;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE N. meningitidis P1.7.16 delta 5 and HPV-16 E7 fusion protein.
 XX
 KM papillomavirus infection; cytosolic; immune stimulation; vaccine;
 KM cancer.
 XX
 OS Neisseria meningitidis.
 OS Human papillomavirus type 16.
 OS Chimeric.
 XX
 PN WO2005032585-A1.
 XX
 PD 14-APR-2005.
 XX
 PF 04-OCT-2004; 2004WO-CU000010.
 XX
 PR 09-OCT-2003; 2003CU-00000224.
 XX
 PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
 XX
 PI Torrens Madrazo IDC, Guillen Nieto GE, Fernandez Molina LE;
 PI Pajon Feyt R, Reyes Acosta O;
 XX
 DR WPI: 2005-296057/30.
 DR N-PSDB; AD242208.
 XX
 XX Vaccine composition for boosting cellular immune response against human
 PT papilloma virus (HPV) antigens, contains HPV antigens linked via
 PT hydrophobic bonds or mixed with very small size proteoliposomes (VSSP's).
 XX
 PS Example 1; SEQ ID NO 7; 62pp; Spanish.
 XX
 CC The invention relates to a novel composition comprising human
 CC papillomavirus (HPV) antigens or portions linked via hydrophobic bonds or
 CC mixed with very small size proteoliposomes (VSSP's). The invention
 CC further comprises a method for treating a tumor expressing an HPV antigen
 CC by administering an effective amount of this composition. The novel
 CC composition has cytostatic activity. The composition is useful for
 CC boosting the immune response against HPV antigens. The compositions are
 CC suitable for use in the pharmaceutical industry as vaccines in human
 CC therapeutics for cancer treatment. The cellular immune response against
 CC HPV antigens is significantly boosted, especially with respect to cell
 CC cytotoxicity, ensuring that cells which exhibit the HPV antigen are
 CC destroyed more effectively. This sequence represents a Neisseria
 CC meningitidis P1.7.16 delta 5 and HPV-16 E7 fusion protein, used in the
 CC expression of HPV antigens of the invention.
 XX
 SQ Sequence 490 AA;

Query Match 97.3%; Score 503; DB 9; Length 490;
 Best Local Similarity 94.9%; Pred. No. 2.5e-55;
 Matches 93; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEHYMDLQPTETDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIIVTFCK 60
 Db 270 IHGDTPTLHEHYMDLQPTETDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIIVTFCK 329

Qy 61 CDSTLRLCVOSTHVDIRTELDLMTGLGIVXPICSOXP 98
 Db 330 CDSTLRLCVOSTHVDIRTELDLMTGLGIVCPICSOXP 367

RESULT 93
 AAB31614
 ID AAB31614 standard; protein; 648 AA.
 XX
 AC AAB31614;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Amino acid sequence of Hsp65-E7 fusion protein.
 XX
 KM Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
 KM lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
 KM E7 protein.
 XX
 OS Synthetic.
 OS Mycobacterium bovis.
 OS Human papillomavirus.
 XX
 PN WO200104344-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 10-JUL-2000; 2000WO-US018828.
 XX
 PR 08-JUL-1999; 99US-0143757P.
 XX
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 XX
 PI Siegel M, Chu NR, Mizeen LA;
 XX
 DR WPI: 2001-138361/14.
 DR N-PSDB; AAF25019.
 XX
 XX Screening for compounds that stimulate Th1-like responses in CD4+ T
 PT lymphocyte cells.
 XX
 PS Example 11; Fig 10A-B; 86pp; English.
 XX
 CC The present sequence represents a fusion protein comprising Mycobacterium
 CC bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7
 CC protein. The fusion protein is used in the method of the invention. The
 CC specification describes a method of determining whether a compound
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
 CC lymphocyte cells. The method comprises contacting naive lymphocytes in
 CC vitro with a fusion protein comprising at least a fragment of Hsp, and
 CC then detecting the Th1-like response exhibited by the cell sample. The
 CC proteins which may be used in the method of the invention are Hsp65,
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
 CC compounds that stimulate Th1-like responses in response to microbial
 CC pathogens
 XX
 SQ Sequence 648 AA;

Query Match 97.3%; Score 503; DB 4; Length 648;
 Best Local Similarity 95.9%; Pred. No. 3.5e-55;
 Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEHYMDLQPTETDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIIVTFCK 60
 Db 1 MDGDTPTLHEHYMDLQPTETDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIIVTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGLGIYXPCISQKP 98
 |||
 Db 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGLGIYPCISQKP 98

RESULT 94

AAB31617
 ID AAB31617 standard; protein; 711 AA.

XX AAB31617;

DT 30-APR-2001 (first entry)

DE Amino acid sequence of Hsp71-E7 fusion protein.

XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
 KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
 KW E7 protein.

OS Synthetic.
 OS Mycobacterium tuberculosis.

OS Human papillomavirus.

XX WO200104344-A2.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-US018828.

XX 08-JUL-1999; 99US-0143757P.

XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX Siegel M, Chu NR, Mizzzen LA;

XX WPI; 2001-138361/14.

DR N-PSDB; AAF25028.

XX Screening for compounds that stimulate Th1-like responses in CD4+ T

PT lymphocyte cells.

XX Example 14; Fig 13A-B; 88pp; English.

XX The present sequence represents a fusion protein comprising Mycobacterium
 CC tuberculosis heat shock protein (Hsp) 71 fused to a HPV16 E7 protein. The
 CC fusion protein is used in the method of the invention. The specification
 CC describes a method of determining whether a compound stimulates a Th1-
 CC like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The
 CC method comprises contacting naive lymphocytes in vitro with a fusion
 CC protein comprising at least a fragment of Hsp, and then detecting the Th1
 CC -like response exhibited by the cell sample. The proteins which may be
 CC used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and
 CC Hsp71. The method may be used to identify compounds that stimulate Th1-
 CC like responses in response to microbial pathogens

XX Sequence 711 AA;

Query Match 97.3%; Score 503; DB 4; Length 711;

Best Local Similarity 95.9%; Pred. No. 4e-55; Mismatches 4; Indels 0; Gaps 0;

Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 MHGDPPTLHEWMLDQPEPTDLYXXYXOLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
 |||
 Db 1 MDGDPPTLHEWMLDQPEPTDLYCYEQUNDSEDEIDGPAQAEPDRAHYNIVTFCK 60
 |||
 Qy 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGLGIYXPCISQKP 98
 |||
 Db 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGLGIYPCISQKP 98

RESULT 95

AAB31618

ID AAB31618 standard; protein; 724 AA.

XX AAB31618;

DT 30-APR-2001 (first entry)

DE Amino acid sequence of E7-Hsp71 fusion protein.

XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
 KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
 KW E7 protein.

OS Synthetic.

OS Human papillomavirus.

XX Mycobacterium tuberculosis.

XX WO200104344-A2.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-US018828.

XX 08-JUL-1999; 99US-0143757P.

XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX Siegel M, Chu NR, Mizzzen LA;

XX WPI; 2001-138361/14.

DR N-PSDB; AAF25031.

XX Screening for compounds that stimulate Th1-like responses in CD4+ T

PT lymphocyte cells.

XX Example 14; Fig 14A-B; 88pp; English.

XX The present sequence represents a fusion protein comprising a HPV16 E7
 CC protein fused to a Mycobacterium tuberculosis heat shock protein (Hsp)
 CC 71. The fusion protein is used in the method of the invention. The
 CC specification describes a method of determining whether a compound
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
 CC lymphocyte cells. The method comprises contacting naive lymphocytes in
 CC vitro with a fusion protein comprising at least a fragment of Hsp, and
 CC then detecting the Th1-like response exhibited by the cell sample. The
 CC proteins which may be used in the method of the invention are Hsp65,
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
 CC compounds that stimulate Th1-like responses in response to microbial
 CC pathogens

XX Sequence 724 AA;

Query Match 97.3%; Score 503; DB 4; Length 724;

Best Local Similarity 95.9%; Pred. No. 4.1e-55; Mismatches 4; Indels 0; Gaps 0;

Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 MHGDPPTLHEWMLDQPEPTDLYXXYXOLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
 |||
 Db 1 MDGDPPTLHEWMLDQPEPTDLYCYEQUNDSEDEIDGPAQAEPDRAHYNIVTFCK 60
 |||
 Qy 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGLGIYXPCISQKP 98
 |||
 Db 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGLGIYPCISQKP 98

RESULT 96

AAB81111

ID AAB81111 standard; protein; 99 AA.

XX AAB81111;

DT 05-NOV-2002 (first entry)

XX HPV E7 antigenic protein.

XX Major histocompatibility complex; MHC; antigen presenting cell; APC;
 KM antigen; cytostatic; virucide; gene therapy; CD8; vaccine; therapeutic;
 KM cancer; viral infection; HPV; E7.
 XX
 OS Human papillomavirus.
 XX
 PN WO200261113-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 01-FEB-2002; 2002WO-US002598.
 XX
 PR 01-FEB-2001; 2001US-0265334P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Wu T, Hung C;
 XX
 DR WPI; 2002-619261/66.
 DR N-PSDB; ABN86677.
 XX
 XX
 PS Disclosure; Page 16; 127pp; English.
 CC The invention relates to a new nucleic acid molecule (I) encoding a
 CC fusion polypeptide useful as a vaccine composition. (I) comprises a first
 CC nucleic acid sequence encoding a first polypeptide or peptide that
 CC promotes processing via the Major Histocompatibility Complex (MHC) class
 CC I pathway (MHC-I-p) and/or promotes development or activity of an
 CC antigen presenting cell (APC). The second nucleic acid sequence is linked
 CC in frame to the first nucleic acid sequence or to a linker nucleic acid
 CC sequence and encodes an antigenic polypeptide or peptide. The methods and
 CC compositions of the present invention are useful as therapeutic vaccine
 CC for cancer and for major viral infections, such as hepatoma and cervical
 CC cancer, that cause morbidity and mortality. They can also be used in
 CC treating animal diseases, such as equine herpesvirus, bovine viruses,
 CC Marek's disease, retroviral and lentiviral diseases and rabies, in the
 CC veterinary medicine context. The present sequence represents the human
 CC papillomavirus (HPV) E7 antigenic protein
 XX
 SQ Sequence 99 AA;
 Query Match 96.7%; Score 500; DB 5; Length 99;
 Best Local Similarity 96.9%; Pred. No. 7.6e-56;
 Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MGGDPTLHRYMDLQPEETDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIVTFCCK 60
 Db 1 MGGDPTLHRYMDLQPEETDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIVTFCCK 60
 QY 61 CDSTLRLCVOSTHVDIRLTLEDLMGTIGIYCPICSQ 96
 Db 61 CDSTLRLCVOSTHVDIRLTLEDLMGTIGIYCPICSQ 96
 RESULT 97
 ABB82376
 ID ABB82376 standard; protein; 99 AA.
 XX
 AC ABB82376;
 XX
 DT 08-JAN-2003 (first entry)
 XX
 DE Modified HPV-E7 amino acid sequence.
 XX
 KM Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
 KM hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; HPV;
 KM E7 protein.

XX
 OS Human papillomavirus.
 XX
 PN WO200274920-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 18-MAR-2002; 2002WO-US008033.
 XX
 PR 16-MAR-2001; 2001US-0276854P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Wu T, Hung C;
 XX
 DR WPI; 2002-740856/80.
 DR N-PSDB; ABV73162.
 XX
 XX
 PS Disclosure; Page 20; 93pp; English.
 CC The invention relates to a nucleic acid molecule that encodes a fusion
 CC polypeptide, comprising a first nucleic acid sequence encoding a
 CC polypeptide that comprises at least one immunogenically-potentiating
 CC polypeptide, optionally, fused in frame with the nucleic acid, a linker
 CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked
 CC in frame to them, and that encodes an antigenic peptide or polypeptide.
 CC The nucleic acid molecule, polypeptides and vectors are useful as
 CC vaccines for enhancing immune responses, primarily cytotoxic T
 CC lymphocytes (CTL), responses to specific antigens such as tumour or viral
 CC antigens, and for inhibiting growth or preventing re-growth of a tumour.
 CC The packaging cell line is useful for generating alphavirus replicon
 CC particles without contamination from replicon-competent virus. The
 CC pathogenic organisms include viruses such as human papilloma virus (HPV),
 CC hepatitis B virus, hepatitis C virus, human immunodeficiency virus,
 CC Epstein Barr virus and herpes simplex virus, intracellular parasites such
 CC as malaria, and bacteria that grow intracellularly such as mycobacteria
 CC and listeria. The present sequence represents a modified HPV E-7 protein
 XX
 SQ Sequence 99 AA;
 Query Match 96.7%; Score 500; DB 5; Length 99;
 Best Local Similarity 96.9%; Pred. No. 7.6e-56;
 Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MGGDPTLHRYMDLQPEETDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIVTFCCK 60
 Db 1 MGGDPTLHRYMDLQPEETDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIVTFCCK 60
 QY 61 CDSTLRLCVOSTHVDIRLTLEDLMGTIGIYCPICSQ 96
 Db 61 CDSTLRLCVOSTHVDIRLTLEDLMGTIGIYCPICSQ 96
 RESULT 98
 ADE21865
 ID ADE21865 standard; protein; 99 AA.
 XX
 AC ADE21865;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE HPV-16 E7 protein SEQ ID NO:7.
 XX
 KM chimeric fusion; translocation; antigenic; cytostatic; immunotherapy;
 KM gene therapy; cancer; tumour; HPV-16; E7 protein.
 XX
 OS Human papillomavirus.

PN WO2003085085-A2.
 XX
 PD 16-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010235.
 XX
 PR 04-APR-2002; 2002US-00115440.
 XX
 PA (UJYO) UNIV JOHNS HOPKINS.
 XX
 F1 Wu T, Hung C;
 XX
 DR WPI; 2003-877027/81.
 DR N-PSDB; ADE21864.
 XX
 PT New nucleic acid encoding a chimeric fusion or fusion polypeptide
 PT comprising a first domain with a translocation polypeptide, and a second
 PT domain with an antigen having at least one antigenic peptide, useful for
 PT treating cancer.
 PS Disclosure; SEQ ID NO 7; 68bp; English.
 XX
 CC The present invention describes a nucleic acid (I) encoding a chimeric
 CC fusion or fusion polypeptide comprising a first domain with a
 CC translocation polypeptide, and a second domain comprising an antigen
 CC having at least one antigenic peptide. Also described: (1) an expression
 CC vector comprising (I) operatively linked to a promoter and optionally, to
 CC one or more regulatory elements that enhance expression of the nucleic
 CC acid in a cell; (2) a particle comprising (I) or the expression vector;
 CC (3) a cell that has been modified to comprise (I) or the expression
 CC vector; (4) a chimeric polypeptide comprising a first domain with a
 CC translocation polypeptide, and a second domain comprising an antigen
 CC having at least one antigenic peptide; (5) a pharmaceutical composition
 CC capable of inducing or enhancing an antigen specific immune response,
 CC comprising (1), expression vector, particle, cell, cell of the particle,
 CC or the chimeric polypeptide; and a carrier or excipient; (6) inducing or
 CC enhancing an antigen specific immune response by administering the
 CC composition described above; (7) increasing the number of CD8 + CTLs
 CC specific for a selected desired antigen in a subject by administering the
 CC composition described above; and (8) inhibiting the growth of a tumour in
 CC a subject by administering the composition described above. (I) has
 CC cytostatic activity, and can be used in immunotherapy, and gene therapy.
 CC The nucleic acids (I), compositions and methods are useful for treating
 CC cancer. The present sequence represents HPV-16 E7, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 99 AA;
 Query Match 96.7%; Score 500; DB 7; Length 99;
 Best Local Similarity 96.9%; Pred. No. 7.6e-56;
 Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDDPAGQAEPPRAHYNIIVTECK 60
 DB 1 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDDPAGQAEPPRAHYNIIVTECK 60
 QY 61 CDSTLRCLCVGOSTHVDIRTDLTDLMTGLIGIYXPCISQ 96
 DB 61 CDSTLRCLCVGOSTHVDIRTDLTDLMTGLIGIYXPCISQ 96
 RESULT 99
 ADO05276
 ID ADO05276 standard; protein; 99 AA.
 XX
 AC ADO05276;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human papillomavirus type 16 E7 protein.
 XX
 KW Translocation domain; bacterial toxin; exotoxin A domain II; E7A;
 KW major histocompatibility complex; MHC class I; vaccine; immune response;

KW CD8+ cytotoxic T lymphocyte; CTL; tumour; E7 antigen.
 XX
 OS Human papillomavirus type 16.
 XX
 PN US2004086845-A1.
 XX
 PD 06-MAY-2004.
 XX
 PR 04-APR-2002; 2002US-00115440.
 XX
 PF 20-OCT-1999; 99US-00421608.
 PR 09-FEB-2000; 2000US-00501097.
 PR 20-OCT-2000; 2000WO-US041422.
 PR 04-APR-2001; 2001US-0281003P.
 XX
 PA (WTTT/) WU T.
 PA (HUNG/) HUNG C.
 XX
 PI Wu T, Hung C;
 XX
 DR WPI; 2004-356187/33.
 DR N-PSDB; ADO05275.
 XX
 PT Novel chimeric polypeptide e.g., Pseudomonas aeruginosa exotoxin A domain
 PT II/human papilloma virus-16 E7 peptide useful for inducing or enhancing
 PT antigen specific immune response, or for inhibiting growth of tumor in
 PT subject.
 PS Claim 10; SEQ ID NO 7; 48bp; English.
 XX
 CC The invention relates to nucleic acid encoding a chimeric polypeptide
 CC comprising a translocation domain of a bacterial toxin and at least one
 CC antigenic peptide. The preferred translocation domain is domain II of
 CC Pseudomonas aeruginosa exotoxin A (ETA/dII) and the preferred antigen is
 CC human papilloma virus type 16 (HPV-16) E7 which is a model tumour
 CC antigen. The antigenic peptide comprises an epitope that binds to and is
 CC presented on the cell surface by major histocompatibility complex (MHC)
 CC class I protein. The nucleic acid of the invention is useful as vaccine
 CC composition for enhancing antigen specific immune response, increasing
 CC the number of CD8+ cytotoxic T lymphocytes (CTLs) and for inhibiting the
 CC growth of a tumour. The present sequence is HPV-16 E7 protein.
 XX
 SQ Sequence 99 AA;
 Query Match 96.7%; Score 500; DB 8; Length 99;
 Best Local Similarity 96.9%; Pred. No. 7.6e-56;
 Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDDPAGQAEPPRAHYNIIVTECK 60
 DB 1 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDDPAGQAEPPRAHYNIIVTECK 60
 QY 61 CDSTLRCLCVGOSTHVDIRTDLTDLMTGLIGIYXPCISQ 96
 DB 61 CDSTLRCLCVGOSTHVDIRTDLTDLMTGLIGIYXPCISQ 96
 RESULT 100
 ADU6377
 ID ADU6377 standard; protein; 99 AA.
 XX
 AC ADU6377;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human papillomavirus type 16 (HPV16) E7 protein - SEQ ID 2.
 XX
 KW vaccine; MHC class I pathway; antigen specific immune response; tumor;
 KW E7 protein; E6 protein.
 XX
 OS Human papillomavirus type 16.
 XX
 PN WO2004098526-A2.

```

XX 18-NOV-2004.
PD
XX
XX 05-MAY-2004; 2004MO-US013756.
PF
XX
XX 05-MAY-2003; 2003US-0467602P.
PR
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX
XX Wu T, Hung CF;
PI
XX
XX WPI: 2004-813972/80.
DR
XX N-PSDB; ADU66361.
XX
XX New nucleic acid molecules encoding a fusion polypeptide comprising an
PT antigen, a signal peptide, and a heat shock protein, useful as a vaccine
PT for inducing or enhancing immune response or for inhibiting or preventing
PT tumor growth.
XX
XX Claim 8; SEQ ID NO 2; 67pp; English.
PS
XX
XX The invention comprises a nucleic acid molecule (DNA vaccine) that
CC encodes a fusion polypeptide which is useful as a vaccine composition.
CC The nucleic acid of the invention contains: a first nucleic acid encoding
CC a polypeptide that promotes processing via the MHC class I pathway; a
CC second sequence encoding a signal peptide; and a third sequence encoding
CC an antigenic polypeptide. The DNA vaccine of the invention is useful for
CC inducing or enhancing an antigen specific immune response, or to inhibit
CC growth or prevent re-growth of a tumor expressing Human papillomavirus
CC (HPV) E7 or E6 protein. The present amino acid sequence represents a
CC human papillomavirus type 16 (HPV16) E7 protein of the invention.
XX
XX Sequence 99 AA;
SQ
XX
XX Query Match          96.7%; Score 500; DB 8; Length 99;
XX Best Local Similarity 96.9%; Pred. No. 7,6e-56;
XX Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 MHGDTPTLHEVMDLQEPETDLYXXQLNDSSEDEIDGPAQAPDRAHNYIVTFCK 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1 MHGDTPTLHEVMDLQEPETDLYCYEQLNDSSEDEIDGPAQAPDRAHNYIVTFCK 60
XX
XX 61 CDSTLRICVOSTHYDIRTLEIDLMGTGIVPCISQ 96
XX ||||||||||||||||||||||||||||||||||||||||||||||||
XX 61 CDSTLRICVOSTHYDIRTLEIDLMGTGIVPCISQ 96
XX

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Search completed: May 27, 2006, 05:10:00
 Job time : 234.273 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:16:46 ; Search time 44.2691 Seconds
(Without alignments)
298.563 Million cell updates/sec

Title: US-10-530-253-13ED

Perfect score: 830
Sequence: 1 MFQDPQRPRLPQLCTELQ.....WTGCMSCRSSRRRETQL 151

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*

- 1: /EMC_Celeerra_SIDS3/prodata/2/iaa/5.COMB.pep:*
- 2: /EMC_Celeerra_SIDS3/prodata/2/iaa/6.COMB.pep:*
- 3: /EMC_Celeerra_SIDS3/prodata/2/iaa/7.COMB.pep:*
- 4: /EMC_Celeerra_SIDS3/prodata/2/iaa/H.COMB.pep:*
- 5: /EMC_Celeerra_SIDS3/prodata/2/iaa/PCUS.COMB.pep:*
- 6: /EMC_Celeerra_SIDS3/prodata/2/iaa/RE.COMB.pep:*
- 7: /EMC_Celeerra_SIDS3/prodata/2/iaa/bocckflle1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	826	99.5	162	1	US-08-316-239B-4
2	823	99.2	158	2	US-09-980-523A-2
3	823	99.2	158	3	US-09-763-616-1
4	823	99.2	162	1	US-08-316-239B-3
5	823	99.2	266	2	US-08-860-165-10
6	823	99.2	266	2	US-09-359-382-10
7	823	99.2	266	2	US-09-367-309A-1
8	823	99.2	273	2	US-09-485-885-4
9	823	99.2	292	2	US-09-485-885-10
10	823	99.2	371	2	US-09-485-885-6
11	823	99.2	390	2	US-09-485-885-14
12	818	98.6	151	2	US-09-701-080C-18
13	779.5	93.9	243	2	US-09-462-993-1
14	519	62.5	172	2	US-08-860-165-12
15	519	62.5	172	2	US-09-359-382-12
16	478	57.6	172	2	US-08-860-165-14
17	478	57.6	172	2	US-09-359-382-14
18	477	57.5	182	1	US-08-117-083-10
19	455.5	54.9	158	1	US-08-247-904B-10
20	455.5	54.9	158	2	US-08-767-942A-19
21	455.5	54.9	271	1	US-08-117-083-14
22	455.5	54.9	278	2	US-09-485-885-21
23	455.5	54.9	383	2	US-09-485-885-23
24	304	36.6	368	2	US-09-000-094-20
25	304	36.6	368	2	US-10-011-749-20
26	304	36.6	375	2	US-09-000-094-22

27	304	36.6	375	2	US-10-011-749-22	Sequence 22, Appl
28	304	36.6	465	2	US-09-000-094-24	Sequence 24, Appl
29	304	36.6	465	2	US-10-011-749-24	Sequence 24, Appl
30	304	36.6	1587	2	US-09-000-094-46	Sequence 46, Appl
31	304	36.6	1587	2	US-10-011-749-46	Sequence 46, Appl
32	163	19.6	30	1	US-08-363-586-4	Sequence 4, Appl
33	163	19.6	30	2	US-09-980-523A-4	Sequence 8, Appl
34	159	19.2	29	2	US-09-980-523A-8	Sequence 4, Appl
35	134.5	16.2	137	2	US-09-913-204-17	Sequence 17, Appl
36	130	15.7	23	2	US-09-980-523A-10	Sequence 10, Appl
37	128	15.4	22	2	US-09-601-729-276	Sequence 276, App
38	124	14.9	22	2	US-09-980-523A-6	Sequence 6, Appl
39	120	14.5	21	1	US-08-934-915-167	Sequence 167, App
40	119	14.3	137	2	US-09-913-204-3	Sequence 3, Appl
41	119	14.3	137	2	US-09-913-204-7	Sequence 7, Appl
42	119	14.3	137	2	US-09-913-204-13	Sequence 13, Appl
43	115	13.9	21	1	US-08-934-915-166	Sequence 166, App
44	115	13.9	32	1	US-08-466-285-2	Sequence 2, Appl
45	115	13.9	32	2	US-08-164-768-2	Sequence 2, Appl
46	114	13.7	20	2	US-09-601-729-278	Sequence 278, App
47	114	13.7	22	2	US-10-612-818-4	Sequence 4, Appl
48	109	13.1	20	1	US-08-934-915-44	Sequence 44, Appl
49	109	13.1	20	1	US-08-934-915-45	Sequence 45, Appl
50	109	13.1	20	1	US-08-934-915-163	Sequence 163, App
51	104	12.5	20	1	US-08-934-915-164	Sequence 164, App
52	104	12.5	20	1	US-08-934-915-165	Sequence 165, App
53	98	11.8	20	1	US-08-934-915-159	Sequence 159, App
54	97	11.7	20	1	US-08-934-915-160	Sequence 160, App
55	97	11.7	20	1	US-08-934-915-161	Sequence 161, App
56	94	11.3	15	3	US-09-641-528B-46524	Sequence 46524, A
57	93	11.2	32	1	US-08-466-285-4	Sequence 4, Appl
58	93	11.2	32	2	US-08-164-768-4	Sequence 4, Appl
59	92	11.1	15	3	US-09-641-528B-46535	Sequence 46535, A
60	92	11.1	20	1	US-08-934-915-162	Sequence 162, App
61	90	10.8	23	1	US-08-363-586-3	Sequence 3, Appl
62	89	10.7	15	3	US-09-641-528B-46517	Sequence 46517, A
63	85	10.2	15	1	US-07-909-122-2	Sequence 2, Appl
64	85	10.2	15	3	US-09-641-528B-46523	Sequence 46523, A
65	85	10.2	15	3	US-09-641-528B-46525	Sequence 46525, A
66	85	10.2	15	3	US-09-641-528B-46526	Sequence 46526, A
67	85	10.2	15	3	US-09-641-528B-46520	Sequence 46520, A
68	84	10.1	15	3	US-09-641-528B-46519	Sequence 46519, A
69	84	10.1	15	3	US-09-641-528B-46534	Sequence 46534, A
70	83	10.0	15	3	US-09-641-528B-46532	Sequence 46532, A
71	83	10.0	15	3	US-09-641-528B-46527	Sequence 46527, A
72	83	10.0	15	3	US-09-641-528B-46536	Sequence 46536, A
73	83	10.0	15	3	US-09-641-528B-46535	Sequence 46535, A
74	82	9.9	15	2	US-08-075-541D-52	Sequence 52, Appl
75	82	9.9	15	3	US-09-641-528B-51199	Sequence 51199, A
76	82	9.9	15	3	US-09-641-528B-51250	Sequence 51250, A
77	82	9.9	15	3	US-09-270-767-11452	Sequence 41152, A
78	81	9.8	15	3	US-09-641-528B-46518	Sequence 46518, A
79	80	9.6	15	3	US-09-641-528B-46520	Sequence 46520, A
80	80	9.6	15	3	US-09-641-528B-47291	Sequence 47291, A
81	80	9.6	15	3	US-09-641-528B-46558	Sequence 46558, A
82	79	9.5	15	3	US-09-641-528B-46532	Sequence 46532, A
83	78	9.4	15	3	US-09-641-528B-46516	Sequence 46516, A
84	78	9.4	15	3	US-09-641-528B-46528	Sequence 46528, A
85	77.5	9.3	165	2	US-09-270-767-11740	Sequence 46577, A
86	77.5	9.3	165	2	US-09-270-767-46957	Sequence 46957, A
87	77.5	9.3	572	2	US-09-949-016-6366	Sequence 46366, App
88	77	9.3	15	3	US-09-641-528B-46521	Sequence 46521, A
89	77	9.3	15	3	US-09-641-528B-50557	Sequence 50557, A
90	77	9.3	15	3	US-09-641-528B-50559	Sequence 50559, A
91	76.5	9.2	14	1	US-07-909-853A-15	Sequence 15, Appl
92	76	9.2	15	3	US-09-641-528B-46529	Sequence 46529, A
93	76	9.2	15	3	US-09-641-528B-46531	Sequence 46531, A
94	76	9.2	15	3	US-09-248-766A-16235	Sequence 16235, A
95	75.5	9.1	187	2	US-09-949-016-6090	Sequence 8090, Ap
96	75.5	9.1	15	3	US-09-641-528B-46533	Sequence 46533, A
97	75	9.0	393	1	US-08-377-309-7	Sequence 7, Appl
98	74.5	9.0	393	2	US-09-186-723-7	Sequence 7, Appl
99	74.5	9.0	393	2	US-09-186-723-7	Sequence 7, Appl

100 74.5 9.0 393 2 US-08-505-012-10

Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-316-239B-4

; Sequence 4, Application US/08316239B

; Patent No. 5679509

; GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.

; APPLICANT: Parmenter, Cheryl A.

; TITLE OF INVENTION: Methods and a Diagnostic Aid for

; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an

; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and

; TITLE OF INVENTION: Cervical Cancer

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jagtiani & Associates

; STREET: 6126 Rocky Way Court

; CITY: Centreville

; STATE: VA

; COUNTRY: USA

; ZIP: 20120-3400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/316,239B

; FILING DATE: 30-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Jagtiani, Ajay A.

; REGISTRATION NUMBER: 35,205

; REFERENCE/DOCKET NUMBER: UNNE-0001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 817-9453

; TELEFAX: (703) 803-9387

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 162 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; US-08-316-239B-4

Query Match 99.5%; Score 826; DB 1; Length 162;

Best Local Similarity 98.7%; Pred. No. 8.2e-86;

Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOOLLREVVDPFAFRDLCTIVRDGPNY 60

DB 8 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOOLLREVVDPFAFRDLCTIVRDGPNY 67

QY 61 AVXDKLKFYSKISEYRHYCYGVYGTLLLEQYNNKPLCDLLIRICINXQKPLCEPEKQRHLD 120

DB 68 AVCDKCLKFYSKISEYRHYCYGVYGTLLLEQYNNKPLCDLLIRICINXQKPLCEPEKQRHLD 127

QY 121 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 151

DB 128 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 158

QY 121 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 151

DB 128 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 158

QY 121 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 151

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QY 121 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 151

DB 128 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 158

QY 121 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 151

DB 128 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 158

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: BOURGAULT VILLADA, ISABELLE

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: CONNAM, FRANCINE

APPLICANT: FERRIES, ESTELLE

TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7

TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: PARTICULARLY IN VACCINATION

FILE REFERENCE: WO91 AO INS

CURRENT APPLICATION NUMBER: US/09/980,523A

CURRENT FILING DATE: 2002-04-29

PRIOR APPLICATION NUMBER: PCT/FR00/01513

PRIOR FILING DATE: 2000-05-31

PRIOR APPLICATION NUMBER: FR 99/07012

PRIOR FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 2

LENGTH: 158

TYPE: PRT

ORGANISM: Human Papillomavirus

US-09-980-523A-2

Query Match 99.2%; Score 823; DB 2; Length 158;

Best Local Similarity 98.0%; Pred. No. 1.7e-85;

Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOOLLREVVDPFAFRDLCTIVRDGPNY 60

DB 8 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOOLLREVVDPFAFRDLCTIVRDGPNY 67

QY 61 AVXDKLKFYSKISEYRHYCYGVYGTLLLEQYNNKPLCDLLIRICINXQKPLCEPEKQRHLD 120

DB 68 AVCDKCLKFYSKISEYRHYCYGVYGTLLLEQYNNKPLCDLLIRICINXQKPLCEPEKQRHLD 127

QY 121 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 151

DB 128 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 158

QY 121 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 151

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QY 121 KKQRFNIRGRWTCRCMSCCRSSRTRETQL 151

Db 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREVYDPAFRLDCTIVRDGPNY 67
Qy 61 AVXDCKLKFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRCNXQKPLCPBEKORHLD 120
Db 68 AVCDKCLKFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRCNXQKPLCPBEKORHLD 127
Qy 121 KKORFHNIRGWRGCMSCCRSSRTRETOL 151
Db 128 KKORFHNIRGWRGCMSCCRSSRTRETOL 158

RESULT 4

US-08-316-239B-3
Sequence 3, Application US/08316239B
Patent No. 5679509
GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centerville
STATE: VA
COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNME-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
FAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 99.2%; Score 823; DB 1; Length 162;
Best Local Similarity 98.0%; Pred. No. 1.8e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREVYDPAFRLDCTIVRDGPNY 60
Db 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREVYDPAFRLDCTIVRDGPNY 67
Qy 61 AVXDCKLKFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRCNXQKPLCPBEKORHLD 120
Db 68 AVCDKCLKFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRCNXQKPLCPBEKORHLD 127
Qy 121 KKORFHNIRGWRGCMSCCRSSRTRETOL 151
Db 128 KKORFHNIRGWRGCMSCCRSSRTRETOL 158

RESULT 5
US-08-860-165-10
Sequence 10, Application US/08860165A
Patent No. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 266
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 99.2%; Score 823; DB 2; Length 266;
Best Local Similarity 98.0%; Pred. No. 3.2e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREVYDPAFRLDCTIVRDGPNY 60
Db 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLRREVYDPAFRLDCTIVRDGPNY 67
Qy 61 AVXDCKLKFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRCNXQKPLCPBEKORHLD 120
Db 68 AVCDKCLKFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRCNXQKPLCPBEKORHLD 127
Qy 121 KKORFHNIRGWRGCMSCCRSSRTRETOL 151
Db 128 KKORFHNIRGWRGCMSCCRSSRTRETOL 158

RESULT 6

US-09-359-382-10
Sequence 10, Application US/09359382
Patent No. 6306397
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 266
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 99.2%; Score 823; DB 2; Length 266;

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Best Local Similarity 98.0%; Pred. No. 3.2e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDQPERPRKLPOLCTELQTTIHDIIECYCKQOQLRREYVDFAFRDLCTIVRDGNPY 60
D 8 MFQDQPERPRKLPOLCTELQTTIHDIIECYCKQOQLRREYVDFAFRDLCTIVRDGNPY 67
QY 61 AVXDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
D 68 AVCDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127
QY 121 KKQRFHNIRGRWTCRMSCCRSSRTRRETOL 151
D 128 KKQRFHNIRGRWTCRMSCCRSSRTRRETOL 158

RESULT 7
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRN
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 99.2%; Score 823; DB 2; Length 266;
Best Local Similarity 98.0%; Pred. No. 3.2e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDQPERPRKLPOLCTELQTTIHDIIECYCKQOQLRREYVDFAFRDLCTIVRDGNPY 60
D 8 MFQDQPERPRKLPOLCTELQTTIHDIIECYCKQOQLRREYVDFAFRDLCTIVRDGNPY 67
QY 61 AVXDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
D 68 AVCDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127
QY 121 KKQRFHNIRGRWTCRMSCCRSSRTRRETOL 151
D 128 KKQRFHNIRGRWTCRMSCCRSSRTRRETOL 158

RESULT 8
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 971953.5
```

```
;; PRIOR FILING DATE: 1997-08-22
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 4
;; LENGTH: 273
;; TYPE: PRN
;; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 99.2%; Score 823; DB 2; Length 273;
Best Local Similarity 98.0%; Pred. No. 3.3e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDQPERPRKLPOLCTELQTTIHDIIECYCKQOQLRREYVDFAFRDLCTIVRDGNPY 60
D 114 MFQDQPERPRKLPOLCTELQTTIHDIIECYCKQOQLRREYVDFAFRDLCTIVRDGNPY 173
QY 61 AVXDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
D 174 AVCDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 233
QY 121 KKQRFHNIRGRWTCRMSCCRSSRTRRETOL 151
D 234 KKQRFHNIRGRWTCRMSCCRSSRTRRETOL 264

RESULT 9
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 971953.5
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRN
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 99.2%; Score 823; DB 2; Length 292;
Best Local Similarity 98.0%; Pred. No. 3.6e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDQPERPRKLPOLCTELQTTIHDIIECYCKQOQLRREYVDFAFRDLCTIVRDGNPY 60
D 133 MFQDQPERPRKLPOLCTELQTTIHDIIECYCKQOQLRREYVDFAFRDLCTIVRDGNPY 192
QY 61 AVXDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
D 193 AVCDCKLFYSKISEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 252
QY 121 KKQRFHNIRGRWTCRMSCCRSSRTRRETOL 151
D 253 KKQRFHNIRGRWTCRMSCCRSSRTRRETOL 283

RESULT 10
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
```

GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Gabizon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Bernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 371
TYPE: PRT
ORGANISM: Homo sapien
US-09-485-885-6

Query Match 99.2%; Score 823; DB 2; Length 371;
Best Local Similarity 98.0%; Pred. No. 4.8e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRLCIVRDGPNY 60
DB 114 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRLCIVRDGPNY 173
QY 61 AVXKCLKFYSKISSEYHYCYSVYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 120
DB 174 AVCDKCLKFYSKISSEYHYCYSLVGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 233
QY 121 KKORFHNIRGRWTCRCMSCCRSSRTTRETOL 151
DB 234 KKORFHNIRGRWTCRCMSCCRSSRTTRETOL 264

RESULT 11
US-09-485-885-14
Sequence 14, Application US/09485885
Patent No. 6342224
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Gabizon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Bernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapien
US-09-485-885-14

Query Match 99.2%; Score 823; DB 2; Length 390;
Best Local Similarity 98.0%; Pred. No. 5.1e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRLCIVRDGPNY 60
DB 133 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRLCIVRDGPNY 192

QY 61 AVXKCLKFYSKISSEYHYCYSVYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 120
DB 193 AVCDKCLKFYSKISSEYHYCYSLVGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 252
QY 121 KKORFHNIRGRWTCRCMSCCRSSRTTRETOL 151
DB 253 KKORFHNIRGRWTCRCMSCCRSSRTTRETOL 283

RESULT 12
US-09-701-080C-18
Sequence 18, Application US/09701080C
Patent No. 6864054
GENERAL INFORMATION:
APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
FILE REFERENCE: N73477C GCM
CURRENT APPLICATION NUMBER: US/09/701,080C
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: GB 9811303.8
PRIOR FILING DATE: 1998-05-26
PRIOR APPLICATION NUMBER: GB 9900157.0
PRIOR FILING DATE: 1999-01-05
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 151
TYPE: PRT
ORGANISM: Human papillomavirus
US-09-701-080C-18

Query Match 98.6%; Score 818; DB 2; Length 151;
Best Local Similarity 97.4%; Pred. No. 6.1e-85;
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRLCIVRDGPNY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRLCIVRDGPNY 60
QY 61 AVXKCLKFYSKISSEYHYCYSVYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 120
DB 61 AVCDKCLKFYSKISSEYHYCYSLVGTLEQYNNKPLCDLLIRCNXOKPLCPBEKQRHLD 120
QY 121 KKORFHNIRGRWTCRCMSCCRSSRTTRETOL 151
DB 121 KKORFHNIRGRWTCRCMSCCRSSRTTRETOL 151

RESULT 13
US-09-462-993-1
Sequence 1, Application US/09462993
Patent No. 6884786
GENERAL INFORMATION:
APPLICANT: KIENV, Marie-Paule
APPLICANT: BIZOUANE, Nadine
APPLICANT: BIZOUANE, Jean-Marc
FILE REFERENCE: 017753-122
CURRENT APPLICATION NUMBER: US/09/462,993
CURRENT FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: PCT/FR98/01576
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: FR 97/09152
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.2
SEQ ID NO 1
LENGTH: 243
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Derived from
OTHER INFORMATION: human papillomavirus, strain HPV-16, E6 protein
OTHER INFORMATION: fused F protein signals, clone E6*TWf.
US-09-462-993-1

Query Match 93.9%; Score 779.5; DB 2; Length 243;
Best Local Similarity 94.7%; Pred. No. 2.5e-80;
Matches 143; Conservative 1; Mismatches 2; Indels 5; Gaps 1;

QY 1 MFQDPQERPRKLPOLCTELQTTIHIIIECVYCKQQLLRREYDPAFRDLCTVYRDGNY 60
DB 36 MFQDPQERPRKLPOLCTELQTTIHIIIECVYCKQQLLRREYDPAFRDLCTVYRDGNY 95
QY 61 AVXDKLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQ 120
DB 96 AVXDKLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQ 150
QY 121 KQRFNIRGRWTCRCMCCRSSRTRRETOL 151
DB 151 KQRFNIRGRWTCRCMCCRSSRTRRETOL 181

RESULT 14
US-08-860-165-12
Sequence 12, Application US/08860165A
Patent No. 6004557

GENERAL INFORMATION:
APPLICANT: EDWARDS, Scirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann

APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 172
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 62.5%; Score 519; DB 2; Length 172;
Best Local Similarity 96.8%; Pred. No. 5.7e-51;
Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 57 GNPYAVXDKLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQ 116
DB 2 GNPYAVXDKLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQ 61
QY 117 RHLDDKKQRFNIRGRWTCRCMCCRSSRTRRETOL 151
DB 62 RHLDDKKQRFNIRGRWTCRCMCCRSSRTRRETOL 96

RESULT 15
US-09-359-382-12
Sequence 12, Application US/09359382
Patent No. 6306397

GENERAL INFORMATION:
APPLICANT: EDWARDS, Scirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann

APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148

CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 172
TYPE: PRT
ORGANISM: Human papillomavirus type 16

US-09-359-382-12

Query Match 62.5%; Score 519; DB 2; Length 172;
Best Local Similarity 96.8%; Pred. No. 5.7e-51;
Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 57 GNPYAVXDKLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQ 116
DB 2 GNPYAVXDKLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCIHXKPLCPBEKQ 61
QY 117 RHLDDKKQRFNIRGRWTCRCMCCRSSRTRRETOL 151
DB 62 RHLDDKKQRFNIRGRWTCRCMCCRSSRTRRETOL 96

RESULT 16
US-08-860-165-14
Sequence 14, Application US/08860165A
Patent No. 6004557

GENERAL INFORMATION:
APPLICANT: EDWARDS, Scirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann

APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 172
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 57.6%; Score 478; DB 2; Length 172;
Best Local Similarity 92.5%; Pred. No. 2.6e-46;
Matches 86; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHIIIECVYCKQQLLRREYDPAFRDLCTVYRDGNY 60
DB 77 MFQDPQERPRKLPOLCTELQTTIHIIIECVYCKQQLLRREYDPAFRDLCTVYRDGNY 136
QY 61 AVXDKLKFYSKISEYRHVCYSVYGTTLLEQYNN 93
DB 137 AVXDKLKFYSKISEYRHVCYSVYGTTLSSH 169

RESULT 17
US-09-359-382-14
Sequence 14, Application US/09359382
Patent No. 6306397

GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRASER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PNO157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 172
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 57.6%; Score 478; DB 2; Length 172;
Best Local Similarity 92.5%; Pred. No. 2,6e-46;
Matches 86; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFODPQRPRLPOLCTELQTTTHDIIIECYCKQQLRREVDFAPRDLCTIVRDGPNY 60
DB 77 MFODPQRPRLPOLCTELQTTTHDIIIECYCKQQLRREVDFAPRDLCTIVRDGPNY 136

QY 61 AYXDKLKFYSKISEYRHYCYSVYGTLEEQYN 93
DB 137 AVCDKLFYSKISEYRHYCYSLYGTLLRSHHH 169

RESULT 18
US-08-117-083-10
Sequence 10 Application US/08117083
Patent No. 5719054
GENERAL INFORMATION:
APPLICANT: Boursnell, Michael E.
APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58783
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

LENGTH: 182 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
OTHER INFORMATION: /note= "Xaa refers to stop codon in
OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match 57.5%; Score 477; DB 1; Length 182;
Best Local Similarity 62.2%; Pred. No. 3,6e-46;
Matches 97; Conservative 5; Mismatches 8; Indels 46; Gaps 4;

QY 1 MFODPQRPRLPOLCTELQTTTHDIIIECYCKQQLRREVDFAPRDLCTIVRDGPNY 60
DB 9 MFODPQRPRLPOLCTELQTTTHDIIIECYCKQQLRREVDFAPRDLCTIVRDGPNY 60

QY 61 AYXDKLKFYSKISEYRHYCYSVYGTLEEQYNKPCDLLIRCTINXKPKLCPKORHLD 120
DB 61 -----ISEYRHYCYSLYGTLEEQY-----EKKORHLD 88

QY 121 KKQRFNIRGRWG-----RCMSCRSRRRRETOL 151
DB 89 KKQRFNIRGRWSCMETIHLHGMNICYIC-NOROVOL 123

RESULT 19
US-08-247-904B-10
Sequence 10 Application US/08247904B
Patent No. 5981899
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Eckstein, Jens W.
APPLICANT: Diacteta, Giulio
TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,904B
FILING DATE: 23-MAY-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-247-904B-10

Query Match 54.9%; Score 455.5; DB 1; Length 158;
Best Local Similarity 56.1%; Pred. No. 8,2e-44;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

[illegible]

RESULT 20
US-08-767-942A-19
; Sequence 19, Application US/08767942A

```

1  GENERAL INFORMATION: Mark
2  APPLICANT: Rolfe, Mark
3  APPLICANT: Chiu, M. Isabel
4  APPLICANT: Berlin, Vivian
5  APPLICANT: Damagnez, Veronique
6  APPLICANT: Diaceta, Giulio
7  APPLICANT: Guillaume, Cottarel
8  TITLE OF INVENTION: UBIOURIN CONJUGATING ENZYMES
9  NUMBER OF SEQUENCES: 45
10 CORRESPONDENCE ADDRESS:
11 ADDRESS: FOLEY, HOAG & ELIOT LLP
12 STREET: One Post Office Square
13 CITY: Boston
14 STATE: MA
15 COUNTRY: USA
16 ZIP: 02109-2170
17
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Floppy disk
20 COMPUTER: IBM PC compatible
21 OPERATING SYSTEM: PC-DOS/MS-DOS
22 SOFTWARE: PatentIn Release #1.0, Version #1.30
23
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/767,942A
26 FILING DATE: 17-DEC-1996
27
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Vincent, Matthew P.
30 REGISTRATION NUMBER: 36,709
31 REFERENCE/DOCKET NUMBER: MIV-029.04
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 617-832-1000
34 TELEFAX: 617-832-7000
35
36 INFORMATION FOR SEQ ID NO: 19:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 158 amino acids
39 TYPE: amino acid
40 TOPOLOGY: linear
41
42 MOLECULE TYPE: protein
43
44 US-08-767-942A-19

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[illegible]

RESULT 21
 US-08-117-083-14
 ; Sequence 14, Application US/08117083
 ; Patent No. 5719054
 ; GENERAL INFORMATION:
 ; APPLICANT: Boursnell, Michael E.
 ; APPLICANT: Inglis, Stephen C.
 ; APPLICANT: Munro, Alan J.
 ; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
 ; TITLE OF INVENTION: Papilloma Virus Proteins
 ; NUMBER OF SEQUENCES: 70
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Walter H. Dreger
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA

```

1 COMPUTER READABLE FORM:
2
3 MEDIUM TYPE: Floppy disk
4 COMPUTER: IBM PC compatible
5 OPERATING SYSTEM: PC-DOS/MS-DOS
6 SOFTWARE: Patent In Release #1.0, Version #1.25
7
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/117,083
10 FILING DATE: 10-SEP-1993
11 CLASSIFICATION: 435
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Dregler, Walter H.
14 REGISTRATION NUMBER: 24,190
15 REFERENCE/DOCKET NUMBER: A-58783
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 415-781-1989
18 TELEFAX: 415-398-3249
19
20 TELEX: 910 277299
21
22 INFORMATION FOR SEQ ID NO: 14:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 271 amino acids
25 TYPE: amino acid
26 STRANDEDNESS: single
27 TOPOLOGY: linear
28 MOLECULE TYPE: protein
29 FEATURE:
30 NAME/KEY: Protein
31 LOCATION: 1..271
32 OTHER INFORMATION: /note="Xaa refers to stop codon in
33 OTHER INFORMATION: the open reading frame."
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35 US-08-117-083-14
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```
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
FILE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 278
TYPE: PRT
ORGANISM: Homo sapien
US-09-485-885-21
```

```
Query Match 54.9%; Score 455.5; DB 2; Length 278;
Best Local Similarity 56.1%; Pred. No. 1.6e-43;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;
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```
QY 2 FODPGERPKLPOLCTELQTHIHIIIECVYCKQOQLRREYVDFAFRLDCTIVYRGNPYA 61
DB 115 FEDPFRARYKLPDLCTELNTSLQDLEITCYCVKTVLETFEVEFAFKLPVYVRDSIPHA 174
QY 62 VXDCKLKFYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRNCINXOKPLCEPEKORHLDK 121
DB 175 ACHKCIDPYSIRLRIHSDSVYGTTLLEKLTNTGYNLIRLRCQKPLNPAEKRLHINE 234
QY 122 KQRFNIRGRTGRCMSCCRSSR-----TRRETQL 151
DB 235 KRPFNINAGHYRGQCHSCCNRAQRLQRRRETQV 269
```

```
RESULT 23
US-09-485-885-23
Sequence 23, Application US/09485885
Patent No. 6342224
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
FILE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 383
TYPE: PRT
ORGANISM: Homo sapien
US-09-485-885-23
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Query Match 54.9%; Score 455.5; DB 2; Length 383;
Best Local Similarity 56.1%; Pred. No. 2.4e-43;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;
```

```
DB 175 ACHKCIDPYSIRLRIHSDSVYGTTLLEKLTNTGYNLIRLRCQKPLNPAEKRLHINE 234
QY 122 KQRFNIRGRTGRCMSCCRSSR-----TRRETQL 151
DB 235 KRPFNINAGHYRGQCHSCCNRAQRLQRRRETQV 269
```

```
RESULT 24
US-09-000-094-20
Sequence 20, Application US/0900094
Patent No. 6365160
GENERAL INFORMATION:
APPLICANT: WEBB, Elizabeth Ann
MARGGETTS, Mary Brigid
COX, John Cooper
FRAZER, Ian
MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
HOLLAND, Stirling John
EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPEPTIDE CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-000-094-20
```

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Query Match 36.6%; Score 304; DB 2; Length 368;
Best Local Similarity 39.8%; Pred. No. 3.4e-26;
Matches 51; Conservative 29; Mismatches 48; Indels 0; Gaps 0;
```



```

GENERAL INFORMATION:
APPLICANT: WEBB, Elizabeth Ann
MARGETTS, Mary Brigid
COX, John Cooper
FRAZER, Ian
MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
Holland
EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,749
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-011-749-24

Query Match          36.6%; Score 304; DB 2; Length 465;
Best Local Similarity 39.8%; Pred. No. 4.5e-26;
Matches 51; Conservative 29; Mismatches 48; Indels 0; Gaps 0;

QY 12 LPQLCTELQTHDILIECYCKQQLLRREYVDFAFRLDCTIVYRGDNFYAVYDKLKFPYS 71
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 13 IDQLCTFNLMTHTQINCVPCKNALTTAEIYSYAKHLKVLFRGGYPPAAACCLIEFHG 72
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 KISEYRHVCYSVGTLLIEQYNNKPLCDLLIRICINOKPLCPBEKORHLDKORFHNIRGR 131
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 73 KINQYRHFYAGYATVVEETKQDILDVILRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 WTGRCMSC 139
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 133 WKGRCLHC 140
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 30
US-09-000-094-46
; Sequence 46, Application US/09000094
; Patent No. 6365160
; GENERAL INFORMATION:
```

```

APPLICANT: WEBB, Elizabeth Ann
MARGETTS, Mary Brigid
COX, John Cooper
FRAZER, Ian
MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
Holland
EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1587 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-000-094-46

Query Match          36.6%; Score 304; DB 2; Length 1587;
Best Local Similarity 39.8%; Pred. No. 2e-25;
Matches 51; Conservative 29; Mismatches 48; Indels 0; Gaps 0;

QY 12 LPQLCTELQTHDILIECYCKQQLLRREYVDFAFRLDCTIVYRGDNFYAVYDKLKFPYS 71
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 699 IDQLCTFNLMTHTQINCVPCKNALTTAEIYSYAKHLKVLFRGGYPPAAACCLIEFHG 758
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 KISEYRHVCYSVGTLLIEQYNNKPLCDLLIRICINOKPLCPBEKORHLDKORFHNIRGR 131
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 759 KINQYRHFYAGYATVVEETKQDILDVILRCYLCHKPLCEVEKVKHILTKARFIKLNCT 818
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 WTGRCMSC 139
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 819 WKGRCLHC 826
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 31
US-10-011-749-46
; Sequence 46, Application US/10011749
; Patent No. 6726912
; GENERAL INFORMATION:
APPLICANT: WEBB, Elizabeth Ann
MARGETTS, Mary Brigid
COX, John Cooper
```



```

; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-601-729-276

Query Match      15.4%; Score 128; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 LRREYDFAFRDLCIVRDGNPY 60
Db 1 LRREYDFAFRDLCIVRDGNPY 23

RESULT 38
US-09-980-523A-6
; Sequence 6, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/01/00100
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-6

Query Match      14.9%; Score 124; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 RREYDFAFRDLCIVRDGNPY 60
Db 1 RREYDFAFRDLCIVRDGNPY 22

RESULT 39
US-08-934-915-167
; Sequence 167, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: CHENG, HWEI-MING
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
```

```

; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Fouch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-167

Query Match      14.5%; Score 120; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 RWTGRMCCSCRSRRTRETOL 151
Db 1 RWTGRMCCSCRSRRTRETOL 21

RESULT 40
US-09-913-204-3
; Sequence 3, Application US/09913204
; Patent No. 6953579
; GENERAL INFORMATION:
; APPLICANT: GISSMAN, Lutz
; APPLICANT: MULLER, Martin
; APPLICANT: MULLER, Herman
; TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES OR
; TITLE OF INVENTION: CHIMERIC CAPSOMERS FROM BPV
; FILE REFERENCE: 035280134PCUS00
; CURRENT APPLICATION NUMBER: US/09/913,204
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/DE00/00426
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: DE 199 05 883.0
; PRIOR FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Bovine papilloma virus
US-09-913-204-3

Query Match      14.3%; Score 119; DB 2; Length 137;
Best Local Similarity 28.9%; Pred. No. 1e-05;
Matches 35; Conservative 16; Mismatches 60; Indels 2; Gaps 2;

Qy 28 LECYCKQQLRREYDFAFRDLCIVRDGNPYAVXDKLAFYKISRYHYCYVYGT 87
Db 15 LDCIMCRPLREYDFAFRDLCIVRDGNPYAVXDKLAFYKISRYHYCYVYGT 74
Qy 88 LEOYKPLCDLLIRCIKXQKPLCEEKQRHLDKKQRFHNIQR-WTGRMCCSCRSR 145
```

Db 75 AELLHGKTLDRICRCYCGKLTNKKRHVLFNEPFCCKRANIRGRCTDCCHGSR 134

QY 146 R 146
Db 135 K 135

RESULT 41
US-09-913-204-7
Sequence 7, Application US/09913204

Patent No. 6953579
GENERAL INFORMATION:
APPLICANT: GISSMAN, Lutz
APPLICANT: MULLER, Martin
TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES OR
FILE REFERENCE: 035280134PCUS00
CURRENT APPLICATION NUMBER: US/09/913,204
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/DE00/00426
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: DE 199 05 883.0
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 137
TYPE: PRT
ORGANISM: Bovine papilloma virus
US-09-913-204-7

Query Match 14.3%; Score 119; DB 2; Length 137;
Best Local Similarity 28.9%; Pred. No. 1e-05; Indels 2; Gaps 2;
Matches 35; Conservative 16; Mismatches 68; Indels 2; Gaps 2;

QY 28 LECVCKQQLRREYDFAFDLCIVYRDGNPYAVXDKLKFYSKISEYRHVCYSVYGT 87
Db 15 LDCWCREPLTEVDFAFCWVDFHVIIRGCGYACTICLENCLATERLWQGVPTGEE 74
QY 88 LEOQYNKPLCDLLIRCTINXQKPLCEEKQRLDKKORFNINR- WTGRCMSCCR-SSRT 145
Db 75 AELLHGKTLDRICRCYCGKLTNKKRHVLFNEPFCCKRANIRGRCTDCCHGSR 134
QY 146 R 146
Db 135 K 135

RESULT 42
US-09-913-204-13
Sequence 13, Application US/09913204
Patent No. 6953579
GENERAL INFORMATION:
APPLICANT: GISSMAN, Lutz
APPLICANT: MULLER, Martin
APPLICANT: MULLER, Herman
TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES OR
FILE REFERENCE: 035280134PCUS00
CURRENT APPLICATION NUMBER: US/09/913,204
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/DE00/00426
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: DE 199 05 883.0
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 137
TYPE: PRT
ORGANISM: Bovine papilloma virus
US-09-913-204-13

Query Match 14.3%; Score 119; DB 2; Length 137;
Best Local Similarity 28.9%; Pred. No. 1e-05; Indels 2; Gaps 2;
Matches 35; Conservative 16; Mismatches 68; Indels 2; Gaps 2;

QY 28 LECVCKQQLRREYDFAFDLCIVYRDGNPYAVXDKLKFYSKISEYRHVCYSVYGT 87
Db 15 LDCWCREPLTEVDFAFCWVDFHVIIRGCGYACTICLENCLATERLWQGVPTGEE 74
QY 88 LEOQYNKPLCDLLIRCTINXQKPLCEEKQRLDKKORFNINR- WTGRCMSCCR-SSRT 145
Db 75 AELLHGKTLDRICRCYCGKLTNKKRHVLFNEPFCCKRANIRGRCTDCCHGSR 134
QY 146 R 146
Db 135 K 135

RESULT 43
US-08-934-915-166
Sequence 166, Application US/08934915

Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESS: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 166:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-166

Query Match 13.9%; Score 115; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3e-06; Indels 0; Gaps 0;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 115 KORHLDKKORFNINIRGRWTGR 135
Db 1 KORHLNKKORFNINIRGRWTGR 21

Qy 4 DPQERPKLPQLCTELQTTIHDIILECYCK 34
||| ||| ||| ||| ::| : |||
Db 1 DPTRRPYKLPDLCTELNTSLQDIEITCYCK 31

```

: Patent No. 6323794
: Sequence 2 Application US/08164768
:
: GENERAL INFORMATION:
: APPLICANT: BLEUL, Conrad
: APPLICANT: AUER, Martin
: APPLICANT: MULDER, Martin
: TITLE OF INVENTION: SEROREACTIVE EPITOPES ON PROTEINS OF
: TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
: ADDRESSEE: DUNNER, L.L.P.
: STREET: 1300 I Street, N.W.
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/164,768
: FILING DATE: 10-DEC-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Forman, David S.
: REGISTRATION NUMBER: 33,694
: REFERENCE/DOCKET NUMBER: 05552.1075-02000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 408-4400
: TELEFAX: (202) 408-4400
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 32 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-164-768-2
:
: Query Match 13.9%; Score 115; DB 2; Length 32;
: Best Local Similarity 64.5%; Pred. No. 5e-06;
: Matches 20; Conservative 3; Mismatches 8; Indels 0; Gaps 0
:
: QY 4 DPOERPRLPOLCTELQTTIHDIIECVCK 34
: 1 DPTRRPYKLPDLCTELNTSLQDIIEITCVCK 31
:
: RESULT 46
: US-09-601-729-278
: Sequence 278, Application US/09601729
: Patent No. 6683052
: GENERAL INFORMATION:
: APPLICANT: THIAM, KADER
: APPLICANT: AURIAULT, CLAUDE
: APPLICANT: GRAS-MASSÉ, HELENE
: APPLICANT: LOING, ESTELLE
: APPLICANT: VERMAERDE, CLAUDE
: APPLICANT: GUILLET, JEAN GERARD
: TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
: TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
: FILE REFERENCE: USB-97-AU-IN
: CURRENT APPLICATION NUMBER: US/09/601,729
: CURRENT FILING DATE: 2000-11-20
: PRIOR APPLICATION NUMBER: PCT/FR99/00259
: PRIOR FILING DATE: 1999-02-05
: PRIOR APPLICATION NUMBER: 98 01439
: PRIOR FILING DATE: 1998-02-06
: NUMBER OF SEQ ID NOS: 281
: SOFTWARE: PatentIn Ver. 2.1

```

```
; SEQ ID NO 278
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-601-729-278

Query Match      13.7%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      114 EKORLDDKKORFHNIRGRWT 133
Db      1 EKORLDDKKORFHNIRGRWT 20

RESULT 47
US-10-612-818-4
; Sequence 4, Application US/10612818
; Patent No. 6933123
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Pap
; TITLE OF INVENTION: Associated Cancers
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/10/612,818
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
US-10-612-818-4

Query Match      13.7%; Score 114; DB 2; Length 22;
Best Local Similarity 95.5%; Pred. No. 4.2e-06;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      55 RDGNPYAVXDCKLKPKYSKISEY 76
Db      1 RDGNPYAVXDCKLKPKYSKISEY 22

RESULT 48
US-08-934-915-44
; Sequence 44, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
```

```
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-44

Query Match      13.1%; Score 109; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      70 YSKISEYRHRYCYSLVGTGLE 89
Db      1 YSKISEYRHRYCYSLVGTGLE 20

RESULT 49
US-08-934-915-45
; Sequence 45, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
```

REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-45

Query Match 13.1%; Score 109; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 GTTLEQYKNKPLCDLLIRCI 104
Db 1 GTTLEQYKNKPLCDLLIRCI 20

RESULT 50
US-08-934-915-163
Sequence 163, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-163

Query Match 13.1%; Score 109; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 70 YKSISEYRHVCYSYVGTTL 89
Db 1 YKSISEYRHVCYSYVGTTL 20

RESULT 51
US-08-934-915-164
Sequence 164, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-164

Query Match 12.5%; Score 104; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.1e-05;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 85 GTTLEQYKNKPLCDLLIRCI 104
Db 1 GTTLEQYKNKPLCDLLIRCI 20

RESULT 52
US-08-934-915-165
Sequence 165, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 165:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-165

Query Match 12.5%; Score 104; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.1e-05;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

;; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
;; TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
;; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
;; NUMBER OF SEQUENCES: 193
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MASON & ASSOCIATES, P.A.
;; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
;; CITY: CLEARWATER
;; STATE: FLORIDA
;; COUNTRY: U.S.A.
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows 3.0
;; SOFTWARE: Microsoft Word 6.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/934,915
;; FILING DATE: 22-SEP-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/949,836
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LOUISE A. Fouché
;; REGISTRATION NUMBER: 37,133
;; REFERENCE/DOCKET NUMBER: 1946.6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 813-538-3800
;; TELEFAX: 813-538-3820
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-934-915-165
;
;; INFORMATION FOR SEQ ID NO: 165:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-934-915-165
;
Query Match 12.5%; Score 104; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.1e-05;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
Qy 100 LIRCINXOKPLCPPEKORHL 119
Db 1 LIRCINXOKPLCPPEKORHL 20
;
RESULT 53
US-08-934-915-159
;; Sequence 159, Application US/08934915
;; Patent No. 5932412
;; GENERAL INFORMATION:
;; APPLICANT: DILLNER, JOAKIM
;; APPLICANT: DILLNER, LENA
;; APPLICANT: CHENG, HWEI-MING
;; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
;; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
;; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
;; TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
;; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
;; NUMBER OF SEQUENCES: 193
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MASON & ASSOCIATES, P.A.
;; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
;; CITY: CLEARWATER
;; STATE: FLORIDA
;; COUNTRY: U.S.A.
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows 3.0
;; SOFTWARE: Microsoft Word 6.0
;; CURRENT APPLICATION DATA:
;;

;; APPLICATION NUMBER: US/08/934,915
;; FILING DATE: 22-SEP-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/949,836
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LOUISE A. Fouché
;; REGISTRATION NUMBER: 37,133
;; REFERENCE/DOCKET NUMBER: 1946.6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 813-538-3800
;; TELEFAX: 813-538-3820
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-934-915-159
;
Query Match 11.8%; Score 98; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 0.00024;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
Qy 10 RRLPOLCTELOTTHDILE 29
Db 1 RRLPOLCTELOTTHDILE 20
;
RESULT 54
US-08-934-915-160
;; Sequence 160, Application US/08934915
;; Patent No. 5932412
;; GENERAL INFORMATION:
;; APPLICANT: DILLNER, JOAKIM
;; APPLICANT: DILLNER, LENA
;; APPLICANT: CHENG, HWEI-MING
;; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
;; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
;; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
;; TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
;; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
;; NUMBER OF SEQUENCES: 193
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MASON & ASSOCIATES, P.A.
;; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
;; CITY: CLEARWATER
;; STATE: FLORIDA
;; COUNTRY: U.S.A.
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows 3.0
;; SOFTWARE: Microsoft Word 6.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/934,915
;; FILING DATE: 22-SEP-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/949,836
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LOUISE A. Fouché
;; REGISTRATION NUMBER: 37,133
;; REFERENCE/DOCKET NUMBER: 1946.6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 813-538-3800
;; TELEFAX: 813-538-3820
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-934-915-160
;; SEQUENCE CHARACTERISTICS:
;;

LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-160

Query Match 11.7%; Score 97; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 0.00031;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 25 DILLECVCCKOOLLREYVD 44
:|||||:|||||:|||||:
Db 1 NILEECVCCKOOLLREYVN 20

RESULT 55
US-08-934-915-161
Sequence 161, Application US/08934915
Patent No. 5932412

GENERAL INFORMATION:
APPLICANT: DILNER, JOAKIM
APPLICANT: DILNER, LENA
APPLICANT: CHENG, HWEI-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Fouchon
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:

INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-161

Query Match 11.7%; Score 97; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 0.00031;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 40 REVYDFARPDICIVYRDGP 59
|||||:|||||:|||||:
Db 1 REVYNFAFRNLCTIVYRGNP 20

RESULT 56

US-09-641-528B-46524
Sequence 46524, Application US/09641528B
Patent No. 7026443

GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Ectaban
APPLICANT: Grey, Howard

TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46524
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46524

Query Match 11.3%; Score 94; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 PHNIRGRWTCRCMSC 139
|||||:|||||:|||||:
Db 1 PHNIRGRWTCRCMSC 15

RESULT 57
US-08-466-285-4
Sequence 4, Application US/08466285
Patent No. 5753233

GENERAL INFORMATION:
APPLICANT: Bleul, Conrad
APPLICANT: Gissmann, Lutz
APPLICANT: Muller, Martin
TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of
TITLE OF INVENTION: Human Papillomavirus (HPV)18
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,285
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,768
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,992
FILING DATE: 21-SEP-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

Qy 40 REVYDFARPDICIVYRDGP 59
|||||:|||||:|||||:
Db 1 REVYNFAFRNLCTIVYRGNP 20

APPLICATION NUMBER: US 07/696,953
FILING DATE: 08-MAY-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 40 15 044.5
FILING DATE: 10-MAY-1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Manepizer, David A.
REGISTRATION NUMBER: 37,540
REFERENCE/DOCKET NUMBER: 05552.1075-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-285-4

Query Match 11.2%; Score 93; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.0016;
Matches 18; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 61 AVXDCKLFYKISEYRHVCYVGTLEQ 90
Db 1 AACHKCIDFYSRIRLHRYSDSVGDTLEK 30

RESULT 58
US-08-164-768-4
Sequence 4, Application US/08164768
Patent No. 6322794
GENERAL INFORMATION:
APPLICANT: BLEUL, Conrad
APPLICANT: GISSMANN, Lutz
APPLICANT: MULLER, Martin
TITLE OF INVENTION: SEROREACTIVE EPITOPES ON PROTEINS OF
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
ADDRESSEE: DUNNER, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,768
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552.1075-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-164-768-4

Query Match 11.2%; Score 93; DB 2; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.0016;
Matches 18; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 61 AVXDCKLFYKISEYRHVCYVGTLEQ 90
Db 1 AACHKCIDFYSRIRLHRYSDSVGDTLEK 30

RESULT 59
US-09-641-528B-46535
Sequence 46535, Application US/09641528B
Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Euseban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46535
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46535

Query Match 11.1%; Score 92; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 RGRWTRGRCMCCRSS 143
Db 1 RGRWTRGRCMCCRSS 15

RESULT 60
US-08-934-915-162
Sequence 162, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEI-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foulch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-162

Query Match 11.1%; Score 92; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 0.0012;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 55 RDGNPYAVXDKCLKFYSKIS 74
|:|||||:|||||
Db 1 RGNPNYAVCNKCLKFYSKIS 20

RESULT 61
US-08-363-586-3
Sequence 3, Application US/08363586
Patent No. 5629161
GENERAL INFORMATION:
APPLICANT: Mueller, Martin
APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
TITLE OF INVENTION: Peptides for the Diagnostic Purpose
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,586
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/909,296
FILING DATE: 09-JUL-1992
APPLICATION NUMBER: EP 9111720.8
FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Madler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02481-1195-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-363-586-3

Query Match 10.8%; Score 90; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQDPQERPRKLPOLC 16
|||||
Db 8 MFQDPQERPRKLPOLC 23

RESULT 62
US-09-641-528B-46517
Sequence 46517, Application US/09641528B
Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Betteban
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46517
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46517

Query Match 10.7%; Score 89; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 CLKFYSKISEYRHYC 80
|||||
Db 1 CLKFYSKISEYRHYC 15

RESULT 63
US-07-909-122-2
Sequence 2, Application US/07909122
Patent No. 5415995
GENERAL INFORMATION:
APPLICANT: SCHOOLNIK, GARY K.
APPLICANT: PALERSKY, JOEL M.
TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
TITLE OF INVENTION: VIRUS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/909,122
; FILING DATE: 19920706
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BENZ, WILLIAM H.
; REGISTRATION NUMBER: 25,952
; REFERENCE/DOCKET NUMBER: 28600-20105.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-909-122-2

Query Match 10.2%; Score 85; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FODPQERPRKLPQLC 16
Db 1 FODPQERPRKLPQLC 15

RESULT 64
US-09-641-528B-46523
; Sequence 46523, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46523
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
;
US-09-641-528B-46523

Query Match 10.2%; Score 85; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 EQQYNKPLCDLLIRC 103
Db 1 EQQYNKPLCDLLIRC 15

RESULT 65
US-09-641-528B-46525
; Sequence 46525, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
```

```

; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46525
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
;
US-09-641-528B-46525

Query Match 10.2%; Score 85; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 GRWMSCCRSSRTRE 148
Db 1 GRWMSCCRSSRTRE 15

RESULT 66
US-09-641-528B-46526
; Sequence 46526, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46526
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
;
US-09-641-528B-46526

Query Match 10.2%; Score 85; DB 3; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0051;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 78 HCYSVYGTTLQOY 92
Db 1 HCYSVYGTTLQOY 15

RESULT 67
US-09-641-528B-51200
; Sequence 51200, Application US/09641528B
; Patent No. 7026443
```



```

; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51200
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-51200

Query Match      10.2%; Score 85; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      107 QKPLCPKPKRHLDK 121
Db      1 QKPLCPKPKRHLDK 15

RESULT 68
US-09-641-528B-46519
; Sequence 46519, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46519
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46519

Query Match      10.1%; Score 84; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      44 DPAFRDLCTVYRDGN 58
Db      1 DPAFRDLCTVYRDGN 15

RESULT 69
US-09-641-528B-46534
; Sequence 46534, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46534
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46534

Query Match      10.1%; Score 84; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      20 OTTHDIILCEYCK 34
Db      1 OTTHDIILCEYCK 15

RESULT 70
US-09-641-528B-46522
; Sequence 46522, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46522
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46522

Query Match      10.0%; Score 83; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      29 ECVYCKQQLLRREYV 43
Db      1 ECVYCKQQLLRREYV 15

RESULT 71
US-09-641-528B-46527
```

```
Sequence 46527, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46527
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46527

Query Match      10.0%; Score 83; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 IHDIILECYCKQQL 37
Db      1 IHDIILECYCKQQL 15

RESULT 72
US-09-641-528B-46536
; Sequence 46536, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46536
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46536

Query Match      10.0%; Score 83; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      42 VYDFARDLCTIVRD 56
Db      1 VYDFARDLCTIVRD 15

RESULT 73
```

```
US-09-641-528B-50556
; Sequence 50556, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50556
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50556

Query Match      10.0%; Score 83; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 IHDIILECYCKQQL 37
Db      1 IHDIILECYCKQQL 15

RESULT 74
US-08-075-541D-52
; Sequence 52, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-075-541D-52

Query Match 9.9%; Score 82; DB 2; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FODPQRRPKLPOLC 16
   :|||||
Db 1 YDPQRRPKLPOLC 15

RESULT 75
US-09-641-528B-51199
; Sequence 51199, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51199
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-51199

Query Match 9.9%; Score 82; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CTELQTTIHDIILC 30
   :|||||
Db 1 CTELQTTIHDIILC 15

RESULT 76
US-09-641-528B-51250
; Sequence 51250, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B

```

```

; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 51250
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-51250

Query Match
Best Local Similarity 9.9%; Score 82; DB 3; Length 15;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 107 OKPLCPBEKORHLDK 121
      |||
      1 OKPLCPBEKORHLDK 15

RESULT 77
US-09-270-767-41452
; Sequence 41452, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-004
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41452
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41452

Query Match
Best Local Similarity 9.9%; Score 82; DB 2; Length 654;
Matches 33; Conservative 15; Mismatches 42; Indels 78; Gaps 6;

QY 14 QLTLEQTTIHDIILECYCKOQLRREYDPAFRLDLCIVYDGNPY----- 60
      |||
      376 QVITALGKTWHPHEFTCMHCSQELGTRNPF-----RDGFYCCPDYHNLFSPPRC 425

QY 61 -----AVADKCLKFKFSKISEVRHY-----CYSYVGTTL-LEQQYNKPLC----- 97
      |||
      426 AYVNGALLDKCYTALDKTWHTEHFFCAQCGQGFGEFGHERGDKPYCRNDYFEMFAPKCN 485

QY 98 -----DLIRICINQ-----KPLCPE 113
      |||
      486 GCNRAIMENYISALNSQWHPDCCVFCVDRCDKKAIVRGKSFYAMEKRPVCPQ 533

RESULT 78
US-09-641-528B-46518
; Sequence 46518, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esben
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001

```

```

; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46518
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46518

Query Match
Best Local Similarity 9.8%; Score 81; DB 3; Length 15;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 80 CYSVYGTLEQOYK 94
DB 1 CYSVYGTLEQOYK 15
```

```

RESULT 79
US-09-641-528B-46520
; Sequence 46520, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46520
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46520
```

```

Query Match
Best Local Similarity 9.6%; Score 80; DB 3; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 DILLECVCCKQQLR 39
DB 1 DILLECVCCKQQLR 15
```

```

RESULT 80
US-09-641-528B-47291
; Sequence 47291, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47291
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-47291
```

```

; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47291
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-47291

Query Match
Best Local Similarity 9.6%; Score 80; DB 3; Length 15;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 125 FHNIRGRTGRCMSC 139
DB 1 FHNIRGRTGRCMSC 15
```

```

RESULT 81
US-09-641-528B-50558
; Sequence 50558, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50558
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50558
```

```

Query Match
Best Local Similarity 9.6%; Score 80; DB 3; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPOLCTELQTTIHI 26
DB 1 LPOLCTELQTTIHI 15
```

```

RESULT 82
US-09-641-528B-46532
; Sequence 46532, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46532
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46532
```

```

; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 46532
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46532

Query Match          9.5%; Score 79; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PRKLPOLCTELQTTI 23
Db      1 PRKLPOLCTELQTTI 15

RESULT 83
US-09-641-528B-46516
; Sequence 46516, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Setite, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 46516
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46516

Query Match          9.4%; Score 78; DB 3; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.032;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      51 CIVRDGNPYAVXDK 65
Db      1 CIVRDGNPYAVCDK 15

RESULT 84
US-09-641-528B-46528
; Sequence 46528, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Setite, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
```

```

; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 46528
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46528

Query Match          9.4%; Score 78; DB 3; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.032;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      101 IRCINXQKPLCEEEK 115
Db      1 IRCINXQKPLCEEEK 15

RESULT 85
US-09-270-767-31740
; Sequence 31740, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 31740
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-31740

Query Match          9.3%; Score 77.5; DB 2; Length 165;
Best Local Similarity 26.0%; Pred. No. 0.64;
Matches 34; Conservative 14; Mismatches 66; Indels 17; Gaps 5;

Qy      29 ECVYCKQQLRREYVDFARDLCTVYRDG-----NPYAVXDK-LKFSKISEYHY 79
Db      30 ECTACDIQMTAKERSIHFDTCIFMREAIRSLNVTLSRYVCNVCLEKFAVTDLLQEHK 89
Qy      80 CYSV-YGTTLEQYVKKPL--CDLLIRICINXQKPLCEEEKORHLDKQRFHNI RGRWTR- 135
Db      90 CTSFHYFPRRLNENGLKLLPDCDFVNVFPAHDLFAHSEEGHINKKREKERTNRNGAGRI 149
Qy      136 ----CMSCCRS 142
Db      150 RQYLCDDIGKS 160

RESULT 86
US-09-270-767-46957
; Sequence 46957, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
```

SEQ ID NO 46957
LENGTH: 165
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-46957

Query Match
Best Local Similarity 26.0%; Score 77.5; DB 2; Length 165;
Matches 34; Conservative 14; Mismatches 66; Indels 17; Gaps 5;

QY 29 ECVCYKQQLRRVYDFARDLCTVYRDG-----NRYAVXDK-LKFSKISRYHY 79
DB 30 ECTACDIQNTAKASIHPTDCIFMRBAIRSLNVTLSRYFVCNVCLEKFANTDLQERH 89
QY 80 CYSV-YGTLLEQYKPL--CDLLRCINXQKPLCEBEQRHLDKQRFHNIRGWTGR- 135
DB 90 CTSFHYFPLNENKLLPDCDCDVNFPAHDFLAHSEKHLKKRKEKRETNMGARI 149
QY 136 ----CMSCRS 142
DB 150 RQYLDICGKS 160

RESULT 87
US-09-949-016-6366
Sequence 6366, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 6366
LENGTH: 572
TYPE: PRT
ORGANISM: Human
US-09-949-016-6366

Query Match
Best Local Similarity 22.4%; Score 77.5; DB 2; Length 572;
Matches 41; Conservative 21; Mismatches 66; Indels 55; Gaps 11;

QY 1 MFOD---PDRPRKLPOLC-----TEIQTTHHLLLECVYKQQLRRVY 43
DB 366 LMQDMHPORONAVNELGCRCHQPLARQPAVRALGOLFHLCFTCHCAQQLQGOQF 425
QY 44 DFAFRDLCTVYRD-----GNPYAVXDK-LKFSKISRYHYCS-----VYGT 87
DB 426 SLEGAAYCEGCTYDLTEKCTGCEP--ITDRMLRAVKG--AYHPCTCYVCARPLSGIS 481
QY 88 -LEQYKPLC-----DLIRICINXQKPLCEBEQRHLDKQRFHNIRGWTGR 136
DB 482 FIDQANRPHCVDPDHYKQYAPRCSVSEPIPEGRDETIVRVVALDKNFM-----KC 534
QY 137 MSC 139
DB 535 YKC 537

RESULT 88
US-09-641-528B-46521
Sequence 46521, Application US/09641528B
Patent No. 7026443

GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.010001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 46521
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46521

Query Match
Best Local Similarity 93.3%; Score 77; DB 3; Length 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 98 DLLIRICINXQKPLCP 112
DB 1 DLLIRICINXQKPLCP 15

RESULT 89
US-09-641-528B-50557
Sequence 50557, Application US/09641528B
Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.010001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 50557
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50557

Query Match
Best Local Similarity 93.3%; Score 77; DB 3; Length 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 LCIVYRDGNPYAVXD 64
DB 1 LCIVYRDGNPYAVCD 15

RESULT 90
US-09-641-528B-50559
Sequence 50559, Application US/09641528B

```
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.010001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50559
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50559

Query Match          9.3%; Score 77; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      35 QQLRREYVDFAFRD 49
DB      1 QQLRREYVDFAFRD 15

RESULT 91
US-09-939-853A-15
; Sequence 15, Application US/09939853A
; Patent No. 6989232
; GENERAL INFORMATION:
; APPLICANT: Burgess et al.
; TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-099
; CURRENT APPLICATION NUMBER: US/09/939,853A
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/228,191
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/267,300
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/269,961
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/277,337
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15
; LENGTH: 785
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-939-853A-15

Query Match          9.2%; Score 76.5; DB 2; Length 785;
Best Local Similarity 24.0%; Pred. No. 5.3;
Matches 31; Conservative 12; Mismatches 33; Indels 53; Gaps 7;
```

```
DB      392 ATDQCFSCC 400

RESULT 92
US-07-909-122-4
; Sequence 4, Application US/07909122
; Patent No. 5415995
; GENERAL INFORMATION:
; APPLICANT: SCHOOLNIK, GARY K.
; APPLICANT: PALERFSKY, JOEL M.
; TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/909,122
; FILING DATE: 19920706
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BENZ, WILLIAM H.
; REGISTRATION NUMBER: 25,952
; REFERENCE/DOCKET NUMBER: 28600-20105.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-909-122-4

Query Match          9.2%; Score 76; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38 LRREYVDFAFRDLC 51
DB      1 LRREYVDFAFRDLC 14

RESULT 93
US-09-641-528B-46529
; Sequence 46529, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.010001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
```

```

; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46529
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46529

Query Match
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 KOOLRREYDFAFR 48
DB 1 KOOLRREYDFAFR 15

RESULT 94
US-09-641-528B-46531
; Sequence 46531, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46531
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46531

Query Match
Best Local Similarity 9.2%; Score 76; DB 3; Length 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 93 NKPLCDLLIRCIHQ 107
DB 1 NKPLCDLLIRCIHQ 15

RESULT 95
US-09-248-796A-16235
; Sequence 16235, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16235
```

```

; LENGTH: 187
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16235

Query Match
Best Local Similarity 22.9%; Pred. No. 1.2;
Matches 33; Conservative 18; Mismatches 54; Indels 39; Gaps 8;

QY 14 QLTBLQI-----TIHIIIEC-----YCK-----OOLRREYDFAFRDLCTIV 54
DB 24 RLCHNRDYYNNHPPYCHHIFCLICGHICPCNDHVFACHHICHCYHGRPCICH 83
QY 55 RDGNFYAVXDKCLKFYS-KISEYRH---YCYSVYGTLEQYNNPLCDLLIRCIHQKP 109
DB 84 -GTYPIYHRSYLSCLRCLCVCHHTCPICHPRIYDYSYLCYRPIHLSYCHNHQ-- 139

QY 110 LCPREKQRH-----LDKQRFHNI 128
DB 140 -----QKHWVYVYIWSKDRFHNI 157

RESULT 96
US-09-949-016-8090
; Sequence 8090, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYOMPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8090
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8090

Query Match
Best Local Similarity 9.1%; Score 75.5; DB 2; Length 250;
Matches 33; Conservative 14; Mismatches 36; Indels 37; Gaps 7;

QY 40 REVDFAPFDLCIVYRDGNPYAVXD-----KCLKFYSKISEYRHICYSVYGTLEQYNN 94
DB 26 RCIDESTRCLCDLYM--HPYCCDLHPYVCL-----CYS-----KRSNC 65
QY 95 PLCDLLIRCIHQKPLCEPEKQRH-----DKQRFHNIIRGRWTCM--SCCRSS 143
DB 66 GLCDLYPCCLGPKYKLYCLRPSLRSLERKAIKRAIIEDEKELAKLR-RTTIRLIASSCCSSN 124

RESULT 97
US-09-641-528B-46533
; Sequence 46533, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46531
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; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 46533
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46533

Query Match
; Score 9.0%; DB 3; Length 15;
; Best Local Similarity 93.3%; Pred. No. 0.07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 59 PVAVDKCLKFYSKI 73
Db 1 PVAVDKCLKFYSKI 15

RESULT 98
US-08-377-309-7
; Sequence 7, Application US/08377309A
; Patent No. 5965528
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
; FILE REFERENCE: 06727/005001
; CURRENT APPLICATION NUMBER: US/08/377,309A
; CURRENT FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 7
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-377-309-7

Query Match
; Score 9.0%; DB 1; Length 393;
; Best Local Similarity 23.4%; Pred. No. 3.9;
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;

Qy 6 GERPKLPQLCTELQTTIHDIIECVYCKQQLRREVYDFAFRDLCIVY----- 54
Db 63 QDEKIMSYICSQ-QDTLSNKITEC--CKLTLE-----RGCTIIHAENDEKREGLS 111
Qy 55 -----RDGNPYAVXDKCLKFYSKISEY--RHVCYSVYGTTLTQQYNKPLCDLLIRC 103
Db 112 PNLNRFGLDRDPNQSSGSKNIFLASFVHEYSRRHPQLAV---SVILRVAKGYQELLEKRC 168
Qy 104 INXQKPL-C---PEKQRLDKQ 123
Db 169 FQTEPNLECDQKGEELQYIOESQ 193

RESULT 99
US-09-186-723-7
; Sequence 7, Application US/09186723
; Patent No. 6288034
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
; FILE REFERENCE: 06727/005002
; CURRENT APPLICATION NUMBER: US/09/186,723
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: 08/377,309
; EARLIER FILING DATE: 1995-01-24
```

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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 7
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-186-723-7

Query Match
; Score 9.0%; DB 2; Length 393;
; Best Local Similarity 23.4%; Pred. No. 3.9;
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;

Qy 6 GERPKLPQLCTELQTTIHDIIECVYCKQQLRREVYDFAFRDLCIVY----- 54
Db 63 QDEKIMSYICSQ-QDTLSNKITEC--CKLTLE-----RGCTIIHAENDEKREGLS 111
Qy 55 -----RDGNPYAVXDKCLKFYSKISEY--RHVCYSVYGTTLTQQYNKPLCDLLIRC 103
Db 112 PNLNRFGLDRDPNQSSGSKNIFLASFVHEYSRRHPQLAV---SVILRVAKGYQELLEKRC 168
Qy 104 INXQKPL-C---PEKQRLDKQ 123
Db 169 FQTEPNLECDQKGEELQYIOESQ 193

RESULT 100
US-08-505-012-10
; Sequence 10, Application US/08505012
; Patent No. 631611
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF CLONED
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,012
; FILING DATE: 21-JUL-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/377,317
; FILING DATE: 24-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06727/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-505-012-10

Query Match
; Score 9.0%; DB 2; Length 393;
; Best Local Similarity 23.4%; Pred. No. 3.9;
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;
```

```

Qy 6 QERPRKLPOLCTELQTTTHDIIIECYCKQOLLREVDPAFRDLCIVY----- 54
    | : : : : : | : | | | | : | : |
Db 63 ODGEKIMSYICSO-ODTISNKITEC--CKLTTL-----RGOCIIHAENDEKEPGLS 111
    | : : : : : | : | | | | : | : |
Qy 55 -----RDGNPYAVXDKCLKFYKISEY--RHYCYSVGTTLLEQYKPKPLCDLLIRC 103
    | | | : : : | : | | | | : | : |
Db 112 PVLNRPFLGDRDPNPFSSGSEKIFLASFVHFYSRRHPQLAV---SVILRYAKGYQELLEKC 168
    | | | : : : | : | | | | : | : |
Qy 104 INXOKPL-C-----PEEKQRHLDKQ 123
    | | | : : : | : | | | | : | : |
Db 169 FQTNPLLECQDKGEELQKYIQESQ 193
    | | | : : : | : | | | | : | : |

```

Search completed: May 27, 2006, 05:18:32
 Job time : 46.2691 secs

GenCore version 5.1.8
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OM protein - protein search, using bw model

Run on: May 27, 2006, 04:59:57 ; Search time 351.727 Seconds
(without alignments)
196.288 Million cell updates/sec

Title: US-10-530-253-13ED

Perfect score: 830

Sequence: 1 MFQDQERRKUPQLCTELQ.....WTGRCMSCRSRTRRETOL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :
1: A_Geneseq.8:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	828	99.8	248	8	AD044062 Amino ac1
2	828	99.8	248	8	AD044064 Amino ac1
3	826	99.5	151	6	AAO22640 HPV-16 pr
4	826	99.5	151	6	AAO22636 HPV prote
5	826	99.5	151	6	AD044072 Amino ac1
6	826	99.5	151	6	AD044072 Amino ac1
7	826	99.5	151	6	AD044060 Amino ac1
8	823	99.2	158	3	AAAY82462 Human pap
9	823	99.2	158	3	AAAR22766 HPV B6 pe
10	823	99.2	158	3	AAAY82462 Human pap
11	823	99.2	158	3	AAAB98420 Human pap
12	823	99.2	158	7	ADP09515 Human pap
13	823	99.2	158	8	ADU66363 Human pap
14	823	99.2	158	8	ADU66363 Human pap
15	823	99.2	158	9	AEA98532 HPV (onco
16	823	99.2	158	9	AEA98532 HPV (onco
17	823	99.2	158	9	AE811990 HPV16 B6
18	823	99.2	158	9	AE811990 HPV16 B6
19	823	99.2	158	10	AE888520 Human pap
20	823	99.2	162	2	AAW35741 Human pap
21	823	99.2	171	5	AAO22922 Human pap
22	823	99.2	188	2	AAAR63865 HPV16 B6/
23	823	99.2	248	8	AD044068 Amino ac1

24	823	99.2	248	8	AD044070 Amino ac1
25	823	99.2	256	8	ADR47005 Human pap
26	823	99.2	256	10	AE840157 Human pap
27	823	99.2	263	2	AAAR27725 HPV 16 B6
28	823	99.2	266	2	AAAR97561 Human pap
29	823	99.2	273	2	AAAY25376 HPV fusio
30	823	99.2	273	2	AAAY02632 Prot. D1/3
31	823	99.2	273	2	AE852634 Fusion pr
32	823	99.2	292	2	AAAY25379 HPV fusio
33	823	99.2	292	2	AAAY02635 CYTA-E6-
34	823	99.2	292	2	AE852642 Fusion pr
35	823	99.2	371	2	AAAY25377 HPV fusio
36	823	99.2	371	2	AAAY02633 Prot. D1/3
37	823	99.2	371	2	AE852638 Fusion pr
38	823	99.2	390	2	AAAY25381 HPV fusio
39	823	99.2	390	2	AAAY02637 CYTA-E6-
40	823	99.2	390	2	AE852646 Fusion pr
41	821	98.9	248	8	AD044066 Amino ac1
42	818	98.6	151	3	AAAY57808 HPV-16 B6
43	815	98.2	158	8	ADL90078 Human pap
44	779.5	93.9	243	2	AAAR93369 Papilloma
45	580	69.9	149	2	AAAR40919 HPV B6 re
46	578	69.6	149	8	AD044077 Amino ac1
47	578	69.6	149	9	AEA98533 HPV (onco
48	572	68.9	180	7	ADP31985 Human pap
49	523	63.0	149	4	AD044075 Amino ac1
50	523	63.0	149	8	AD044075 Amino ac1
51	523	63.0	149	9	AEA98537 HPV (onco
52	523	63.0	149	9	AEA98865 HPV-31 Bn
53	523	63.0	149	9	AEA98865 HPV prote
54	520	62.7	149	4	AD044076 Amino ac1
55	520	62.7	149	9	AEA98853 HPV (onco
56	520	62.7	149	9	AEA98853 HPV prote
57	520	62.7	149	9	AEA98866 HPV-33 Bn
58	520	62.7	149	9	AEA98879 HPV (onco
59	498	60.0	149	8	AD044083 Amino ac1
60	496	59.8	149	9	AD044083 Amino ac1
61	496	59.8	149	9	AEA98534 HPV (onco
62	496	59.8	149	9	AEA98870 HPV-58 Bn
63	496	59.8	149	9	AEA98870 HPV-58 Bn
64	487	58.7	148	8	AD044081 Amino ac1
65	487	58.7	148	9	AEA98536 HPV (onco
66	487	58.7	148	9	AEA98868 HPV-52 Bn
67	487	58.7	148	9	AEA98868 HPV-52 Bn
68	484	58.3	148	9	AEA98878 HPV (onco
69	483	58.2	148	9	AEA98858 HPV (onco
70	478	57.6	172	2	AAAR97563 Human pap
71	468.5	56.4	158	8	AD044085 Amino ac1
72	468.5	56.4	158	9	AEA98880 HPV (onco
73	468	56.4	172	2	AAAR97562 Human pap
74	460	55.4	151	8	AD044080 Amino ac1
75	460	55.4	151	9	AEA98543 HPV (onco
76	459.5	55.4	158	8	AD044079 Amino ac1
77	459.5	55.4	158	9	AEA98548 HPV (onco
78	459.5	55.4	158	9	AEA98867 HPV-45 Bn
79	455.5	54.9	158	2	AAAR63866 HPV18 B6/
80	455.5	54.9	158	2	AAAR63866 HPV18 B6/
81	455.5	54.9	158	2	AAAR63866 HPV18 B6/
82	455.5	54.9	158	2	AAAR63866 HPV18 B6/
83	455.5	54.9	158	4	AD044074 Amino ac1
84	455.5	54.9	158	8	AD044074 Amino ac1
85	455.5	54.9	158	9	AEA98547 HPV (onco
86	455.5	54.9	158	9	AEA98547 HPV (onco
87	455.5	54.9	158	9	AEA98547 HPV (onco
88	455.5	54.9	158	9	AEA98547 HPV (onco
89	455.5	54.9	158	9	AEA98547 HPV (onco
90	455.5	54.9	158	5	AAO22924 Human pap
91	455.5	54.9	172	2	AAAR27728 HPV 18 B6
92	455.5	54.9	278	2	AAAY25385 HPV fusio
93	455.5	54.9	278	2	AAAY25385 HPV fusio
94	455.5	54.9	278	2	AAAY25385 HPV fusio
95	455.5	54.9	278	2	AAAY25385 HPV fusio
96	455.5	54.9	383	2	AAAY02642 Prot. D1/3
			383	9	AE852657 Fusion pr

QY 1 MFQDPOBRPRKLPOLCTELQTTIHDIILBECVCKQQLRREYVDFAFRDLCTIYVRDGNPY 60
 DB 8 MFQDPOBRPRKLPOLCTELQTTIHDIILBECVCKQQLRREYVDFAFRDLCTIYVRDGNPY 67
 QY 61 AVXDKCLKFKYSKISEYRHYCYSVYGTLLBEOQYNKPLCDLLIRINCINXOKPLCPBEKORHLD 120
 DB 68 AVCDKCLKFKYSKISEYRHYCYSVYGTLLBEOQYNKPLCDLLIRINCINXOKPLCPBEKORHLD 127
 QY 121 KKQRFNINRGWTRGCMSCCRSSRTRETOL 151
 DB 128 KKQRFNINRGWTRGCMSCCRSSRTRETOL 158

RESULT 7
 ID ADO44060 standard; protein; 248 AA.
 XX ADO44060;
 AC ADO44060;
 DT 15-JUL-2004 (first entry)
 DE Amino acid sequence of an E6E7 fusion protein.
 XX B6 protein; E7 protein: fusion protein; HPV16; HPV-associated cancer;
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
 XX Human papillomavirus type 16.
 OS Synthetic.
 OS MO2004030636-A2.
 PN 15-APR-2004.
 PD 02-OCT-2003; 2003MO-US031726.
 PF 03-OCT-2002; 2002US-0415929P.
 PR (AMHP) WYETH HOLDINGS CORP.
 PA Smith L, Cassetti MC;
 PI WPI; 2004-316328/29.
 DR N-PSDB; ADO44061.
 XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.
 PS Example 1; Page 67-68; 101pp; English.
 XX The present sequence represents an E6E7 fusion protein, comprising wild
 CC type E6 and E7 polypeptides from human papillomavirus type 16 (HPV16).
 CC The specification describes human papillomavirus E6 and E7 polypeptides,
 CC where the E7 polypeptide has mutations at any one or more of the amino
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of
 CC there sequence given in ADO44072. The polypeptides of the invention are
 CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.
 XX Sequence 248 AA;
 SQ

Query Match 99.5%; Score 826; DB 8; Length 248;
 Best Local Similarity 98.7%; Pred. No. 7.7e-84;
 Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFQDPOBRPRKLPOLCTELQTTIHDIILBECVCKQQLRREYVDFAFRDLCTIYVRDGNPY 60

DB 1 MFQDPOBRPRKLPOLCTELQTTIHDIILBECVCKQQLRREYVDFAFRDLCTIYVRDGNPY 60
 QY 61 AVXDKCLKFKYSKISEYRHYCYSVYGTLLBEOQYNKPLCDLLIRINCINXOKPLCPBEKORHLD 120
 DB 61 AVCDKCLKFKYSKISEYRHYCYSVYGTLLBEOQYNKPLCDLLIRINCINXOKPLCPBEKORHLD 120
 QY 121 KKQRFNINRGWTRGCMSCCRSSRTRETOL 151
 DB 121 KKQRFNINRGWTRGCMSCCRSSRTRETOL 151

RESULT 8
 ID ADU66364 standard; protein; 151 AA.
 XX ADU66364;
 AC ADU66364;
 DT 10-FEB-2005 (first entry)
 DE Human papillomavirus type 16 (HPV16) E6 protein - SEQ ID 5.
 XX vaccine; MHC class I pathway; antigen specific immune response; tumor;
 KM E7 protein; E6 protein.
 XX Human papillomavirus type 16.
 OS MO2004098526-A2.
 PN 18-NOV-2004.
 PD 05-MAY-2004; 2004MO-US013756.
 PF 05-MAY-2003; 2003US-0467602P.
 PR (UYJO) UNIV JOHNS HOPKINS.
 PA Wu T, Hung CF;
 PI WPI; 2004-813972/80.
 DR New nucleic acid molecules encoding a fusion polypeptide comprising an
 XX antigen, a signal peptide, and a heat shock protein, useful as a vaccine
 PT for inducing or enhancing immune response or for inhibiting or preventing
 PT tumor growth.
 PS Disclosure; SEQ ID NO 5; 67pp; English.
 XX The invention comprises a nucleic acid molecule (DNA vaccine) that
 CC encodes a fusion polypeptide which is useful as a vaccine composition.
 CC The nucleic acid of the invention contains: a first nucleic acid encoding
 CC a polypeptide that promotes processing via the MHC class I pathway; a
 CC second sequence encoding a signal peptide; and a third sequence encoding
 CC an antigenic polypeptide. The DNA vaccine of the invention is useful for
 CC inducing or enhancing an antigen specific immune response, or to inhibit
 CC growth or prevent re-growth of a tumor expressing Human papillomavirus
 CC (HPV) E7 or E6 protein. The present amino acid sequence represents a
 CC human papillomavirus type 16 (HPV16) E6 protein of the invention.
 XX Sequence 151 AA;
 SQ

Query Match 99.2%; Score 823; DB 8; Length 151;
 Best Local Similarity 98.0%; Pred. No. 9.2e-84;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFQDPOBRPRKLPOLCTELQTTIHDIILBECVCKQQLRREYVDFAFRDLCTIYVRDGNPY 60
 DB 1 MFQDPOBRPRKLPOLCTELQTTIHDIILBECVCKQQLRREYVDFAFRDLCTIYVRDGNPY 60
 QY 61 AVXDKCLKFKYSKISEYRHYCYSVYGTLLBEOQYNKPLCDLLIRINCINXOKPLCPBEKORHLD 120
 DB 61 AVCDKCLKFKYSKISEYRHYCYSVYGTLLBEOQYNKPLCDLLIRINCINXOKPLCPBEKORHLD 120

Qy 121 KKQRFHNIIRGRWTCRSCCRSSRTRETOL 151
 |||
 Db 121 KKQRFHNIIRGRWTCRSCCRSSRTRETOL 151

RESULT 9
 ID AAR22766 standard; peptide; 158 AA.
 AAR22766

XX AAR22766;
 AC AAR22766;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-SEP-1992 (first entry)
 XX
 DE HPV E6 peptide.

XX Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.
 XX Synthetic.
 OS Homo sapiens.

XX MO9205248-A.

XX 02-APR-1992.

XX 26-SEP-1991; 91WO-US007081.

XX 26-SEP-1990; 90US-00588384.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Thomas EK, Chen L, Blake J, Hellestrom K, Hellestrom I, Hu SL;

XX WPI; 1992-132119/16.

XX Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and
 PT recombinant cells encoding them, useful in treatment and prophylaxis of
 PT cervical warts or cancer resulting from HPV infection.

XX PS Disclosure; Fig 7; 81pp; English.

XX The peptide is the sequence of the human papillomavirus HPV 16 E6
 CC nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)
 CC of HPV 16 E6 were synthesised by standard Merrifield synthesis. Examples
 CC of such peptides are E6 1-20, 8-20, 119-134 or 148-158. Compositions
 CC contg. these peptides, antibodies against the peptides, or recombinant
 CC cells contg. the gene encoding the immuno- genic peptides may be utilised
 CC in methods for inhibiting and treating HPV infection and tumour
 CC initiation and progression e.g. in the prevention or retardation of
 CC cervical warts and cervical carcinoma resulting from HPV infection. See
 CC also AAR22767. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 25-MAR-2003 to correct PI field.)

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 2; Length 158;
 Best Local Similarity 98.0%; Pred. No. 9.7e-84;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIYVRDGNPY 60
 |||
 Db 8 MFQDPQRPRLPOLCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIYVRDGNPY 67
 Qy 61 AVXDCKLKFYSKISEYHNYCYSVYGTLEQYNNKPLCDLIRICINXOKPLCPBEKQRLHD 120
 |||
 Db 68 AVCDKCLKFYSKISEYHNYCYSLYGTLEQYNNKPLCDLIRICINXOKPLCPBEKQRLHD 127
 Qy 121 KKQRFHNIIRGRWTCRSCCRSSRTRETOL 151
 |||
 Db 128 KKQRFHNIIRGRWTCRSCCRSSRTRETOL 158

RESULT 10

AA82462
 ID AA82462 standard; protein; 158 AA.
 XX
 AC AA82462;
 XX
 DT 30-JUN-2000 (first entry)
 XX
 DE Human papillomavirus E6 protein containing two zinc finger motifs.

XX Chelated zinc finger; therapeutic; treatment; prophylaxis; HPV;
 KM mammalian papillomavirus; antiviral; cytostatic; cervical cancer; lesion;
 KM wart.

XX Human papillomavirus.

XX Key Location/Qualifiers
 FT Misc-difference 37. .73 /note= "forms a zinc finger motif"
 FT Misc-difference 110. .146 /note= "forms a zinc finger motif"

XX MO200014063-A1.

XX 16-MAR-2000.

XX 03-SEP-1999; 99WO-AU000724.

XX 04-SEP-1998; 98AU-00005733.

XX 15-JUL-1999; 99AU-00001645.

XX (MOLE-) INST MOLECULAR & CELL BIOLOGY.

XX (HUGH/) HUGHES E J L.

XX Bernard H, Tan YJ, Beerheide W, Ting AE, Sim MM;

XX WPI; 2000-256917/22.

XX Polysulfide and dithionodisulfide agents, useful for the treatment or
 PT prophylaxis of diseases caused by mammalian papillomavirus, are
 PT disruptors of a chelated metal cation domain in an HPV gene encoded
 PT protein.

XX Disclosure; Fig 1; 78pp; English.

XX The present invention describes an agent used in the treatment or
 CC prophylaxis of a disease caused or exacerbated by MPV (mammalian
 CC papillomavirus) comprising a compound capable of reducing, inhibiting or
 CC otherwise decreasing the activity of a protein encoded by an HPV gene by
 CC facilitating disruption of a chelated metal cation domain present in the
 CC protein. An agent of the present invention can be used to treat cervical
 CC cancer or its HPV associated precursor lesions or other HPV associated
 CC cancers and/or warts. The present sequence represents a human
 CC papillomavirus E6 protein containing two zinc finger motifs, as given in
 CC the exemplification of the present invention

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 3; Length 158;
 Best Local Similarity 98.0%; Pred. No. 9.7e-84;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIYVRDGNPY 60
 |||
 Db 8 MFQDPQRPRLPOLCTELQTTIHDIIECYCKQQLRREVDFAFRDLCIYVRDGNPY 67
 Qy 61 AVXDCKLKFYSKISEYHNYCYSVYGTLEQYNNKPLCDLIRICINXOKPLCPBEKQRLHD 120
 |||
 Db 68 AVCDKCLKFYSKISEYHNYCYSLYGTLEQYNNKPLCDLIRICINXOKPLCPBEKQRLHD 127
 Qy 121 KKQRFHNIIRGRWTCRSCCRSSRTRETOL 151
 |||
 Db 128 KKQRFHNIIRGRWTCRSCCRSSRTRETOL 158

RESULT 11
ID AAB98420 standard; protein; 158 AA.
XX
AC AAB98420;
XX
DT 22-AUG-2001 (first entry)
XX
DE Human papillomavirus protein HPV16 E6.
XX
KM Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
KM epitope; T cell; identification; vaccine; infection; genital wart;
KM neoplastic growth; antiviral.
OS
XX Human papillomavirus.
OS
PN WO20014179-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033549.
XX
PR 10-DEC-1999; 99US-0172705P.
PR 15-AUG-2000; 2000US-00641528.
XX
XX (EPIM-) EPIMMUNE INC.
PI Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
XX WPI; 2001-381497/40.
XX
PT An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT treating HPV infections.
XX
XX Disclosure; Page 20-21; 756pp; English.
XX
XX The present invention describes an isolated prepared human papillomavirus
CC (HPV) epitope (1). (1) has antiviral activity, and can be used in vaccine
CC production. Peptides and corresponding nucleic acid compositions from the
CC present invention are useful for stimulating an immune response to HPV by
CC stimulating the production of CTL or HTL responses, specifically in the
CC treatment or prophylaxis of HPV infection, in persons who have not
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
CC can also be used in a tetramer staining assay to assess peripheral blood
CC mononuclear cells for the presence of antigen-specific CTLs following
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune
CC recall responses or evaluate the efficacy of a vaccine. The vaccine
CC compositions are useful for removing warts or treating HPV infections.
CC The epitopes for inclusion in an epitope-base vaccine may be selected
CC from conserved regions of viral or tumour-associated antigens, which
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
CC that may be present in whole antigens can be avoided with the use of
CC epitope-base vaccines. An additional advantage is the ability to combine
CC selected epitopes (CTL and HTL) and to modify the composition of the
CC epitopes achieving enhanced immunogenicity, the major benefit of the
CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
CC polypeptide sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 4; Length 158;
Best Local Similarity 98.0%; Pred. No. 9.7e-84;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBRPKLPLQCTELQTTTHDIILCEVCYKQQLLRREVDFAFRDLCIYRRGNPY 60
DB 8 MFODPOBRPKLPLQCTELQTTTHDIILCEVCYKQQLLRREVDFAFRDLCIYRRGNPY 67
QY 61 AVXDCKLKFYSKISEYRHVCYSYVGTLEQYNNKPLCDLLIRICINOKPLCPBEKORHLD 120
DB 68 AVCDCKLKFYSKISEYRHVCYSYVGTLEQYNNKPLCDLLIRICINOKPLCPBEKORHLD 127

QY 121 KKORFHNIRGRWTRGCMSCCRSSRTRETQL 151
DB 128 KKORFHNIRGRWTRGCMSCCRSSRTRETQL 158

RESULT 12
ID ADF09515 standard; protein; 158 AA.
XX
AC ADF09515;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human papillomavirus 16 E6 SEQ ID NO:16.
XX
KM human; protein-protein interaction; virocid; cyostatic; vaccine;
KM human papilloma virus; HPV; cancer.
XX
OS Human papillomavirus.
OS
PN WO2003068940-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004594.
XX
PR 14-FEB-2002; 2002US-0356911P.
XX
XX (CURA-) CURAGEN CORP.
PA (HOFF) HOFFMANN LA ROCHE INC.
XX
XX Jackson A, Ooi CE, Lewin DA, Cuthill S;
XX WPI; 2003-689668/65.
XX
DR N-PSDB; ADF09607.
XX
PT New purified complex comprising a first polypeptide and a second
PT polypeptide, useful for identifying agents for treating/preventing a
PT condition involving altered level of the complex e.g. human papilloma
PT virus infection, or cancer.
XX
PS Example 3; SEQ ID NO 16; 156pp; English.
XX
XX The invention relates to a novel purified complex comprising a first
CC polypeptide and a second polypeptide, where the polypeptides comprise
CC defined amino acid sequences listed in the specification, and where the
CC first polypeptide binds to the second polypeptide. A complex of the
CC invention has virucide and cytostatic activity, and may have a use as a
CC vaccine. The complex is useful for identifying agents for treating or
CC preventing a conditions involving altered level of the complex, e.g.
CC human papilloma virus (HPV) infection, or cancer. The compositions,
CC antibodies, vectors and methods are useful for treating such diseases.
CC The sequences shown in ADF09500-ADF09583 represent proteins of the
CC invention.
XX
SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 7; Length 158;
Best Local Similarity 98.0%; Pred. No. 9.7e-84;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBRPKLPLQCTELQTTTHDIILCEVCYKQQLLRREVDFAFRDLCIYRRGNPY 60
DB 8 MFODPOBRPKLPLQCTELQTTTHDIILCEVCYKQQLLRREVDFAFRDLCIYRRGNPY 67
QY 61 AVXDCKLKFYSKISEYRHVCYSYVGTLEQYNNKPLCDLLIRICINOKPLCPBEKORHLD 120
DB 68 AVXDCKLKFYSKISEYRHVCYSYVGTLEQYNNKPLCDLLIRICINOKPLCPBEKORHLD 127
QY 121 KKORFHNIRGRWTRGCMSCCRSSRTRETQL 151
DB 128 KKORFHNIRGRWTRGCMSCCRSSRTRETQL 158

RESULT 13
 ADU66363 standard; protein, 158 AA.
 XX ADU66363;
 XX 10-FEB-2005 (first entry)
 DT
 XX Human papillomavirus type 16 (HPV16) E6 protein - SEQ ID 4.
 DE
 XX vaccine; MHC class I pathway; antigen specific immune response; tumor;
 KM E7 protein; E6 protein.
 XX
 OS Human papillomavirus type 16.
 PN MO2004098526-A2.
 XX
 PD 18-NOV-2004.
 XX
 PF 05-MAY-2004; 2004MO-US013756.
 XX
 PR 05-MAY-2003; 2003US-0467602P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Wu T, Hung CF;
 DR WPI; 2004-813972/80.
 XX
 PT New nucleic acid molecules encoding a fusion polypeptide comprising an
 PT antigen, a signal peptide, and a heat shock protein, useful as a vaccine
 PT for inducing or enhancing immune response or for inhibiting or preventing
 PT tumor growth.
 PT
 XX
 PS Claim 11; SEQ ID NO 4; 67pp; English.
 XX
 CC The invention comprises a nucleic acid molecule (DNA vaccine) that
 CC encodes a fusion polypeptide which is useful as a vaccine composition.
 CC The nucleic acid of the invention contains: a first nucleic acid encoding
 CC a polypeptide that promotes processing via the MHC class I pathway; a
 CC second sequence encoding a signal peptide; and a third sequence encoding
 CC an antigenic polypeptide. The DNA vaccine of the invention is useful for
 CC inducing or enhancing an antigen specific immune response, or to inhibit
 CC growth or prevent re-growth of a tumor expressing Human papillomavirus
 CC (HPV) E7 or E6 protein. The present amino acid sequence represents a
 CC human papillomavirus type 16 (HPV16) E6 protein of the invention.
 CC
 XX
 SQ Sequence 158 AA;
 Query Match 99.2%; Score 823; DB 8; Length 158;
 Best Local Similarity 98.0%; Pred. No. 9.7e-84;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFODPOBRPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIYVRDGNPY 60
 DB 8 MFODPOBRPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIYVRDGNPY 67
 QY 61 AVXDCKLKFYSKISEYRHVCYSVYGTTLBEOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
 DB 68 AVCDKCKLKFYSKISEYRHVCYSVYGTTLBEOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127
 QY 121 KQRFNINRGWTRGCMSCCRSSRTRETOL 151
 DB 128 KQRFNINRGWTRGCMSCCRSSRTRETOL 158
 RESULT 14
 ID AEA40817 standard; protein, 158 AA.
 XX AEA40817;
 AC AEA40817;

XX
 DT 28-JUL-2005 (first entry)
 XX
 DE Anti-apoptotic vector HPV E6 antigenic protein, SEQ ID 7.
 XX
 KM immunogenicity; immunogenicity-potentiating polypeptide; IPP; T-cell;
 KM vaccine; immune stimulation; tumor; cytostatic.
 XX
 OS Human papillomavirus - 16.
 XX
 PN MO2005047501-A1.
 PD 26-MAY-2005.
 XX
 PF 24-FEB-2004; 2004MO-US005292.
 XX
 PR 24-FEB-2003; 2003US-0449429P.
 PR 18-JUL-2003; 2003US-0488527P.
 PR 31-DEC-2003; 2003US-0533792P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Wu T, Hung CF, Kim T;
 XX
 DR WPI; 2005-367009/37.
 DR GENBANK; NC_001526.
 XX
 PT New nucleic acid composition comprising a first nucleic acid vector
 PT encoding an anti-apoptotic polypeptide and a second nucleic acid vector
 PT encoding an anti-apoptotic polypeptide, useful as an immunogen for
 PT inhibiting the growth of a tumor.
 PT
 XX
 PS Disclosure; SEQ ID NO 7; 158pp; English.
 XX
 CC The invention relates to a novel nucleic acid composition useful as an
 CC immunogen. The composition comprises a combination of: a first nucleic
 CC acid vector comprising a first sequence encoding an antigenic polypeptide
 CC or peptide, and optionally, a second sequence linked to the first
 CC sequence and encoding an immunogenicity-potentiating polypeptide (IPP);
 CC and a second nucleic acid vector encoding an anti-apoptotic polypeptide.
 CC When the second vector is administered with the first vector to a
 CC subject, a T cell mediated immune response to the antigenic polypeptide
 CC or peptide is induced that is greater in magnitude and/or duration than
 CC an immune response induced by administration of the first vector alone.
 CC The invention further includes: a particle comprising a material that is
 CC suitable for introduction into a cell or an animal by particle
 CC bombardment, bound to which is the first and second vectors or
 CC composition; a pharmaceutical composition capable of inducing or
 CC enhancing an antigen specific immune response, comprising the particle
 CC and a carrier or an excipient; inducing or enhancing an antigen specific
 CC immune response in a subject; increasing the numbers of CD8+ CTLs
 CC specific for a selected desired antigen in a subject; and inhibiting the
 CC growth of a tumor in a subject. The nucleic acid composition is useful as
 CC an immunogen for inhibiting the growth of a tumor, hence it has
 CC cytostatic activity. This sequence represents an anti-apoptotic vector HPV
 CC E6 antigenic protein of the invention.
 CC
 XX
 SQ Sequence 158 AA;
 Query Match 99.2%; Score 823; DB 9; Length 158;
 Best Local Similarity 98.0%; Pred. No. 9.7e-84;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFODPOBRPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIYVRDGNPY 60
 DB 8 MFODPOBRPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIYVRDGNPY 67
 QY 61 AVXDCKLKFYSKISEYRHVCYSVYGTTLBEOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
 DB 68 AVCDKCKLKFYSKISEYRHVCYSVYGTTLBEOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127
 QY 121 KQRFNINRGWTRGCMSCCRSSRTRETOL 151
 DB 128 KQRFNINRGWTRGCMSCCRSSRTRETOL 151

Db 128 KKORFNHNRGRWTCRMSCCRSTRTRETOL 158

RESULT 15

AEA98532

ID AEA98532 standard; protein; 158 AA.

AC AEA98532;

DT 08-SEP-2005 (first entry)

DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 13.

KM Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;

KW cancer; cervix tumor; cytostatic.

OS Human papillomavirus type 16.

PN US2005142541-A1.

PD 30-JUN-2005.

PF 23-DEC-2004; 2004US-00021949.

PR 23-DEC-2003; 2003US-0532373P.

PA (ARBO-) ARBOR VITA CORP.

PI Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;

DR WPI; 2005-457781/46.

PT New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing cancer.

PS Disclosure; SEQ ID NO 13; 161pp; English.

CC The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC least three different oncogenic HPV strains. Also included are a CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV CC E6 protein in a sample, a method of detecting the presence of an CC oncogenic HPV E6 protein in a sample and a system for detecting the CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide, CC where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins CC of at least three different oncogenic HPV strains). The antibody CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 9; Length 158;

Best Local Similarity 98.0%; Pred. No. 9,7e-84;

Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDDPQRPRLPOLCTELQTTIHDIILCEVCYKQQLLRREYVDFARDCIYVRDGNPY 60
 DB 8 MFQDDPQRPRLPOLCTELQTTIHDIILCEVCYKQQLLRREYVDFARDCIYVRDGNPY 67
 QY 61 AYVDCIKLKFYSKISEYHVCYSYVGTLLBQYNNKPLCDLIRINCINXOKPLCPBEKORHLD 120
 DB 68 AYVDCIKLKFYSKISEYHVCYSYVGTLLBQYNNKPLCDLIRINCINXOKPLCPBEKORHLD 127
 QY 121 KKORFNHNRGRWTCRMSCCRSTRTRETOL 151
 DB 128 KKORFNHNRGRWTCRMSCCRSTRTRETOL 158

RESULT 16

AEB11990

ID AEB11990 standard; protein; 158 AA.

AC AEB11990;

DT 08-SEP-2005 (first entry)

DE HPV16 E6 protein.

KM Tumor-associated antigen; vaccine; papilloma; cytostatic; neoplaasm;

KW cancer; HPV16 E6.

OS Human papillomavirus type 16.

PN WO2005060993-A1.

PD 07-JUL-2005.

PF 24-DEC-2003; 2003WO-NL000929.

PR 24-DEC-2003; 2003WO-NL000929.

PA (UYLE-) UNIV LEIDEN MEDICAL CENT.

PI Van Der Burg SH, Drijfhout JW;

DR WPI; 2005-497704/50.

PT Producing a synthetic protein of a pathogen or tumor comprises chemically PT synthesizing two or more fragments of 2-80 contiguous amino acids of PT sequence; the sequence of two or more fragments are neighboring and non- PT overlapping.

PS Claim 11; SEQ ID NO 2; 53pp; English.

CC The invention relates to a method of producing a synthetic protein CC comprising an amino acid sequence that is at least 80% identical to a CC naturally occurring antigenic protein of a pathogen or tumor comprising CC chemically synthesizing two or more fragments, chemically ligating the C- CC termini of a fragment to the N-terminus of a neighboring fragment to CC produce the synthetic protein or its part and optionally repeating the CC second step to sequentially ligate a further neighboring fragment CC obtained from the second step. The invention also relates to a CC composition comprising the protein and a method for treating or CC preventing human papillomavirus (HPV) associated disease by administering CC to the subject the protein or composition in a therapeutically effective CC amount. In producing a synthetic protein, the neighboring non-overlapping CC fragments are selected to comprise N-terminal cysteine or glycine CC residues. The naturally occurring protein is an HPV protein, e.g. E2, E6 CC or E7 protein from HPV16, HPV18, HPV31, HPV33 or HPV45. The composition CC further comprises an anti-CD40 antibody. The composition is useful as a CC vaccine for preventing or treating HPV associated disease, such as CC cancer. This sequence represents an HPV16 E6 protein used in the method CC of the invention.

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 9; Length 158;

Best Local Similarity 98.0%; Pred. No. 9,7e-84;

Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDDPQRPRLPOLCTELQTTIHDIILCEVCYKQQLLRREYVDFARDCIYVRDGNPY 60
 DB 8 MFQDDPQRPRLPOLCTELQTTIHDIILCEVCYKQQLLRREYVDFARDCIYVRDGNPY 67
 QY 61 AYVDCIKLKFYSKISEYHVCYSYVGTLLBQYNNKPLCDLIRINCINXOKPLCPBEKORHLD 120
 DB 68 AYVDCIKLKFYSKISEYHVCYSYVGTLLBQYNNKPLCDLIRINCINXOKPLCPBEKORHLD 127
 QY 121 KKORFNHNRGRWTCRMSCCRSTRTRETOL 151
 DB 128 KKORFNHNRGRWTCRMSCCRSTRTRETOL 158

Db 128 KKQRFHNIRGRWTCRMCSSRSRTRETQL 158

RESULT 17
AEC98863
ID AEC98863 standard; protein; 158 AA.
XX
AC AEC98863;
XX
DT 01-DEC-2005 (first entry)
XX
DE HPV_16 Envelope protein E6.
XX
KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
KM epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
XX
OS Human papillomavirus type 16.
PN WO2005089164-A2.
PD 29-SEP-2005.
PE 03-JAN-2005; 2005WO-US000077.
XX
PR 31-DEC-2003; 2003US-0533211P.
PR 02-JUL-2004; 2004US-0584652P.
XX
PA (EPIM-) EPIMMUNE INC.
PA (INNO-) INNOGENETICS NV.
PA (CHES/) CHESNUT R.
PA (NEMM/) NEWMAN M J.
PA (MOTH/) MOTHE B.
PA (BAKE/) BAKER D.
PA (SOUT/) SOUTHWOOD S.
PA (BABE/) BABE L M.
PA (CHEN/) CHEN Y.
PA (DEYO/) DEYOUNG L M.
PA (HUAN/) HUANG M T F.
PA (POME/) POWER S D.
XX
PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;
PI Chen Y, Deyoung LM, Huang MTF, Power SD;
DR WPI: 2005-658982/67.
XX
PT New polynucleotide comprises a multi-epitope construct comprising nucleic
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
PT (CTL) epitopes, useful in preparing a vaccine against HPV.
XX
XX Example 10; Page 349; 518bp; English.
XX
PS The invention relates to a new polynucleotide comprising a multi-epitope
CC construct comprising nucleic acids encoding the human papillomavirus
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that
CC are directly or indirectly joined to one another in the same reading
CC frame, a vaccine minigene. Also included are a vector comprising the
CC multi-epitope construct, a polypeptide comprising an amino acid sequence
CC encoded by the polynucleotide, a composition (comprising the
CC polynucleotide, vector and/or polypeptide and a carrier), a cell
CC (comprising the polynucleotide, vector or polypeptide), inducing an
CC immune response against human papillomavirus virus (HPV) and making the
CC polynucleotide, vector or polypeptide. The epitopes are derived from
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the
CC epitopes in the vaccine protein are disclosed in the tables referred to
CC in the claims of the specification. The polynucleotide, vector or
CC polypeptide is useful in preparing a composition for inducing an immune
CC response against human papillomavirus virus (HPV) and thus providing a
CC defense against HPV infection and HPV-related cancers. The present
CC sequence is an HPV protein used to derive epitopes for the vaccine of the
CC invention.
XX
SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 9; Length 158;
Best Local Similarity 98.0%; Pred. No. 9,7e-84;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDPQRPRLPOLCTELQTTIHDIILECVCKQQLREYVDFAFRDLCTIYRDGNY 60
Db 8 MFQDPQRPRLPOLCTELQTTIHDIILECVCKQQLREYVDFAFRDLCTIYRDGNY 67
Qy 61 AYADKCLKFYSKISEYHNYCYSVYGTLLERQYKPLCDLLIRCNXKPLCPREKQRLD 120
Db 68 AVCQCKLKFYSKISEYHNYCYSLYGTLLERQYKPLCDLLIRCNXKPLCPREKQRLD 127
Qy 121 KKQRFHNIRGRWTCRMCSSRSRTRETQL 151
Db 128 KKQRFHNIRGRWTCRMCSSRSRTRETQL 158

RESULT 18
AEC96391
ID AEC96391 standard; protein; 158 AA.
XX
AC AEC96391;
XX
DT 01-DEC-2005 (first entry)
XX
DE HPV protein E6 from HPV16.
XX
KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
KM epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
XX
OS Human papillomavirus type 16.
PN WO2005089164-A2.
PD 29-SEP-2005.
PE 03-JAN-2005; 2005WO-US000077.
XX
PR 31-DEC-2003; 2003US-0533211P.
PR 02-JUL-2004; 2004US-0584652P.
XX
PA (EPIM-) EPIMMUNE INC.
PA (INNO-) INNOGENETICS NV.
PA (CHES/) CHESNUT R.
PA (NEMM/) NEWMAN M J.
PA (MOTH/) MOTHE B.
PA (BAKE/) BAKER D.
PA (SOUT/) SOUTHWOOD S.
PA (BABE/) BABE L M.
PA (CHEN/) CHEN Y.
PA (DEYO/) DEYOUNG L M.
PA (HUAN/) HUANG M T F.
PA (POME/) POWER S D.
XX
PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;
PI Chen Y, Deyoung LM, Huang MTF, Power SD;
DR WPI: 2005-658982/67.
XX
PT New polynucleotide comprises a multi-epitope construct comprising nucleic
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
PT (CTL) epitopes, useful in preparing a vaccine against HPV.
XX
XX Disclosure; Page 56; 518bp; English.
XX
PS The invention relates to a new polynucleotide comprising a multi-epitope
CC construct comprising nucleic acids encoding the human papillomavirus
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that
CC are directly or indirectly joined to one another in the same reading
CC frame, a vaccine minigene. Also included are a vector comprising the
CC multi-epitope construct, a polypeptide comprising an amino acid sequence
CC encoded by the polynucleotide, a composition (comprising the

CC polynucleotide, vector and/or polypeptide and a carrier), a cell
 CC (comprising the polynucleotide, vector or polypeptide), inducing an
 CC immune response against human papillomavirus virus (HPV) and making the
 CC polynucleotide, vector or polypeptide. The epitopes are derived from
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the
 CC epitopes in the vaccine protein are disclosed in the tables referred to
 CC in the claims of the specification. The polynucleotide, vector or
 CC polypeptide is useful in preparing a composition for inducing an immune
 CC response against human papillomavirus virus (HPV) and thus providing a
 CC defense against HPV infection and HPV-related cancers. The present
 CC sequence is an HPV protein used to derive epitopes for the vaccine of the
 CC invention.

SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 9; Length 158;
 Best Local Similarity 98.0%; Pred. No. 9.7e-84;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPERPRKLTQLCTELTTHDIIIECVYCKQQLRREYDFAFRDLCIYRDGNPY 60
 DB 8 MFQDPERPRKLTQLCTELTTHDIIIECVYCKQQLRREYDFAFRDLCIYRDGNPY 67

QY 61 AVXDKCLKFYSKISEYRHVCYVGTLEQYNNKPLCDLLIRCNXOKPLCPBEKORHLD 120
 DB 68 AVCDCKLKFYSKISEYRHVCYSLYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKORHLD 127

QY 121 KKQRFNIRGRWTCRCMSCRSSRTRETOL 151
 DB 128 KKQRFNIRGRWTCRCMSCRSSRTRETOL 158

RESULT 19
 AEF88520
 ID AEF88520 standard; protein; 158 AA.
 AC AEF88520;
 DT 20-APR-2006 (first entry)

DE Human papillomavirus type 16 (HPV16) E7 protein.
 XX
 XX
 XX Vaccine; gene therapy; papillomavirus infection; virucide; infection;
 KM uterine cervix tumor; cytostatic; gynecology and obstetrics; neoplasm;
 KW lung tumor; respiratory disease; E7 protein.
 XX
 XX Human papillomavirus type 16.
 OS
 XX
 XX US2006039919-A1.
 PN
 XX
 PD 23-FEB-2006.
 XX
 PF 18-AUG-2005; 2005US-00206138.
 XX
 PR 20-AUG-2004; 2004TW-00125128.
 XX
 PA (HEAL-) HEALTHBANKS BIOTECH CO LTD.
 XX
 PI Chang H, Liao C, Cheng W;
 XX
 DR WPI; 2006-172399/18.
 XX
 PT New fusion protein comprising E7 peptide sequence of human papillomavirus
 PT type 16, useful for inhibiting or preventing cancer, e.g. cervical or
 PT lung cancer.
 XX
 PS Claim 4; SEQ ID NO 3; 19pp; English.

CC The present invention relates to novel fusion protein for inhibiting or
 CC preventing cancer induced by human papillomavirus type 16 (HPV16). The
 CC fusion protein comprises an E7 peptide sequence of human papillomavirus
 CC type 16, a translocating peptide for translocation and a peptide fragment

CC having a carboxyl terminal section. The fusion protein of the invention
 CC is useful as vaccines and for inhibiting or preventing human
 CC papillomavirus infection and cancers such as cervical and lung cancer.
 CC The invention is useful in gene therapy. The present sequence is the
 CC human papillomavirus type 16 (HPV16) E7 protein.

SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 10; Length 158;
 Best Local Similarity 98.0%; Pred. No. 9.7e-84;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPERPRKLTQLCTELTTHDIIIECVYCKQQLRREYDFAFRDLCIYRDGNPY 60
 DB 8 MFQDPERPRKLTQLCTELTTHDIIIECVYCKQQLRREYDFAFRDLCIYRDGNPY 67

QY 61 AVXDKCLKFYSKISEYRHVCYVGTLEQYNNKPLCDLLIRCNXOKPLCPBEKORHLD 120
 DB 68 AVCDCKLKFYSKISEYRHVCYSLYGTLEQYNNKPLCDLLIRCNXOKPLCPBEKORHLD 127

QY 121 KKQRFNIRGRWTCRCMSCRSSRTRETOL 151
 DB 128 KKQRFNIRGRWTCRCMSCRSSRTRETOL 158

RESULT 20
 AAM35741
 ID AAM35741 standard; protein; 162 AA.
 AC AAM35741;
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 16-FEB-1998 (first entry)

DE Human papillomavirus type 16 E6 protein.
 XX
 XX Complete genome; circular; human papillomavirus type 16; HPV16 E6;
 KW cervical dysplasia; cervical cancer; cervical smear.
 XX
 XX Human papillomavirus type 16.
 OS
 XX
 XX Key Location/Qualifiers
 FH
 FT Misc-difference 90
 FT Misc-difference 159 /note= "Mutated to Val in the variant"
 FT /note= "End of protein sequence even though 3 amino acid
 FT residues are given following on"
 XX
 XX US5679509-A.
 PN
 XX
 PD 21-OCT-1997.
 XX
 PF 30-SEP-1994; 94US-00316239.
 XX
 PR 28-SEP-1993; 93US-00127906.
 XX
 PA (UTNE-) UNIV NEW MEXICO STATE.
 XX
 PI Wheeler CM, Parmenter CA;
 XX
 DR WPI; 1997-525714/48.
 DR N-PSDB; AAT94723.
 XX
 XX Evaluating risk of cervical dysplasia or cervical cancer - by detecting
 XX variant form of human papilloma virus 16.
 XX
 PS Claim 7; Col 23-24; 33pp; English.

CC Methods have been developed for distinguishing a subset of human
 CC papilloma virus (HPV) that is associated with an increased risk of
 CC developing cervical dysplasia or cervical cancer. The methods involve:
 CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the
 CC sample and determining if the base at position 350 of the E6 gene (see

CC AAT94723 and AAT94724 for comparison) is T or G, where the presence of G
 CC at position 350 is associated with an increased risk of developing
 CC cervical dysplasia or cervical cancer; and (2) preparing a cervical
 CC sample to expose any HPV-16 E6 protein in the sample and determining if
 CC the amino acid at position 83 of the protein (see position 90 in AAM5741
 CC and AAM5742 for comparison) is Val or Leu, where the presence of Val at
 CC position 83 that is associated with an increased risk of developing
 CC cervical dysplasia or cervical cancer. The present sequence represents
 CC the reference protein sequence for HPV-16 E6. The 350G variant correlates
 CC well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:4;
 CC for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for CIN III;
 CC 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)
 CC
 XX
 SQ Sequence 162 AA;
 Query Match 99.2%; Score 823; DB 2; Length 162;
 Best Local Similarity 98.0%; Pred. No. 1e-83;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVRDGMPY 60
 DB 8 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVRDGMPY 67
 QY 61 AVXDCKLKFYSKISEYRHVCYSVGTLEQYKNKPLCDLLIRICINXQKPLCPBEKQRLHD 120
 DB 68 AVCDCKLKFYSKISEYRHVCYSVGTLEQYKNKPLCDLLIRICINQKPLCPBEKQRLHD 127
 QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
 DB 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158
 RESULT 21
 ID AAO22922 standard; protein; 171 AA.
 XX
 AC AAO22922;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE Human papillomavirus-16 (HPV16) E6T-protein sequence.
 XX
 KM Virucide; cytostatic; B6; E7 fusion protein; HPV; immunogenic; vaccine;
 KM fusion partner; immunogenicity; HPV infection; neoplasm; HPV16;
 KM human papillomavirus-16; E6T-sequence.
 OS
 XX Human papillomavirus.
 PN
 XX EPI243655-A1.
 PD
 XX 25-SEP-2002.
 XX
 PF 23-MAR-2001; 2001EP-00107271.
 XX
 PR 23-MAR-2001; 2001EP-00107271.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 FI Cid-Atregui A, Zur Hausen H;
 XX
 DR WPI; 2002-724952/79.
 DR N-PSDB; AAL53420.
 XX
 XX A new DNA sequence encoding a fusion protein comprising a mutagenized HPV
 PT (human papillomavirus) B6 or E7 coding sequence and a sequence encoding a
 PT highly immunogenic fusion partner is useful to vaccinate against HPV
 XX infection.
 XX
 PS Disclosure; Fig 2; 34pp; English.
 XX
 CC The invention relates to a new DNA sequence encodes an B6 or E7 fusion
 CC protein of HPV, where at least 20% of the original codons are replaced by
 CC codons which lead to enhanced translation in a mammalian cell, containing

CC a mutation which results in production of a truncated non-functional
 CC protein, and encoding a highly immunogenic polypeptide fusion partner
 CC capable of enhancing immunogenicity of the B6 or E7 protein in the
 CC mammalian host. The invention is used as a vaccine for the prevention or
 CC treatment of an HPV infection or a neoplasm associated with HPV
 CC infection. This sequence represents the human papillomavirus-16 (HPV16)
 CC E6T-protein sequence of the invention
 XX
 SQ Sequence 171 AA;
 Query Match 99.2%; Score 823; DB 5; Length 171;
 Best Local Similarity 98.0%; Pred. No. 1.1e-83;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVRDGMPY 60
 DB 13 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVRDGMPY 72
 QY 61 AVXDCKLKFYSKISEYRHVCYSVGTLEQYKNKPLCDLLIRICINXQKPLCPBEKQRLHD 120
 DB 73 AVCDCKLKFYSKISEYRHVCYSVGTLEQYKNKPLCDLLIRICINQKPLCPBEKQRLHD 132
 QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
 DB 133 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 163
 RESULT 22
 ID AAR63865 standard; protein; 188 AA.
 XX
 AC AAR63865;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-JUN-1995 (first entry)
 XX
 DE HPV16 E6/E7 proteins.
 XX
 KM HPV; HPV16; E6 protein; E7 protein; diagnosis; cervical dysplasia;
 KM cervix cancer.
 OS
 XX Human papillomavirus; strain 16.
 FH
 XX Key Location/Qualifiers
 FT Protein 1..158
 FT /label= B6_protein
 FT 159..188
 FT /label= E7_protein
 XX
 PN W09426934-A2.
 XX
 PD 24-NOV-1994.
 XX
 PF 06-MAY-1994; 94WO-US005085.
 XX
 PR 06-MAY-1993; 93US-00058920.
 XX
 PA (BAKT) BAXTER DIAGNOSTICS INC.
 XX
 PI Brown JT;
 XX
 DR WPI; 1995-006821/01.
 DR P-PSDB; AAO75470.
 XX
 XX Human papilloma virus detection assay - by amplification using self
 PT sustained sequence replication and hybridisation with a detector probe.
 XX
 PS Disclosure; Page 24-26; 79pp; English.
 XX
 CC The sequences of the B6 and E7 polypeptide-encoding regions of human
 CC papillomavirus (HPV) 16 and 18 are given in AAO75470-71 and the encoded
 CC proteins in AAR63865-66, respectively. Probes and primers based on these

CC sequences were used for HPV infection diagnosis; expression of E6 and E7
 CC is diagnostic for cervical cancer or pre-malignant states. (Updated on
 CC 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise
 CC OS field)
 CC
 XX
 SQ Sequence 188 AA;

Query Match 99.2%; Score 823; DB 2; Length 188;
 Best Local Similarity 98.0%; Pred. No. 1,2e-83;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAPRDLCTIVRDGNPY 60
 DB 8 MFQDPERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAPRDLCTIVRDGNPY 67
 QY 61 AVXDKCLKFYSKISEYHVCYVGTTLBOQYNKPLCDLLIRGINXKPLCPBEKORHLD 120
 DB 68 AVCDKCLKFYSKISEYHVCYVGTTLBOQYNKPLCDLLIRGINCKPLCPBEKORHLD 127
 QY 121 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 151
 DB 128 KKQRFNIRGRWTRGCMSCCRSSRTRETOL 158

RESULT 23
 ADO44068
 ID ADO44068 standard; protein; 248 AA.
 XX
 AC ADO44068;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Amino acid sequence of a fusion protein designated E7E6Term.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
 XX Human papillomavirus type 16.
 OS Synthetic.
 XX
 PN WO2004030636-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 02-OCT-2003; 2003WO-US031726.
 XX
 PR 03-OCT-2002; 2002US-0415929P.
 XX
 PA (AMHP) WYETH HOLDINGS CORP.
 XX
 PI Smith L, Cassetti MC;
 XX
 DR WPI; 2004-316328/29.
 DR N-PSDB; ADO44069.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.
 XX
 XX

PS Claim 22; Page 73-74; 101pp; English.

XX The present sequence represents a fusion protein, comprising E7 and E6
 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
 CC protein is designated E7E6Term, and comprises an E7 amino terminus (where
 CC residues 24 and 26 have been replaced with glycine) and an E6 carboxy
 CC terminus (where residues 63 and 106 have been replaced with glycine).
 CC E7E6Term is representative of fusion proteins of the invention. The
 CC specification describes human papillomavirus E6 and E7 polypeptides,
 CC where the E7 polypeptide has mutations at any one or more of the amino
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of

CC there sequence given in ADO44072. The polypeptides of the invention are
 CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.
 CC
 XX
 SQ Sequence 248 AA;

Query Match 99.2%; Score 823; DB 8; Length 248;
 Best Local Similarity 98.7%; Pred. No. 1,7e-83;
 Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQDPERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAPRDLCTIVRDGNPY 61
 DB 99 FQDPERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAPRDLCTIVRDGNPY 158
 QY 62 VXDCKCLKFYSKISEYHVCYVGTTLBOQYNKPLCDLLIRGINXKPLCPBEKORHLD 121
 DB 159 VGDCKCLKFYSKISEYHVCYVGTTLBOQYNKPLCDLLIRGINCKPLCPBEKORHLD 218
 QY 122 KORFNIRGRWTRGCMSCCRSSRTRETOL 151
 DB 219 KORFNIRGRWTRGCMSCCRSSRTRETOL 248

RESULT 24
 ADO44070
 ID ADO44070 standard; protein; 248 AA.
 XX
 AC ADO44070;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Amino acid sequence of a fusion protein designated E7E6Term.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
 KM gene; ss.
 XX
 PN Human papillomavirus type 16.
 OS Synthetic.
 XX
 PD WO2004030636-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 02-OCT-2003; 2003WO-US031726.
 XX
 PR 03-OCT-2002; 2002US-0415929P.
 XX
 PA (AMHP) WYETH HOLDINGS CORP.
 XX
 PI Smith L, Cassetti MC;
 XX
 DR WPI; 2004-316328/29.
 DR N-PSDB; ADO44071.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.
 XX
 XX

PS Claim 22; Page 75-76; 101pp; English.

XX The present sequence represents a fusion protein, comprising E7 and E6
 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
 CC protein is designated E7E6Term, and comprises an E7 amino terminus
 CC (where residues 24, 26 and 91 have been replaced with glycine) and an E6
 CC carboxy terminus (where residues 63 and 106 have been replaced with
 CC glycine). E7E6Term is representative of fusion proteins of the
 CC invention. The specification describes human papillomavirus E6 and E7

CC polypeptides, where the E7 polypeptide has mutations at any one or more
CC of the amino acids corresponding to amino acids 24, 26 or 91 of the
CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
CC mutations at any one or more of the amino acids corresponding to amino
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
CC the invention are useful for treating or preventing human papillomavirus
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC and nucleic acids encoding the fusion proteins are useful for generating
CC immune responses against HPV. They are also useful for treating lower
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
CC the reproductive system, including penile and vulvar cancer.

XX Sequence 248 AA;

SO Query Match 99.2%; Score 823; DB 8; Length 248;
Best Local Similarity 98.7%; Pred. No. 1.7e-83;
Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQDPERPRKLPOLCTELQTTIHDIIEECVCKQQLREYVDFAFRDLCIYRDGNFYA 61
Db 99 FQDPERPRKLPOLCTELQTTIHDIIEECVCKQQLREYVDFAFRDLCIYRDGNFYA 158

QY 62 VXDCKLKFYSKISEYRHVCYSVGTTLLEQYNNKPLCDLLIRICINXQKPLCPEEKQRLDK 121
Db 159 VGDKCLKFYSKISEYRHVCYSVGTTLLEQYNNKPLCDLLIRICINQKPLCPEEKQRLDK 218

QY 122 KQRFHNIRGRWTRCSCSSRTRRETOL 151
Db 219 KQRFHNIRGRWTRCSCSSRTRRETOL 248

RESULT 25
ADRA47005
ID ADRA47005 standard; protein; 256 AA.

XX AC ADRA47005;

DT 18-NOV-2004 (first entry)

DE Human papillomavirus type 16 E7 protein for Dengue virus vaccine.

XX cytostatic; virucide; dengue virus; recombinant replicon; deletion;
KM prem protein; C protein; NS1 protein signal; vaccine; cervical cancer;
KM viral disease; antigen; dendritic cell; immune response;
KM human papillomavirus.

XX Human papillomavirus type 16.

XX OS WO2004072274-A1.

XX PN 26-AUG-2004.

XX PD 30-JAN-2004; 2004WO-CN000088.

XX PF 30-JAN-2003; 2003CN-00115272.

XX PR 30-JAN-2003; 2003CN-00115273.

XX PA (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.

XX PA (TENG-) TENGGEN BIOMEDICAL CO.

XX PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.

XX PI Pang X;

XX DR WPI; 2004-625870/60.

XX DR N-PSDB; ADRA47004.

XX Virus-like particle vaccines containing dengue virus recombinant replicon
PT as core for carrier, applicable in preventives or/and remedies for tumors
PT like cervical cancer and viral diseases.

PS Example 2; SEQ ID NO 2; 38pp; Chinese.

XX A dengue virus recombinant replicon has a deletion of the complete coding

CC sequence for prem protein of dengue virus and also includes elements of
CC e.g. the non-coding region in the whole of the 5'-end, the coding region
CC of the front 20 amino acids in the C protein, and the coding region of
CC NS1 protein signal; coding regions of all non-structural proteins. The
CC obtained vaccines are useful in producing preventives or/and remedies for
CC cancer like cervical cancer and viral diseases. Such vaccines can
CC efficiently express antigen in infected cells, which is because dengue
CC virus can infect dendritic cells, and can effectively present antigen to
CC provide immunity effect. Different types of dengue virus can be used to
CC repeatedly produce efficient immune response thereby strengthening the
CC body's immune system against the pathogen that contains such antigen.
CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC expressing system using of the full-length dengue virus cDNA clone
CC (pBS/FLN2). The recombinant virus vectors were transfected into baby
CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC lines. This sequence corresponds to the HPV type 16 E7 protein whose
CC encoding gene is used as the gene of interest in the recombinant replicon
CC of the invention.

XX Sequence 256 AA;

SO Query Match 99.2%; Score 823; DB 8; Length 256;
Best Local Similarity 98.0%; Pred. No. 1.7e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPERPRKLPOLCTELQTTIHDIIEECVCKQQLREYVDFAFRDLCIYRDGNFY 60
Db 106 MFQDPERPRKLPOLCTELQTTIHDIIEECVCKQQLREYVDFAFRDLCIYRDGNFY 165

QY 61 AVXDCKLKFYSKISEYRHVCYSVGTTLLEQYNNKPLCDLLIRICINXQKPLCPEEKQRLDK 120
Db 166 AVXDCKLKFYSKISEYRHVCYSVGTTLLEQYNNKPLCDLLIRICINQKPLCPEEKQRLDK 225

QY 121 KQRFHNIRGRWTRCSCSSRTRRETOL 151
Db 226 KQRFHNIRGRWTRCSCSSRTRRETOL 256

RESULT 26
AEFA0157
ID AEFA0157 standard; protein; 256 AA.

XX AC AEFA0157;

DT 23-MAR-2006 (first entry)

DE Human papillomavirus 16 (HPV-16) E7-E6 oncoprotein.

XX Vaccine; virus-like particle; replicon; therapeutic; cancer; cytostatic;
KM neoplasm; viral infection; virucide; infection; oncoprotein.

XX Human papillomavirus type 16.

XX OS US2006018928-A1.

XX PN 26-JAN-2006.

XX PD 29-JUL-2005; 2005US-00192923.

XX PF 30-JAN-2003; 2003CN-00115272.

XX PR 30-JAN-2003; 2003CN-00115273.

XX PR 30-JAN-2004; 2004WO-00072274.

XX PA (PANG/) PANG X.

XX PI Pang X;

XX DR WPI; 2006-109169/11.

XX DR N-PSDB; AEFA0156.

XX New recombinant DEN replicons with a deletion of prem, useful for
PT producing a drug for the prophylaxis and treatment of cancer or viral
PT infection.

CC preferably a deletion mutant comprising at least half, and preferably two
CC thirds of full length E6 or E7 protein starting from the N- or C-
CC terminal, or is a full length E6 moiety fused to a full length E7 moiety.
CC The variant optionally has a linkage moiety and a foreign protein or
CC peptide which facilitates the purification of, and enhances the
CC immunogenicity of, the fusion protein. This sequence is a full length
CC E6/E7 fusion protein. (Updated on 27-AUG-2003 to correct OS field.)
XX

SQ Sequence 266 AA;

Query Match 99.2%; Score 823; DB 2; Length 266;
Best Local Similarity 98.0%; Pred. No. 1.8e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRRPRKLPOLCTELQTTIHDIILECVCKQQLRREVYDFARFDLCIVYRDGNPY 60
DB 8 MFQDPQRRPRKLPOLCTELQTTIHDIILECVCKQQLRREVYDFARFDLCIVYRDGNPY 67

QY 61 AVXDCKLKFYSKISEYHNYCYVYGTTLLEQYNNKPLCDLLIRCTNXOKPLCPPEKQKHLD 120
DB 68 AVCDCKLKFYSKISEYHNYCYSLVGTTLLEQYNNKPLCDLLIRCTNCKPLCPPEKQKHLD 127

QY 121 KKQRFHNIRGRWTCRCMSCSSRTRETOL 151
DB 128 KKQRFHNIRGRWTCRCMSCSSRTRETOL 158

RESULT 29
AAV25376
ID AAV25376 standard; protein; 273 AA.

XX AAV25376;

DT 06-SEP-1999 (first entry)

DE HPV fusion protein D1/3-E6-His/HPV16.

XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KM immunological fusion partner; Cpg oligonucleotide; immune response;
KM HIV antigen; prevention; treatment.

XX Synthetic.

OS Human papillomavirus.

XX WO9933868-A2.

PD 08-JUL-1999.

PF 18-DEC-1998; 98WO-EP008563.

PR 24-DEC-1997; 97GB-00027262.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Dalemans WLJ, Gerard CMG;

DR WPI: 1999-405485/34.

DR N-PSDB; AAX78792.

PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
induce immune response to HPV.

PS Example II; Page 48-49; 62pp; English.

CC AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAV25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory Cpg
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours
XX

SQ Sequence 273 AA;

Query Match 99.2%; Score 823; DB 2; Length 273;
Best Local Similarity 98.0%; Pred. No. 1.9e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRRPRKLPOLCTELQTTIHDIILECVCKQQLRREVYDFARFDLCIVYRDGNPY 60
DB 114 MFQDPQRRPRKLPOLCTELQTTIHDIILECVCKQQLRREVYDFARFDLCIVYRDGNPY 173

QY 61 AVXDCKLKFYSKISEYHNYCYVYGTTLLEQYNNKPLCDLLIRCTNXOKPLCPPEKQKHLD 120
DB 174 AVCDCKLKFYSKISEYHNYCYSLVGTTLLEQYNNKPLCDLLIRCTNCKPLCPPEKQKHLD 233

QY 121 KKQRFHNIRGRWTCRCMSCSSRTRETOL 151
DB 234 KKQRFHNIRGRWTCRCMSCSSRTRETOL 264

RESULT 30

AAV2632
ID AAV2632 standard; protein; 273 AA.

XX AAV2632;

DT 17-OCT-2003 (revised)

DT 22-JUN-1999 (first entry)

DE Prot. D1/3-E6-His/HPV16 protein.

XX Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KM tumour; lesion; benign; malignant; virus; infection.

XX Human papillomavirus.

OS Haemophilus influenzae.

XX WO9910375-A2.

PD 04-MAR-1999.

PF 17-AUG-1998; 98WO-EP005285.

PR 22-AUG-1997; 97GB-00017953.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;

PI Lombardo-Bencheikh A;

DR WPI: 1999-190587/16.

DR N-PSDB; AAX29781.

PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
treatment or prophylaxis of HPV induced lesions.

PS Disclosure; Fig 3; 95pp; English.

CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B protein
CC D. The sequence also contains a histidine tag at the C-terminus of the
CC encoded protein. The protein can be used in a vaccine, for immuno-
CC therapeutically treating HPV induced tumour lesions (benign or malignant)
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX

SQ Sequence 273 AA;

Query Match 99.2%; Score 823; DB 2; Length 273;
Best Local Similarity 98.0%; Pred. No. 1.9e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRRPRKLPOLCTELQTTIHDIILECVCKQQLRREVYDFARFDLCIVYRDGNPY 60

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Db      114 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCTIYRDGNPY 173
Qy      61 AVXDKCLKFYSKISEYRHYCYSYGTTLEQYNNKPLCDLLIRNCINXOKPLCPBEKORHLD 120
Db      174 AVCDKCLKFYSKISEYRHYCYSLYGTTLEQYNNKPLCDLLIRNCINXOKPLCPBEKORHLD 233
Qy      121 KKQRFNINIRGRWTRGCMSCCRSSRTRETOL 151
Db      234 KKQRFNINIRGRWTRGCMSCCRSSRTRETOL 264

RESULT 31
AEDS2634
ID      AEDS2634 standard; protein; 273 AA.
XX
AC      AEDS2634;
XX
DT      29-DEC-2005 (first entry)
XX
DE      Fusion protein D1/3-E6-His/HPV16.
XX
KM      Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KM      virucide; uterine cervix tumor; E6; D protein.
XX
OS      Haemophilus influenzae; strain 772.
OS      Human papillomavirus type 16.
OS      Synthetic.
OS      Chimeric.
XX
PN      IN9801903-14.
XX
PD      04-MAR-2005.
XX
PF      24-AUG-1998; 98IN-CH001903.
XX
PR      22-AUG-1997; 97EP-00179535.
XX
PA      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI      Tyrell AMR;
XX
DR      WPI: 2005-557648/57.
DR      N-PSDB; AEDS2633.
XX
PT      Vaccine.
XX
PS      Example 4; Fig 3; 96pp; English.
XX
CC      The invention relates to human Papilloma virus (HPV) fusion proteins,
CC      linked to an immunological fusion partner that provides T helper epitopes
CC      to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC      are useful in the treatment or prophylaxis of HPV induced lesions
CC      (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
CC      proteins (singly, as an E6-E7 fusion or mutated) were fused to either
CC      Haemophilus influenzae D protein (20-127), the C-terminus of
CC      Streptococcus pneumoniae Lyta protein (cLyta) or chloroform. The present
CC      sequence represents an HPV-H. influenzae D protein, fusion protein of the
CC      invention.
XX
SQ      Sequence 273 AA;

Query Match      99.2%; Score 823; DB 9; Length 273;
Best Local Similarity 98.0%; Pred. No. 1.9e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      121 KKQRFNINIRGRWTRGCMSCCRSSRTRETOL 151
Db      234 KKQRFNINIRGRWTRGCMSCCRSSRTRETOL 264

RESULT 32
AA125379
ID      AA125379 standard; protein; 292 AA.
XX
AC      AA125379;
XX
DT      06-SEP-1999 (first entry)
XX
DE      HPV fusion protein CLYTA-E6-His/HPV16.
XX
KM      Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KM      immunological fusion partner; Cpg oligonucleotide; immune response;
KM      HPV antigen; prevention; treatment.
XX
OS      Synthetic.
OS      Human papillomavirus.
XX
PN      WO933868-A2.
XX
PD      08-JUL-1999.
XX
PF      18-DEC-1998; 98WO-EP008563.
XX
PR      24-DEC-1997; 97GB-00027262.
XX
PA      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI      Dalemans WILJ, Gerard CMG;
XX
DR      WPI: 1999-405485/34.
DR      N-PSDB; AAX78795.
XX
PT      Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT      induce immune response to HPV.
XX
PS      Example VI; Page 52-53; 62pp; English.
XX
CC      AAX78791-X78801 represent nucleic acid sequences which encode novel
CC      constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC      HPV (represented in AA125379-Y25386). These constructs are optionally
CC      linked to an immunological fusion partner and an immunomodulatory Cpg
CC      oligonucleotide. The products of the invention can be used to induce an
CC      immune response in a patient to an HPV antigen. They can also be used for
CC      preventing or treating HPV induced tumours
XX
SQ      Sequence 292 AA;

Query Match      99.2%; Score 823; DB 2; Length 292;
Best Local Similarity 98.0%; Pred. No. 2e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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RESULT 33
AA12635
ID      AA12635 standard; protein; 292 AA.

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XX AC AAY02635;
XX DT 17-OCT-2003 (revised)
XX DT 22-JUN-1999 (first entry)
XX DE CLYTA-E6-His protein.
XX KM Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;
XX KM lesion; benign; malignant; virus; infection.
XX OS Human papillomavirus.
XX OS Streptococcus pneumoniae.
XX OS Chimeric.
XX PN MO9910375-A2.
XX PD 04-MAR-1999.
XX PF 17-AUG-1998; 98MO-EP005285.
XX PR 22-AUG-1997; 97GB-00017953.
XX PS (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Bruck C, Cabezon Silva T, Deliese AEF, Gerard CMG;
XX PI Lombardo-Bencheikh A;
XX DR WPI; 1999-190587/16.
XX DR N-PSDB; AAX29784.
XX PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX PT treatment or prophylaxis of HPV induced lesions.
XX PS Disclosure; Fig 10; 95pp; English.
XX CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
XX CC protein from Human papillomavirus (HPV) linked to an immunological fusion
XX CC partner, in this case, a fragment of the Streptococcus pneumoniae CLYTA
XX CC protein of the encoded protein. The protein can be used in a vaccine, for
XX CC immuno-therapeutically creating HPV induced tumour lesions (benign or
XX CC malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 292 AA;

Query Match 99.2%; Score 823; DB 2; Length 292;
Best Local Similarity 98.0%; Pred. No. 2e-83; 2; Indels 0; Gaps 0;
Matches 148; Conservative 1; Mismatches 2;

QY 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 60
DB 133 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 192
QY 61 AVXDCKLKFSKISEYRHYCYSYGTTLEOQYNKPLCDLLIRICINXOKPLCPBEKQRHLD 120
DB 193 AVCDKCLKFSKISEYRHYCYSLYGTLEOQYNKPLCDLLIRICINXOKPLCPBEKQRHLD 252
QY 121 KKORFHNIRGRWTCRMCSCCSSRTRRETOL 151
DB 253 KKORFHNIRGRWTCRMCSCCSSRTRRETOL 283

RESULT 34
AED52642 standard; protein; 292 AA.
XX AC AED52642;
XX KM AED52642;
XX DT 29-DEC-2005 (first entry)
XX DE Fusion protein clyta-E6-His/HPV16.
XX

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KM Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KM virucide; uterine cervix tumor; E7; Lyta.
XX OS Streptococcus pneumoniae.
XX OS Human papillomavirus type 16.
XX OS Synthetic.
XX OS Chimeric.
XX PN IN9801903-14.
XX PD 04-MAR-2005.
XX PF 24-AUG-1998; 98IN-CH001903.
XX PR 22-AUG-1997; 97EP-00179535.
XX PS (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Tyrell AMR;
XX DR WPI; 2005-557648/57.
XX DR N-PSDB; AED52641.
XX PT Vaccine.
XX PS Example 10; Fig 10; 96pp; English.
XX CC The invention relates to human Papilloma virus (HPV) fusion proteins,
XX CC linked to an immunological fusion partner that provides T helper epitopes
XX CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
XX CC are useful in the treatment or prophylaxis of HPV induced lesions
XX CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
XX CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
XX CC Haemophilus influenzae D protein (20-127), the C-terminus of
XX CC Streptococcus pneumoniae Lyta protein (clyta) or thiorodoxin. The present
XX CC sequence represents an HPV-Lyta, fusion protein of the invention.
XX SQ Sequence 292 AA;

Query Match 99.2%; Score 823; DB 9; Length 292;
Best Local Similarity 98.0%; Pred. No. 2e-83; 2; Indels 0; Gaps 0;
Matches 148; Conservative 1; Mismatches 2;

QY 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 60
DB 133 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 192
QY 61 AVXDCKLKFSKISEYRHYCYSYGTTLEOQYNKPLCDLLIRICINXOKPLCPBEKQRHLD 120
DB 193 AVCDKCLKFSKISEYRHYCYSLYGTLEOQYNKPLCDLLIRICINXOKPLCPBEKQRHLD 252
QY 121 KKORFHNIRGRWTCRMCSCCSSRTRRETOL 151
DB 253 KKORFHNIRGRWTCRMCSCCSSRTRRETOL 283

RESULT 35
AAY25377 standard; protein; 371 AA.
XX AC AAY25377;
XX DT 06-SEP-1999 (first entry)
XX DE HPV fusion protein DL/3-E6E7-His/HPV16.
XX KM Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
XX KM immunological fusion partner; CpG oligonucleotide; immune response;
XX KM HPV antigen; prevention; treatment.
XX OS Synthetic.
XX OS Human papillomavirus.
XX

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PN W09933868-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1998; 98MO-EP008563.
XX
PR 24-DEC-1997; 97GB-00027262.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PI Dalemans W.L.J., Gerard CMG;
XX WPI; 1999-405485/34.
XX N-PSDB; AAX78793.
XX
XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT induce immune response to HPV.
XX
XX Example III; Page 50; 62pp; English.
XX
XX AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAY25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory Cpg
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours
XX
SQ Sequence 371 AA;

Query Match 99.2%; Score 823; DB 2; Length 371;
Best Local Similarity 98.0%; Pred. No. 2.7e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDDPQPRPKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDGPNY 60
DB 114 MFQDDPQPRPKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDGPNY 173
QY 61 AVXDCKLKFYSKISEYRHYCYSYGTTLEQYNNKPLCDLLIRICINQKPLCPBEKQRLD 120
DB 174 AVCDCKLKFYSKISEYRHYCYSLYGTLEQYNNKPLCDLLIRICINQKPLCPBEKQRLD 233
QY 121 KKQRFNIRGRMTGRCMSCCRSSRTRETOL 151
DB 234 KKQRFNIRGRMTGRCMSCCRSSRTRETOL 264

RESULT 36
AAY02633
ID AAY02633 standard; protein; 371 AA.
XX
AC AAY02633;
XX
DT 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)
XX
DE Prot. D1/3-E6-E7-His/HPV16 protein.
XX
XX Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KM tumour; lesion; benign; malignant; virus; infection.
XX
XX Human papillomavirus.
OS Haemophilus influenzae.
OS Chimeric.
XX
XX W09910375-A2.
XX
XX 04-MAR-1999.
XX
XX 17-AUG-1998; 98MO-EP005285.
XX
XX 22-AUG-1997; 97GB-00017953.
XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
PI Lombardo-Bencheikh A;
XX
XX WPI; 1999-190587/16.
XX N-PSDB; AAX29782.
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT treatment or prophylaxis of HPV induced lesions.
XX
XX Disclosure; Fig 6; 95pp; English.
XX
XX This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B protein
CC D. The sequence also contains a histidine tag at the C-terminus of the
CC encoded protein. The protein can be used in a vaccine, for immuno-
CC therapeutically treating HPV induced tumour lesions (benign or malignant)
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 371 AA;

Query Match 99.2%; Score 823; DB 2; Length 371;
Best Local Similarity 98.0%; Pred. No. 2.7e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDDPQPRPKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDGPNY 60
DB 114 MFQDDPQPRPKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDGPNY 173
QY 61 AVXDCKLKFYSKISEYRHYCYSYGTTLEQYNNKPLCDLLIRICINQKPLCPBEKQRLD 120
DB 174 AVCDCKLKFYSKISEYRHYCYSLYGTLEQYNNKPLCDLLIRICINQKPLCPBEKQRLD 233
QY 121 KKQRFNIRGRMTGRCMSCCRSSRTRETOL 151
DB 234 KKQRFNIRGRMTGRCMSCCRSSRTRETOL 264

RESULT 37
AED52638
ID AED52638 standard; protein; 371 AA.
XX
AC AED52638;
XX
DT 29-DEC-2005 (first entry)
XX
DE Fusion protein D1/3-E6-E7-His/HPV16.
XX
XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KM virucide; uterine cervix tumor; E7; D protein.
XX
XX Haemophilus influenzae; strain 772.
OS Synthetic.
OS Chimeric.
XX
XX IN9801903-14.
XX
XX 04-MAR-2005.
XX
XX 24-AUG-1998; 98IN-CH001903.
XX
XX 22-AUG-1997; 97BP-00179535.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Tyrell AMR;
XX
XX WPI; 2005-557648/57.
XX N-PSDB; AED52637.
XX

```

XX XX Vaccine.
PT XX
XX XX Example 6; Fig 6; 96pp; English.
XX
CC The invention relates to human Papilloma virus (HPV) fusion proteins,
CC linked to an immunological fusion partner that provides T helper epitopes
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC are useful in the treatment or prophylaxis of HPV induced lesions
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
CC Haemophilus influenzae D protein (20-127), the C-terminus of
CC Streptococcus pneumoniae Lyta protein (ClayA) or thiodoxin. The present
CC sequence represents an HPV-H. influenzae D protein, fusion protein of the
CC invention.
XX
SQ Sequence 371 AA:
Query Match 99.2%; Score 823; DB 9; Length 371;
Best Local Similarity 98.0%; Pred. No. 2.7e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MFQDPQPRPKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTVYRDGNPY 60
DB 114 MFQDPQPRPKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTVYRDGNPY 173
QY 61 AVXDCKLFYSKISEYRHYCYSVYGTTLQYNNKPLCDLLIRCIINXOKPLCPPEKORHLD 120
DB 174 AVCDCKLFYSKISEYRHYCYSLYGTTLQYNNKPLCDLLIRCIINXOKPLCPPEKORHLD 233
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 234 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 264
QY
DB
RESULT 38
AAV25381
ID AAV25381 standard; protein; 390 AA.
XX
AC AAV25381;
XX
DT 06-SEP-1999 (first entry)
XX
DE HPV fusion protein CLYTA-E6E7-His/HPV16.
XX
KM Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KM immunological fusion partner; CpG oligonucleotide; immune response;
KM HPV antigen; prevention; treatment.
XX
OS Synthetic.
OS Human papillomavirus.
XX
PN WO933868-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1998; 98WO-EP008563.
XX
PR 24-DEC-1997; 97GB-00027262.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Dalemans WLJ, Gerard CMG;
XX
DR WPI: 1999-405485/34.
XX
PT N-PSDB; AAX78797.
XX
PS Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
XX induce immune response to HPV.
XX
PS Example VIII; Page 55-56; 62pp; English.
XX
CC AAX78791-X78801 represent nucleic acid sequences which encode novel

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CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAV25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours
XX
SQ Sequence 390 AA:
Query Match 99.2%; Score 823; DB 2; Length 390;
Best Local Similarity 98.0%; Pred. No. 2.9e-83;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MFQDPQPRPKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTVYRDGNPY 60
DB 133 MFQDPQPRPKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTVYRDGNPY 192
QY 61 AVXDCKLFYSKISEYRHYCYSVYGTTLQYNNKPLCDLLIRCIINXOKPLCPPEKORHLD 120
DB 193 AVCDCKLFYSKISEYRHYCYSLYGTTLQYNNKPLCDLLIRCIINXOKPLCPPEKORHLD 252
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 253 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 283
QY
DB
RESULT 39
AAV2637
ID AAV2637 standard; protein; 390 AA.
XX
AC AAV2637;
XX
DT 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)
XX
DE CLYTA-E6E7-His protein.
XX
KM Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;
KM lesion; benign; malignant; virus; infection.
XX
OS Human papillomavirus.
OS Streptococcus pneumoniae.
OS Chimeric.
XX
PN WO9910375-A2.
XX
PD 04-MAR-1999.
XX
PF 17-AUG-1998; 98WO-EP005285.
XX
PR 22-AUG-1997; 97GB-00017953.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
XX
DR Lombardo-Bencheikh A;
XX
DR WPI: 1999-190587/16.
XX
PT N-PSDB; AAX29786.
XX
PS Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX treatment or prophylaxis of HPV induced lesions.
XX
PS Disclosure; Fig 14; 95pp; English.
XX
CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Streptococcus pneumoniae CLYTA
CC protein of the encoded protein. The protein can be used in a vaccine, for
CC immuno-therapeutically treating HPV induced tumour lesions (benign or
CC malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX

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SO Sequence 390 AA:

Query Match 99.2%; Score 823; DB 2; Length 390;
 Best Local Similarity 98.0%; Pred. No. 2.9e-83;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTIHDIILECVYCKQQLRREVDFAFRDLCTIVYRGNPY 60
 DB 133 MFQDPQRPRLPOLCTELQTTIHDIILECVYCKQQLRREVDFAFRDLCTIVYRGNPY 192
 QY 61 AVXDCKLKFKYSKISEYRHVCYSYVGTLEQQYNKPLCDLLIRNCINXQKPLCPBEKORHLD 120
 DB 193 AVCDKCLKFKYSKISEYRHVCYSYVGTLEQQYNKPLCDLLIRNCINXQKPLCPBEKORHLD 252

QY 121 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 151
 DB 253 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 283

RESULT 40
 AED52646
 ID AED52646 standard; protein; 390 AA.
 AC AED52646;
 DT 29-DEC-2005 (first entry)
 DE Fusion protein clyCA-E6-E7-His/HPV16.
 XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
 KM virucide; uterine cervix tumor; E7; Lyta.
 XX Streptococcus pneumoniae.
 OS Human papillomavirus type 16.
 OS Synthetic.
 OS Chimeric.
 PN IN9801903-14.
 PD 04-MAR-2005.
 PF 24-AUG-1998; 98IN-CH001903.
 PR 22-AUG-1997; 97EP-00179535.
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PI Tyrell AMR;
 DR WPI; 2005-557648/57.
 DR N-PSDB; AED52645.
 PT Vaccine.
 PS Example 12; Fig 14; 96pp; English.
 CC The invention relates to human Papilloma virus (HPV) fusion proteins,
 CC linked to an immunological fusion partner that provides T helper epitopes
 CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
 CC are useful in the treatment or prophylaxis of HPV induced lesions
 CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
 CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
 CC Haemophilus influenzae D protein (20-127), the C-terminus of
 CC Streptococcus pneumoniae Lyta protein (cLYCA) or chloroixin. The present
 CC sequence represents an HPV-Lyta, fusion protein of the invention.
 SO Sequence 390 AA:

Query Match 99.2%; Score 823; DB 9; Length 390;
 Best Local Similarity 98.0%; Pred. No. 2.9e-83;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTIHDIILECVYCKQQLRREVDFAFRDLCTIVYRGNPY 60

DB 133 MFQDPQRPRLPOLCTELQTTIHDIILECVYCKQQLRREVDFAFRDLCTIVYRGNPY 192
 QY 61 AVXDCKLKFKYSKISEYRHVCYSYVGTLEQQYNKPLCDLLIRNCINXQKPLCPBEKORHLD 120
 DB 193 AVCDKCLKFKYSKISEYRHVCYSYVGTLEQQYNKPLCDLLIRNCINXQKPLCPBEKORHLD 252

QY 121 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 151
 DB 253 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 283

RESULT 41
 ADO44066
 ID ADO44066 standard; protein; 248 AA.
 AC ADO44066;
 DT 15-JUL-2004 (first entry)
 DE Amino acid sequence of an E7E6 fusion protein.
 XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
 XX Human papillomavirus type 16.
 OS Synthetic.
 PN WO2004030636-A2.
 PD 15-APR-2004.
 PF 02-OCT-2003; 2003WO-US031726.
 PR 03-OCT-2002; 2002US-0415929P.
 PA (AMHP) WYETH HOLDINGS CORP.
 PI Smith L, Cassecci MC;
 DR WPI; 2004-316328/29.
 DR N-PSDB; ADO44067.
 PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.
 PS Example 1; Page 72-73; 101pp; English.
 CC The present sequence represents an E7E6 fusion protein, comprising wild
 CC type E7 and E6 polypeptides from human papillomavirus type 16 (HPV16).
 CC The specification describes human papillomavirus E6 and E7 polypeptides,
 CC where the E7 polypeptide has mutations at any one or more of the amino
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of
 CC the sequence given in ADO44072. The polypeptides of the invention are
 CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.
 SO Sequence 248 AA:

Query Match 98.9%; Score 821; DB 8; Length 248;
 Best Local Similarity 98.7%; Pred. No. 2.8e-83;
 Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FQDPQRPRLPOLCTELQTTIHDIILECVYCKQQLRREVDFAFRDLCTIVYRGNPY 61

```
Db      99 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQOQLLREVVDPFAFRDLCTIVYRDGNPY 158
Qy      62 VXDCKLKFYSKISSEYRHVCYSVYGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQKRLHD 121
Db      159 VCDCKLKFYSKISSEYRHVCYSVYGTTLLEQYNNKPLCDLLIRICINQKPLCPBEKQKRLHD 218
Qy      122 KORFHNIRGRWTRGRCMCCRSSRTRRETQL 151
Db      219 KORFHNIRGRWTRGRCMCCRSSRTRRETQL 248

RESULT 42
AAV57808
ID AAV57808 standard; peptide: 151 AA.
AC AAV57808;
DT 20-MAR-2000 (first entry)
DE HPV-16 E6 protein amino acid sequence.
XX
XX Transcriptional adaptor motif; TRAM; TRAM interaction motif; TRIM;
XX cIAP binding protein; transcriptional regulation; cytoskeletal; antiviral;
XX cell cycle inhibitor; viral transcription inhibitor; cancer; tumour;
XX viral disease; viral infection; cell cycle; apoptosis; growth arrest.
XX
XX Human papillomavirus.
XX
XX W09961608-A2.
XX
XX 02-DEC-1999.
XX
XX 26-MAY-1999; 99WO-GB001668.
XX
XX 26-MAY-1998; 98GB-00011303.
XX
XX 05-JAN-1999; 99GB-00000157.
XX
XX (MOLE-) INST MOLECULAR & CELL BIOLOGY.
XX
XX O'Connor MJ, Zimmermann H;
XX
XX WPI; 2000-072620/06.
XX
XX Novel polypeptides cells useful for treating viral disease and cancer.
XX
XX Example 2; Fig 9; 73pp; English.
XX
XX The present invention describes a polypeptide comprising a
XX transcriptional adaptor motif (TRAM) or a TRAM-interaction motif (TRIM)
XX (I). (I) can be used for identifying compounds (II) comprising a
XX polypeptide capable of disrupting an interaction between a TRAM sequence
XX and/or a TRIM sequence. Polypeptides which bind to a TRAM sequence or a
XX TRIM sequence are identified by incubating the polypeptide with (I) and
XX determining if the polypeptide interacts with (I). Compound (II) is
XX useful for preparing a pharmaceutical composition and for disrupting an
XX interaction between TRAM sequence and TRIM sequence in vitro, thereby
XX inhibiting viral transcription or cell cycle progression in mammalian
XX cells especially cancer cell. Compounds which disrupt interaction between
XX TRIM/TRAM containing polypeptides can be used therapeutically to prevent
XX or treat viral diseases and tumours. The polypeptides reduce
XX susceptibility of cells to viral infection and regulate cell cycle
XX including apoptosis and growth arrest and can be used to produce
XX antibodies against the TRIM or TRAM sequences. HPV types associated with
XX high risk or low risk of cervical cancer can be distinguished based on
XX the ability of E6 polypeptides to bind to cIAP binding protein (CBP) TRAM
XX sequence. The present sequence represents a HPV-16 E6 protein amino acid
XX sequence from an example from the present invention
XX
XX Sequence 151 AA;
XX
XX Query Match 98.6%; Score 818; DB 3; Length 151;
XX Best Local Similarity 97.4%; Pred. No. 3.3e-83;
XX Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
Qy      1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQOQLLREVVDPFAFRDLCTIVYRDGNPY 60
Db      1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQOQLLREVVDPFAFRDLCTIVYRDGNPY 60
Qy      61 AVXDCKLKFYSKISSEYRHVCYSVYGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQKRLHD 120
Db      61 AVCDCKLKFYSKISSEYRHVCYSVYGTTLLEQYNNKPLCDLLIRICINQKPLCPBEKQKRLHD 120
Qy      121 KORFHNIRGRWTRGRCMCCRSSRTRRETQL 151
Db      121 KORFHNIRGRWTRGRCMCCRSSRTRRETQL 151

RESULT 43
ADL90078
ID ADL90078 standard; protein: 158 AA.
AC ADL90078;
DT 17-JUN-2004 (first entry)
DE Human papillomavirus 16-E6 protein, SEQ ID 18.
XX
XX Immune response; immunoglobulin; Ig; E6.
XX
XX Human papillomavirus.
XX
XX W02004027049-A2.
XX
XX 01-APR-2004.
XX
XX 18-SEP-2003; 2003WO-US030188.
XX
XX 20-SEP-2002; 2002US-0412219P.
XX
XX 14-MAR-2003; 2003WO-US007995.
XX
XX (ASTR-) ASTRAL INC.
XX
XX Bot A, Wang L, Smith D, Phillips B;
XX
XX WPI; 2004-295415/27.
XX
XX Generating an immune response to an antigen, useful for generating
XX desired T cell responses comprises administering an immunoglobulin having
XX one peptide epitope of the antigen attached to the immunoglobulin.
XX
XX Disclosure; Fig 1G; 154pp; English.
XX
XX The present invention relates to a method for generating an immune
XX response to an antigen in a patient. The method comprises administering
XX to the patient an immunoglobulin (Ig) or its portion where the Ig has at
XX least one peptide epitope of the antigen attached to the Ig or its
XX portion and administering the immunoglobulin or its portion in
XX conjunction with a RNA segment. The present sequence is an antigen
XX sequence, used to illustrate the invention.
XX
XX Sequence 158 AA;
XX
XX Query Match 98.2%; Score 815; DB 8; Length 158;
XX Best Local Similarity 97.4%; Pred. No. 7.6e-83;
XX Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQOQLLREVVDPFAFRDLCTIVYRDGNPY 60
Db      8 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQOQLLREVVDPFAFRDLCTIVYRDGNPY 67
Qy      61 AVXDCKLKFYSKISSEYRHVCYSVYGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQKRLHD 120
Db      68 AVCDCKLKFYSKISSEYRHVCYSVYGTTLLEQYNNKPLCDLLIRICINQKPLCPBEKQKRLHD 127
Qy      121 KORFHNIRGRWTRGRCMCCRSSRTRRETQL 151
Db      121 KORFHNIRGRWTRGRCMCCRSSRTRRETQL 151
```


Db 128 KKORFNIRGRWTCMCCRSSRTRRETOL 158

RESULT 44

AAW9369

ID AAW9369 standard; peptide; 243 AA.

AC AAW9369;

DT 17-OCT-2003 (revised)

DT 21-MAY-1999 (first entry)

DE Papillomavirus E6/protein F signal peptide fusion protein.

XX Antitumour; immunogen; intracellular localisation; cancer; dysplasia;

KW signal peptide; papillomavirus; infection; cervix uteri.

XX Human papillomavirus.

OS Measles virus.

OS Chimeric.

XX MO9903885-A1.

PD 28-JAN-1999.

PF 17-JUL-1998; 98MO-FR001576.

PR 18-JUL-1997; 97PR-00009152.

PA (TRGE) TRANSGENE SA.

PI Kieny M, Balloul J, Bizouarne N;

DR WPI; 1999-132161/11.

PT Antitumour composition containing immunogenic polypeptide with altered

PT localisation - or vector expressing this polypeptide, particularly for

PT treating or preventing cervical cancer associated with human papilloma

PT virus.

XX Claim 16; Page 54-55; 74pp; French.

CC The invention relates to an antitumour composition containing a

CC therapeutic or prophylactic agent or one or more immunogenic

CC polypeptides, where at least one polypeptide is modified so that its

CC intracellular localisation is different from that of the native

CC polypeptide. This sequence represents an example of a modified

CC immunogenic protein and corresponds to the E6 protein from human

CC papillomavirus fused to the measles virus protein F signal peptide. The

CC compositions, vectors and particles are used to treat or prevent cancers

CC and tumours, specifically those associated with papillomavirus infection

CC (e.g. cancer or low grade dysplasia of the cervix uteri). (Updated on 17-

CC OCT-2003 to standardise OS field)

XX Sequence 243 AA;

Query Match 93.9%; Score 779.5; DB 2; Length 243;

Best Local Similarity 94.7%; Pred. No. 1.2e-78;

Matches 143; Conservative 1; Mismatches 2; Indels 5; Gaps 1;

QY 1 MFQDPOERPRKLPOLCTELQTTIHDIILBCVYCKQQLRREYVDFARDCIYVRDGNPY 60

DB 36 MFQDPOERPRKLPOLCTELQTTIHDIILBCVYCKQQLRREYVDFARDCIYVRDGNPY 95

QY 61 AVXDCKLKFYSKISEYRHYCYVYGTTLBOQYNKPLCDLLIRICINXOKPLCPBEKORHLD 120

DB 96 AVCDKCLKFYSKISEYRHYCYVYGTTLBOQYNKPLCDLLIRICINXOKPLCPBEKORHLD 150

QY 121 KKORFNIRGRWTCMCCRSSRTRRETOL 151

DB 151 KKORFNIRGRWTCMCCRSSRTRRETOL 181

RESULT 45

AA40919

ID AA40919 standard; protein; 149 AA.

AC AA40919;

DT 22-FEB-1994 (first entry)

DE HPV E6 region product.

KW Human papilloma virus; HPV; benign; malignant.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 30..33

FT Disulfide-bond 63..66

PN JP05192200-A.

PD 03-AUG-1993.

PF 19-AUG-1991; 91JP-00230839.

PR 20-AUG-1990; 90JP-00217067.

PA (TAKI) TAKARA SHUZO CO LTD.

DR WPI; 1993-277497/35.

DR N-PSDB; AAQ48575.

XX Detecting benign and/or malignant human papilloma virus - by detecting

XX DNA sequence of E6 and/or E7 region of human papilloma virus.

XX Disclosure; Page 16-17; 18pp; Japanese.

XX Probes are designed to detect benign and/or malignant human papilloma

XX virus. The probes bind to the E6 and/or E7 region of human papilloma

XX virus

XX Sequence 149 AA;

Query Match 69.9%; Score 580; DB 2; Length 149;

Best Local Similarity 71.5%; Pred. No. 1.5e-56;

Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFQDPOERPRKLPOLCTELQTTIHDIILBCVYCKQQLRREYVDFARDCIYVRDGNPY 60

DB 1 MFQDPAERPRKLPOLCTELQTTIHDIILBCVYCKQQLRREYVDFARDCIYVRDGNPY 60

QY 61 AVXDCKLKFYSKISEYRHYCYVYGTTLBOQYNKPLCDLLIRICINXOKPLCPBEKORHLD 120

DB 61 GVCMKCLKFYSKISEYRHYCYVYGTTLBOQYNKPLCDLLIRICINXOKPLCPBEKORHLD 120

QY 121 KKORFNIRGRWTCMCCRSSRTRRETOL 151

DB 121 EKORFNIRGRWTCMCCRSSRTRRETOL 149

RESULT 46

ADO44077

ID ADO44077 standard; protein; 149 AA.

AC ADO44077;

DT 15-JUL-2004 (first entry)

DE Amino acid sequence of the E6 polypeptide of HPV35.

XX E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;

XX cervical cancer; immune response; lower gastrointestinal tract cancer;

XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

XX	Human papillomavirus type 35.
XX	WO2004030636-A2.
XX	15-APR-2004.
XX	02-OCT-2003; 2003WO-US011726.
XX	03-OCT-2002; 2002US-0415929P.
XX	(AMHP) WYETH HOLDINGS CORP.
XX	Smith L, Casasetti MC;
XX	WPI: 2004-316328/29.
XX	N-PESDB; ADO44104.
XX	New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
XX	Disclosure; Page 80; 101pp; English.
XX	ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.
XX	ADO44098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides,
XX	where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of the sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
XX	Sequence 149 AA;
XX	Query Match 69.6%; Score 578; DB 8; Length 149;
XX	Best Local Similarity 71.5%; Pred. No. 2.5e-56;
XX	Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;
QY	1 MFQDPQERPRKLPQLCTELQTTHDIILECYCKQKOLLREYYDFAPFRLCTIVRDGNPY 60
DB	1 MFQDDAEPRPYKXLDHCNEVEBSIHEICINCYCKQKOLRSEYYDFACVLDCTIVREGOPY 60
QY	61 AVXDXCLFYSKISSEYRHYCVSVGCTTEEGQVNRKPLCDLLIRCLINXOKPLCEEKQRHLD 120
DB	61 GCMCKCLFYSKISSEYRHYCVSVGCTTEELKQCKNKLCHLLIRCLICQKPLCEVEKQRHLE 120
QY	121 KQRFPHNIRGRWTGRGMSGCCSSRTRETEL 151
DB	121 EKGRFPHNIGRWTGRGMSCKMK--TRRETEV 149
XX	RESULT 47
XX	AEA98533
XX	AEA98533 standard; protein; 149 AA.
XX	AEA98533;
XX	08-SEP-2005 (first entry)
XX	HPV (oncogenic strain) E6 amino acid sequence SEQ ID 14.
XX	Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;
XX	cancer; cervix tumor; cytostatic.
XX	Human papillomavirus; strain 35.
XX	US2005142541-A1.

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XX      30-JUN-2005.
PD      XX
XX      23-DEC-2004; 2004US-00021949.
PF      XX
XX      23-DEC-2003; 2003US-0532373P.
PR      XX
XX      (ARBO-) ARBOR VITA CORP.
PA      XX
XX      Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;
XX      WPI, 2005-457781/46.
XX      DR
XX      New antibody composition comprising a mixture of monoclonal antibodies
PT      PT for oncogenic strains of human papilloma virus, useful for diagnosing
PT      cancer.
PS      Disclosure; SEQ ID NO 14; 161pp; English.
PS      XX
XX      The invention relates to an antibody composition comprising a mixture of
CC      CC monoclonal antibodies that specifically bind to E6 proteins of human
CC      CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one
CC      CC of the monoclonal antibodies specifically binds to E6 proteins of at
CC      CC least three different oncogenic HPV strains. Also included are a
CC      CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,
CC      CC comprising the antibody composition above), a method of detecting an HPV
CC      CC E6 protein in a sample, a method of detecting the presence of an
CC      CC oncogenic HPV E6 protein in a sample and a system for detecting the
CC      CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a
CC      CC first and a second binding partner for an oncogenic HPV E6 polypeptide,
CC      CC where the first binding partner is a PDZ domain protein and the second
CC      CC binding partner is an antibody that specifically binds to the E6 proteins
CC      CC of at least three different oncogenic HPV strains). The antibody
CC      CC composition, kit, methods, and system are useful for diagnosing cancer,
CC      CC particularly cervical cancer. The present sequence is an HPV E6 protein.
SQ      SQ Sequence 149 AA;

Query Match          69.6%; Score 578; DB 9; Length 149;
Best Local Similarity 71.5%; Pred. No. 2.5e-56;
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1.

QY      1 MFODQGERPKLPQLCTELQTTIHDIILECYCKOGLLRREYDFAFRLDCIVYRDNMP 60
DB      1 MFQDAERPYKLHDDCNEVESIHEICLVACYKQELORSEYDFACYPDLCIVREGOPY 60
QY      61 AVXDCLFLFYSKISERYHCYSVVGTLEDOYNRPCLCDLLIRCIINXQKPLCEEEKQRHLD 120
DB      61 GVCMKCLFLFYKISYRWRYRSVYGTELKEKCNNQDLGHLILRCITCGKPLCEVEQRHLE 120
QY      121 KKQRFHNIRGRWTCGSCCSSSRTTRTQTOL 151
DB      121 EKRRFHNIIGRWTCGSCSWKP--TRRETREV 149

RESULT 48
ID      ADFJ1985 standard; protein; 160 AA.
AC      ADFJ1985;
XX      DT
XX      12-FEB-2004 (first entry)
DE      Human papillomavirus fusion gene.
XX      KW human papillomavirus; cervix cancer.
XX      OS Homo sapiens.
XX      CN1381583-A.
PD      27-NOV-2002.
XX      XX

```

PF 24-APR-2002; 2002CN-00117143.
XX
XX 24-APR-2002; 2002CN-00117143.
XX
XX (ONCO-) INST ONCOLOGY TUMOR HOSPITAL CHINESE ACA.
XX
XX
PI Zhao Q;
XX
XX WPI; 2003-258260/26.
DR N-PSDB; ADF31984.
XX
XX Human papillomavirus E6/E7 fusion gene and its efficient expression
PT carrier and fusion protein vaccine.
XX
XX Claim 8; SEQ ID NO 2; 16pp; Chinese.
XX
XX The present invention relates to human papillomavirus E6/E7 fusion gene,
CC its preparing process, the process for configuring the efficient
CC expression carrier containing the gene and resultant expression carrier,
CC the fusion protein prepared from the gene, and the application of the
CC fusion gene and expression protein to medical science and medicine to
CC treat cervix cancer are disclosed. The present sequence represents the
CC human papillomavirus fusion gene.
XX
XX Sequence 180 AA;
SQ
Query Match 68.9%; Score 572; DB 7; Length 180;
Best Local Similarity 93.8%; Pred. No. 1.5e-55;
Matches 106; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 MFQDPORPRKLPOLCTELQTTIHDIILECYCKQQLRRVYVAFAPDLCIVYRDGPNY 60
DB 8 MFQDPORPRKLPOLCTELQTTIHDIILECYCKQQLRRVYVAFAPDLCIVYRDGPNY 67
QY 61 AVXDCKLFYSKISEYHYCYSVYGTLEOQYNRPCLDLIRCIHXOKPLCPE 113
DB 68 AVGCKLKFYSKISEYHYRYSLVGTLEOQYNRPCLDLIRCIHXOKPLCPE 120
RESULT 49
AAB98434
ID AAB98434 standard; protein; 149 AA.
XX
XX AAB98434;
XX
XX 22-AUG-2001 (first entry)
XX
XX Human papillomavirus protein HPV31 E6.
XX
XX Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
KM epitope; T cell; identification; vaccine; infection; genital wart;
KM neoplastic growth; antiviral.
XX
XX Human papillomavirus.
OS
XX
XX W0200141799-A1.
PN
XX
XX 14-JUN-2001.
PD
XX
XX 11-DEC-2000; 2000WO-US033549.
PF
XX
XX 10-DEC-1999; 99US-0122705P.
PR 15-AUG-2000; 2000US-00641528.
XX
XX (BIM-) BEIMMUNE INC.
PA
XX
XX Sette A, Sidney J, Southwood S, Chesnut R, Cells B, Grey HM;
PI WPI; 2001-381497/40.
DR
XX
XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT treating HPV infections.
XX

PS Disclosure; Page 23; 756pp; English.
XX
XX The present invention describes an isolated prepared human papillomavirus
CC (HPV) epitope (1). (1) has antiviral activity, and can be used in vaccine
CC production. Peptides and corresponding nucleic acid compositions from the
CC present invention are useful for stimulating an immune response to HPV by
CC stimulating the production of CTL or HTL responses, specifically in the
CC treatment or prophylaxis of HPV infection, in persons who have not
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
CC can also be used in a tetramer staining assay to assess peripheral blood
CC mononuclear cells for the presence of antigen-specific CTLs following
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune
CC recall responses or evaluate the efficacy of a vaccine. The vaccine
CC compositions are useful for removing warts or treating HPV infections.
CC The epitopes for inclusion in an epitope-base vaccine may be selected
CC from conserved regions of viral or tumor-associated antigens, which
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
CC that may be present in whole antigens can be avoided with the use of
CC epitope-base vaccines. An additional advantage is the ability to combine
CC selected epitopes (CTL and HTL) and to modify the composition of the
CC epitopes achieving enhanced immunogenicity, the major benefit of the
CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
CC polypeptide sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 149 AA;
SQ
Query Match 63.0%; Score 523; DB 4; Length 149;
Best Local Similarity 64.9%; Pred. No. 3.6e-50;
Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;
QY 1 MFQDPORPRKLPOLCTELQTTIHDIILECYCKQQLRRVYVAFAPDLCIVYRDGPNY 60
DB 1 MFQDPORPRKLPOLCTELQTTIHDIILECYCKQQLRRVYVAFAPDLCIVYRDGPNY 60
QY 61 AVXDCKLFYSKISEYHYCYSVYGTLEOQYNRPCLDLIRCIHXOKPLCPEKORHLD 120
DB 61 AVCTCKLKFYSKISEYHYRYSLVGTLEOQYNRPCLDLIRCIHXOKPLCPEKORHLD 120
QY 121 KQRFHNIRGRWTRGCMSCCRSRTRETQI 151
DB 121 KKKRFHNIRGRWTRGCIACWR--RPRRETQV 149
RESULT 50
ADO44075
ID ADO44075 standard; protein; 149 AA.
XX
XX ADO44075;
XX
XX 15-JUN-2004 (first entry)
XX
XX Amino acid sequence of the E6 polypeptide of HPV31.
XX
XX E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
XX
XX Human papillomavirus type 31.
OS
XX
XX W02004030636-A2.
PN
XX
XX 15-APR-2004.
PD
XX
XX 02-OCT-2003; 2003WO-US031726.
PF
XX
XX 03-OCT-2002; 2002US-0415929P.
PR (AMHP) WYETH HOLDINGS CORP.
PA
XX
XX Smith L, Caesetti MC;
PI WPI; 2004-316328/29.
DR
XX

DR N-PSDB; ADO44102.
 XX
 PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.
 XX
 XX Disclosure; Page 78-79; 101pp; English.
 XX
 CC ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.
 CC ADO44098 is the consensus sequence derived from these polypeptides. The
 CC specification describes human papillomavirus E6 and E7 polypeptides.
 CC where the E7 polypeptide has mutations at any one or more of the amino
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of
 CC the sequence given in ADO44072. The polypeptides of the invention are
 CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancer, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.
 CC
 XX Sequence 149 AA;
 SQ
 Query Match 63.0%; Score 523; DB 8; Length 149;
 Best Local Similarity 64.9%; Pred. No. 3.6e-50;
 Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;
 QY 1 MFQDPQERRPKLPOLCTELQTTIHDIIECYCYCKQQLRREYDPAFRDLCTIVRDGMPY 60
 Db 1 MFKNPAERPRKLHLSALEIPYDELRLNCVCYCKQLTEVLDPAFTDLTVYRDDTPH 60
 QY 61 AVXDKCLKFYKISIEYRHVCYSVGTTLFQOYNKPLCDLIRCTINXOKPLCPBEKQRHLD 120
 Db 61 GVCIKCLAFYSKVSSEFRWRYRSVGTTEKLTNKGICDLIRCTICORPLCPBEKQRHLD 120
 QY 121 KKORFHNRIGRWTCSCCSSRTRRETQL 151
 Db 121 KKKRFHNIIGRWTCRCIACWR--RPRTEYQV 149

RESULT 51
 AEA98537
 ID AEA98537 standard; protein; 149 AA.
 AC AEA98537;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 18.
 XX
 KW Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;
 KW cancer; cervix tumor; cytostatic.
 XX
 OS Human papillomavirus; strain 31.
 XX
 PN US2005142541-A1.
 XX
 PD 30-JUN-2005.
 XX
 PF 23-DEC-2004; 2004US-00021949.
 XX
 PR 23-DEC-2003; 2003US-0532373P.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 PI Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;
 XX MPI; 2005-457781/46.
 XX
 PT New antibody composition comprising a mixture of monoclonal antibodies
 PT for oncogenic strains of human papilloma virus, useful for diagnosing

PT cancer.
 XX
 PS Disclosure; SEQ ID NO 18; 161pp; English.
 XX
 CC The invention relates to an antibody composition comprising a mixture of
 CC monoclonal antibodies that specifically bind to E6 proteins of human
 CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one
 CC of the monoclonal antibodies specifically binds to E6 proteins of at
 CC least three different oncogenic HPV strains. Also included are a
 CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,
 CC comprising the antibody composition above), a method of detecting an HPV
 CC E6 protein in a sample, a method of detecting the presence of an
 CC oncogenic HPV E6 protein in a sample and a system for detecting the
 CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a
 CC first and a second binding partner for an oncogenic HPV E6 polypeptide,
 CC where the first binding partner is a PDZ domain protein and the second
 CC binding partner is an antibody that specifically binds to the E6 proteins
 CC of at least three different oncogenic HPV strains). The antibody
 CC composition, kit, methods, and system are useful for diagnosing cancer,
 CC particularly cervical cancer. The present sequence is an HPV E6 protein.
 CC
 XX Sequence 149 AA;
 SQ
 Query Match 63.0%; Score 523; DB 9; Length 149;
 Best Local Similarity 64.9%; Pred. No. 3.6e-50;
 Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;
 QY 1 MFQDPQERRPKLPOLCTELQTTIHDIIECYCYCKQQLRREYDPAFRDLCTIVRDGMPY 60
 Db 1 MFKNPAERPRKLHLSALEIPYDELRLNCVCYCKQLTEVLDPAFTDLTVYRDDTPH 60
 QY 61 AVXDKCLKFYKISIEYRHVCYSVGTTLFQOYNKPLCDLIRCTINXOKPLCPBEKQRHLD 120
 Db 61 GVCIKCLAFYSKVSSEFRWRYRSVGTTEKLTNKGICDLIRCTICORPLCPBEKQRHLD 120
 QY 121 KKORFHNRIGRWTCSCCSSRTRRETQL 151
 Db 121 KKKRFHNIIGRWTCRCIACWR--RPRTEYQV 149

RESULT 52
 AEC98865
 ID AEC98865 standard; protein; 149 AA.
 AC AEC98865;
 XX
 DT 01-DEC-2005 (first entry)
 XX
 DE HPV_31 Envelope protein E6.
 XX
 KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
 KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
 XX
 OS Human papillomavirus type 31.
 XX
 PN WO2005089164-A2.
 XX
 PD 29-SEP-2005.
 XX
 PF 03-JAN-2005; 2005WO-US000077.
 XX
 PR 31-DEC-2003; 2003US-0533211P.
 XX
 PR 02-JUL-2004; 2004US-0584652P.
 XX
 PA (EPTM-) EPTMONE INC.
 PA (INNO-) INNOGENETICS NV.
 PA (CHES-) CHESNUT R.
 PA (NEWM-) NEWMAN M J.
 PA (MOTH-) MOTH B.
 PA (BAKE-) BAKER D.
 PA (SOUT-) SOUTHWOOD S.
 PA (BABE-) BABE L M.
 PA (CHEN-) CHEN Y.

XX AAB98447;
AC
XX
XX 22-AUG-2001 (first entry)
DT
XX
DE Human papillomavirus protein HPV33 E6.
XX
XX Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
KM epitope; T cell; identification; vaccine; infection; genital wart;
XX neoplastic growth; antiviral.
XX
OS Human papillomavirus.
XX
XX WO200141799-A1.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US033549.
XX
XX 10-DEC-1999; 99US-0172705P.
XX
XX 15-AUG-2000; 2000US-00641528.
XX
XX (EPRIM-) EPRIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
PI
XX WPI; 2001-381497/40.
XX
XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT treating HPV infections.
XX
XX
XX Disclosure: Page 26; 756pp; English.
XX
XX The present invention describes an isolated prepared human papillomavirus
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine
CC production. Peptides and corresponding nucleic acid compositions from the
CC present invention are useful for stimulating an immune response to HPV by
CC stimulating the production of CTL or HTL responses, specifically in the
CC treatment or prophylaxis of HPV infection, in persons who have not
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
CC can also be used in a tetramer staining assay to assess peripheral blood
CC mononuclear cells for the presence of antigen-specific CTLs following
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune
CC recall responses or evaluate the efficacy of a vaccine. The vaccine
CC compositions are useful for removing warts or treating HPV infections.
CC The epitopes for inclusion in an epitope-base vaccine may be selected
CC from conserved regions of viral or tumour-associated antigens, which
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
CC that may be present in whole antigens can be avoided with the use of
CC epitope-base vaccines. An additional advantage is the ability to combine
CC selected epitopes (CTL and HTL) and to modify the composition of the
CC epitopes achieving enhanced immunogenicity, the major benefit of the
CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
CC polypeptide sequences used in the exemplification of the present
CC invention
XX
XX
SQ Sequence 149 AA;
Query Match 62.7%; Score 520; DB 4; Length 149;
Best Local Similarity 63.6%; Pred. No. 7.9e-50;
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

RESULT 55
ADO44076
ID ADO44076 standard; protein, 149 AA.
XX
XX ADO44076;
AC
XX
XX 15-JUN-2004 (first entry)
DT
XX
DE Amino acid sequence of the E6 polypeptide of HPV33.
XX
XX E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
XX
OS Human papillomavirus type 33.
XX
XX WO2004030636-A2.
XX
XX 15-APR-2004.
XX
XX 02-OCT-2003; 2003WO-US031726.
XX
XX 03-OCT-2002; 2002US-0415929P.
XX
XX (AMHP) WYETH HOLDINGS CORP.
XX
XX Smith L, Cassetti MC;
PI
XX WPI; 2004-316328/29.
XX
XX N-PSDB; ADO44103.
XX
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
XX cancers, e.g. cervical cancer.
XX
XX
XX Disclosure: Page 79-80; 101pp; English.
XX
XX ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.
CC ADO44098 is the consensus sequence derived from these polypeptides. The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.
XX
XX
SQ Sequence 149 AA;
Query Match 62.7%; Score 520; DB 8; Length 149;
Best Local Similarity 63.6%; Pred. No. 7.9e-50;
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

RESULT 56
AEA98535
ID AEA98535 standard; protein, 149 AA.
XX
XX AEA98535;
AC
XX
XX 08-SEP-2005 (first entry)
DT
DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 16.
XX
XX Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;
XX
XX cancer; cervix tumor; cytostatic.
XX
XX Human papillomavirus; strain 33.
OS
XX US2005142541-A1.
PN
XX 30-JUN-2005.
PD
XX 23-DEC-2004; 2004US-00021949.
PF
XX 23-DEC-2003; 2003US-0532373P.
PR
XX (ARBO-) ARBOR VITA CORP.
PA
XX Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;
PI
XX WPI; 2005-457781/46.
DR
XX
XX New antibody composition comprising a mixture of monoclonal antibodies
PT
PT for oncogenic strains of human papilloma virus, useful for diagnosing
PT cancer.
PS
XX Disclosure; SEQ ID NO 16; 161pp; English.
XX
XX The invention relates to an antibody composition comprising a mixture of
CC
CC monoclonal antibodies that specifically bind to E6 proteins of human
CC
CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one
CC
CC of the monoclonal antibodies specifically binds to E6 proteins of at
CC
CC least three different oncogenic HPV strains. Also included are a
CC
CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,
CC
CC comprising the antibody composition above), a method of detecting an HPV
CC
CC E6 protein in a sample, a method of detecting the presence of an
CC
CC oncogenic HPV E6 protein in a sample and a system for detecting the
CC
CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a
CC
CC first and a second binding partner for an oncogenic HPV E6 polypeptide,
CC
CC where the first binding partner is a PDZ domain protein and the second
CC
CC binding partner is an antibody that specifically binds to the E6 proteins
CC
CC of at least three different oncogenic HPV strains). The antibody
CC
CC composition, kit, methods, and system are useful for diagnosing cancer,
CC
CC particularly cervical cancer. The present sequence is an HPV E6 protein.
XX
XX
SQ Sequence 149 AA;
Query Match 62.7%; Score 520; DB 9; Length 149;
Best Local Similarity 63.6%; Pred. No. 7.9e-50;
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECVYCKOQLRRREYDAPFDLCTVYRDNQPY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECVYCKOQLRRREYDAPFDLCTVYRDNQPY 60
QY 61 AYXDKCLPKYSKISISYRHYCSVYGTTLBQOYNKPLCDLLIRICINXQKPLCEEKQRHLD 120
DB 61 GICKCLFLSKISISYRHYCSVYGTTLBQOYNKPLCDLLIRICINXQKPLCEEKQRHLD 120
QY 121 KKQRFNIRGRWTRGCMSCGRSSRTTRRETOL 151
DB 121 LMKRFNIRGRWTRGCMSCGRSSRTTRRETOL 151

RESULT 57
AEC96412

ID AEC96412 standard; protein, 149 AA.
XX
XX AEC96412;
AC
XX
XX 01-DEC-2005 (first entry)
DT
XX
XX HPV protein E6 from HPV33.
DE
XX
XX Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
XX
XX epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
XX
XX Human papillomavirus type 33.
OS
XX WO2005089164-A2.
PN
XX 29-SEP-2005.
PD
XX 03-JAN-2005; 2005WO-US000077.
PF
XX 31-DEC-2003; 2003US-0533211P.
PR
XX 02-JUL-2004; 2004US-0584652P.
PS
XX (EPI-M-) EPIMUNE INC.
PA
XX (INNO-) INNOGENETICS NV.
PA
XX (CHES-) CHESNUT R.
PA
XX (NEMM-) NEMMAN M J.
PA
XX (MOTH-) MOTH B.
PA
XX (BAKE-) BAKER D.
PA
XX (SOUT-) SOUTHWOOD S.
PA
XX (BABE-) BABE L M.
PA
XX (CHEN-) CHEN Y.
PA
XX (DEYO-) DEYOUNG L M.
PA
XX (HUAN-) HUANG M T F.
PA
XX (POWE-) POWER S D.
PI
XX
PI Chen R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;
PI Chen Y, Deyoung LM, Huang MTF, Power SD;
DR
XX WPI; 2005-658982/67.
XX
XX New polynucleotide comprises a multi-epitope construct comprising nucleic
PT
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
PT (CTL) epitopes, useful in preparing a vaccine against HPV.
PS
XX Disclosure; Page 61; 518pp; English.
XX
XX The invention relates to a new polynucleotide comprising a multi-epitope
CC
CC construct comprising nucleic acids encoding the human papillomavirus
CC
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16 E1.214, and that
CC
CC are directly or indirectly joined to one another in the same reading
CC
CC frame, a vaccine minigene. Also included are a vector comprising the
CC
CC multi-epitope construct, a polypeptide comprising an amino acid sequence
CC
CC encoded by the polynucleotide, a composition (comprising the
CC
CC polynucleotide, vector and/or polypeptide and a carrier), a cell
CC
CC (comprising the polynucleotide, vector or polypeptide), inducing an
CC
CC immune response against human papillomavirus virus (HPV) and making the
CC
CC polynucleotide, vector or polypeptide. The epitopes are derived from
CC
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
CC
CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the
CC
CC epitopes in the vaccine protein are disclosed in the tables referred to
CC
CC in the claims of the specification. The polynucleotide, vector or
CC
CC polypeptide is useful in preparing a composition for inducing an immune
CC
CC response against human papillomavirus virus (HPV) and thus providing a
CC
CC defense against HPV infection and HPV-related cancers. The present
CC
CC sequence is an HPV protein used to derive epitopes for the vaccine of the
CC
CC invention.
XX
XX
SQ Sequence 149 AA;
Query Match 62.7%; Score 520; DB 9; Length 149;
Best Local Similarity 63.6%; Pred. No. 7.9e-50;
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

Oy		1 MFODPOEPRKLPQLCTELQTTIHDIILECVYCKQQALLREYYDPAFRLCLVIRGNGY 60
Dd		1 MFODEEKPRTLHDCQALETTHINIEIQVCBECKPLOSSEYDDFAFLTVYREGNPF 60
Oy		61 AVXDCTLFYSXISSEYRHYCYSVGTLEEQYNKKPLCDLILRCINCINKQKPLCEPEKQRHD 120
Dd		61 GICIKCLAFLSKISSEYRHNYSVGNLTLEGTYAKKLINELIICIQRPLCPGEKKRRHD 120
Oy		121 KKQRFHNIRGRWTFGRCMSCCRSSRTFRREFOL 151
Dd		121 LNKRFHNISGRWGACCAACWRSS--RRRETAL 149
 RESULT_58 AEC98866 ID AEC98866 standard; protein; 149 AA.		
XX	AEC98866;	
AC		
XX		
DT	01-DEC-2005	(first entry)
XX		
DE	HPV_33 Envelope protein E6.	
XX		
KM	Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;	
KW	epitope mapping; immune stimulation; cytotoxic T-lymphocyte.	
XX		
OS	Human papillomavirus type 33.	
XX		
PN	WO2005089164-A2.	
XX		
PD	29-SEP-2005.	
XX		
PF	03-JAN-2005; 2005MO-US000077.	
PR	31-DEC-2003; 2003US-0533211P.	
ER	02-JUL-2004; 2004US-0584652P.	
XX		
PA	(EPIM-) EPIMUNE INC.	
PA	(INNO-) INNOGENETICS NV.	
PA	(CHES/) CHESNUT R.	
PA	(NEWM/) NEWMAN M J.	
PA	(MOTH/) MOTHE B.	
PA	(BAKE/) BAKER D.	
PA	(SOUT/) SOUTHWOOD S.	
PA	(BABE/) BABE L M.	
PA	(CHEN/) CHEN Y.	
PA	(DEYO/) DEYOUING L M.	
PA	(HUAN/) HUANG M T F.	
PA	(POWER) POWER S D.	
XX		
P1	Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM,	
P1	Chen Y, Deyoung LM, Huang MTF, Power SD;	
XX		
XX	WPI; 2005-658982/67.	
PT	New polynucleotide comprises a multi-epitope construct comprising nucleic	
PT	acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte	
PT	(CTL) epitopes, useful in preparing a vaccine against HPV.	
XX		
PS	Example 10; Page 349; 518bp; English.	
XX		
CC	The invention relates to a new polynucleotide comprising a multi-epitope	
CC	construct comprising nucleic acids encoding the human papillomavirus	
CC	(HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that	
CC	are directly or indirectly joined to one another in the same reading	
CC	frame, a vaccine minigene. Also included are a vector comprising the	
CC	multi-epitope construct, a polypeptide comprising an amino acid sequence	
CC	encoded by the polynucleotide, a composition (comprising the	
CC	polynucleotide, vector and/or polypeptide and a carrier), a cell	
CC	(comprising the polynucleotide, vector or polypeptide), inducing an	
CC	immune response against human papillomavirus virus (HPV), and making the	
CC	polynucleotide, vector or polypeptide. The epitopes are derived from	
CC	different strains of HPV and are from the E1, E2, E6 and E7 proteins. The	

[illegible]

CC first and a second binding partner for an oncogenic HPV E6 polypeptide,
CC where the first binding partner is a PDZ domain protein and the second
CC binding partner is an antibody that specifically binds to the E6 proteins
CC of at least three different oncogenic HPV strains). The antibody
CC composition, kit, methods, and system are useful for diagnosing cancer,
CC particularly cervical cancer. The present sequence is an HPV E6 protein.
XX

XX Sequence 149 AA;

Query Match 60.0%; Score 498; DB 9; Length 149;

Best Local Similarity 60.1%; Pred. No. 2.3e-47;
Matches 89; Conservative 22; Mismatches 37; Indels 0; Gaps 0;

QY 1 MFQDQEPRLKLPOLCTELQTTIHDIIECVYCKQQLRRRYDPAFRLDCIVYRDGMPY 60
DB 1 MFQDDEKPRNLHDLQALFETVH8ISLPVQCKKTLRNEVYDFLFTDLKIVYRCGMPY 60
QY 61 AVXDKLKFYSKISEYRHYSVYGTTLGQYNKPLCDLLIRCIINXQKPLCEPEKQRLHD 120
DB 61 GYCKQCLRLSKISYSEYRHYSVYGTTLGQYNKPLCDLLIRCIINXQKPLCEPEKQRLHD 120
QY 121 KKQRFHNIRGRWTRGRCMSCCRSSRTTRRE 148
DB 121 RKGRFHNISNRWTRGRCSCVCMRPTQTQ 148

RESULT 60

ADO44083
ID ADO44083 standard; protein; 149 AA.

XX ADO44083;

DT 15-JUN-2004 (first entry)

XX Amino acid sequence of the E6 polypeptide of HPV58.

DE E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;

KW cervical cancer; immune response; lower gastrointestinal tract cancer;

XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

OS Human papillomavirus type 58.

XX WO2004030636-A2.

PN 15-APR-2004.

PD 02-OCT-2003; 2003WO-US031726.

XX 02-OCT-2003; 2003WO-US031726.

PR 03-OCT-2002; 2002US-0415929P.

XX (AMHP) WYETH HOLDINGS CORP.

PA Smith L, Casasetti MC;

XX MPI; 2004-316328/29.

DR N-PSDB; ADO44110.

XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,

PT useful for treating or preventing human papillomavirus (HPV)-associated

XX cancers, e.g. cervical cancer.

PT Discloure; Page 84-85; 101pp; English.

XX ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.

CC ADO44074-ADO44085 is the consensus sequence derived from these polypeptides.

CC The specification describes human papillomavirus E6 and E7 polypeptides.

CC where the E7 polypeptide has mutations at any one or more of the amino

CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in

CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any

CC one or more of the amino acids corresponding to amino acids 63 or 106 of

CC the sequence given in ADO44072. The polypeptides of the invention are

CC useful for treating or preventing human papillomavirus (HPV)-associated

CC cancers, such as cervical cancer. The fusion proteins and nucleic acids

CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.
XX

XX Sequence 149 AA;

Query Match 59.8%; Score 496; DB 8; Length 149;

Best Local Similarity 61.6%; Pred. No. 3.9e-47;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

QY 1 MFQDQEPRLKLPOLCTELQTTIHDIIECVYCKQQLRRRYDPAFRLDCIVYRDGMPY 60
DB 1 MFQDDEKPRNLHDLQALFETVH8ISLPVQCKKTLRNEVYDFLFTDLKIVYRDGMPY 60
QY 61 AVXDKLKFYSKISEYRHYSVYGTTLGQYNKPLCDLLIRCIINXQKPLCEPEKQRLHD 120
DB 61 AVCKVCLRLSKISYSEYRHYSVYGTTLGQYNKPLCDLLIRCIINXQKPLCEPEKQRLHD 120
QY 121 KKQRFHNIRGRWTRGRCMSCCRSSRTTRRETQ 151
DB 121 LKGRFHNISGRWTRGRCVCMRPTQTQ 149

RESULT 61

AEA98534
ID AEA98534 standard; protein; 149 AA.

XX AEA98534;

DT 08-SEP-2005 (first entry)

XX HPV (oncogenic strain) E6 amino acid sequence SEQ ID 15.

DE Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;

KW cancer; cervix tumor; cytostatic.

OS Human papillomavirus; strain 58.

XX US2005142541-A1.

PN 30-JUN-2005.

PD 23-DEC-2004; 2004US-00021949.

XX 23-DEC-2004; 2004US-00021949.

PR 23-DEC-2003; 2003US-0532373P.

XX (ARBO-) ARBOR VITA CORP.

PA Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;

XX MPI; 2005-457781/46.

DR New polypeptide comprising a mixture of monoclonal antibodies

XX for oncogenic strains of human papilloma virus, useful for diagnosing

XX cancer.

PT Discloure; SEQ ID NO 15; 161pp; English.

XX The invention relates to an antibody composition comprising a mixture of

XX monoclonal antibodies that specifically bind to E6 proteins of human

XX papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one

XX of the monoclonal antibodies specifically binds to E6 proteins of at

XX least three different oncogenic HPV strains. Also included are a

XX diagnostic kit (for detecting an HPV E6 polypeptide in a sample,

XX comprising the antibody composition above), a method of detecting an HPV

XX E6 protein in a sample, a method of detecting the presence of an

XX oncogenic HPV E6 protein in a sample and a system for detecting the

XX presence of an oncogenic HPV E6 polypeptide in a sample (comprising a

XX first and a second binding partner for an oncogenic HPV E6 polypeptide,

XX where the first binding partner is a PDZ domain protein and the second

XX binding partner is an antibody that specifically binds to the E6 proteins

XX of at least three different oncogenic HPV strains). The antibody

XX
PI Chesnut R, Newman MJ, Moche B, Baker D, Southwood S, Babe LM;
PI Chen Y, Deyoung LM, Huang MTF, Power SD;
XX
DR WPI, 2005-658982/67.
XX
PT New polynucleotide comprises a multi-epitope construct comprising nucleic
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
PT (CTL) epitopes, useful in preparing a vaccine against HPV.
XX
PS Disclosure; Page 66; 518pp; English.
XX
CC The invention relates to a new polynucleotide comprising a multi-epitope
CC construct comprising nucleic acids encoding the human papillomavirus
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that
CC are directly or indirectly joined to one another in the same reading
CC frame, a vaccine minigene. Also included are a vector comprising the
CC multi-epitope construct, a polypeptide comprising an amino acid sequence
CC encoded by the polynucleotide, a composition (comprising the
CC polynucleotide, vector and/or polypeptide and a carrier), a cell
CC (comprising the polynucleotide, vector or polypeptide), inducing an
CC immune response against human papillomavirus virus (HPV) and making the
CC polynucleotide, vector or polypeptide. The epitopes are derived from
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the
CC epitopes in the vaccine protein are disclosed in the tables referred to
CC in the claims of the specification. The polynucleotide, vector or
CC polypeptide is useful in preparing a composition for inducing an immune
CC response against human papillomavirus virus (HPV) and thus providing a
CC defense against HPV infection and HPV-related cancers. The present
CC sequence is an HPV protein used to derive epitopes for the vaccine of the
CC invention.
XX
SQ Sequence 149 AA;

Query Match 59.8%; Score 496; DB 9; Length 149;
Best Local Similarity 61.6%; Pred. No. 3.9e-47;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;
QY 1 MFQDQPERPKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRLDCTVYRDGNY 60
DB 1 MFQDAEKRRTLHDCQALETSVHEIEKVCCKTLQSEVYDFVFADLRIVYRDGNY 60
QY 61 AVXDCLKFKYSKISRYHCVSVGTLEQOYNKPLCDLLIRICINXQKPLCEBKQRHD 120
DB 61 AVCKVCLRLSLKISRYHCVSVGTLEQOYNKPLCDLLIRICINXQKPLCEBKQRHD 120
QY 121 KQRFHNIRGRWTGRCMSCCRSSRTFRRTOL 151
DB 121 LMKRFHNISGRWTGRCACVCRP--RRKOTOV 149

RESULT 64
ADO44081
ID ADO44081 standard; protein; 148 AA.
XX
AC ADO44081;
XX
DT 15-JUL-2004 (first entry)
XX
DE Amino acid sequence of the E6 polypeptide of HPV52.
XX
XX E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;
XX cervical cancer; immune response; lower gastrointestinal tract cancer;
XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
XX
OS Human papillomavirus type 52.
XX
XX WO2004030636-A2.
XX
XX 15-APR-2004.
XX
XX 02-OCT-2003; 2003WO-US031726.

XX
PR 03-OCT-2002; 2002US-0415929P.
XX
XX (AMHP) WYETH HOLDINGS CORP.
XX
XX Smith L, Cassecci MC;
XX
XX WPI, 2004-316328/29.
XX
XX N-PSDB; ADO44108.
XX
PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.
XX
PS Disclosure; Page 83; 101pp; English.
XX
CC ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.
CC ADO44098 is the consensus sequence derived from these polypeptides. The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.
XX
SQ Sequence 148 AA;

Query Match 58.7%; Score 487; DB 8; Length 148;
Best Local Similarity 61.7%; Pred. No. 3.9e-46;
Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;
QY 1 MFQDQPERPKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFRLDCTVYRDGNY 60
DB 1 MFEDATPRRTLHDLCEVLESVHEIRLQCVQCKKELRREYKPLFTDLRTVYRDGNY 60
QY 61 AVXDCLKFKYSKISRYHCVSVGTLEQOYNKPLCDLLIRICINXQKPLCEBKQRHD 120
DB 61 GVCIMCLFPLSKISRYHCVSVGTLEQOYNKPLCDLLIRICINXQKPLCEBKQRHD 120
QY 121 KQRFHNIRGRWTGRCMSCCR 141
DB 121 ANKRFHNIRGRWTGRCSECMR 141

RESULT 65
AEA98536
ID AEA98536 standard; protein; 148 AA.
XX
XX AEA98536;
XX
DT 08-SEP-2005 (first entry)
XX
DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 17.
XX
XX Papillomavirus infection; virulence; E6 protein; diagnosis; antibody;
XX cancer; cervix tumor; cytostatic.
XX
XX Human papillomavirus; strain 52.
XX
XX US2005142541-A1.
XX
XX 30-JUN-2005.
XX
XX 23-DEC-2004; 2004US-00021949.
XX
XX 23-DEC-2003; 2003US-0532373P.
XX

PA	(ARB0-)ARBOR VITRA CORP.
XX	
PL	Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;
XX	
DR	WPI, 2005-457781/46.
XX	
PT	New antibody composition comprising a mixture of monoclonal antibodies
PT	for oncogenic strains of human papilloma virus, useful for diagnosing
PT	cancer.
XX	
PS	Disclosure; SEQ ID NO 17; 161pp; English.
XX	
CC	The invention relates to an antibody composition comprising a mixture of
CC	monoclonal antibodies that specifically bind to E6 proteins of human
CC	papilloma virus (HPV) strains 16, 18, 31, 33 and 45 where at least one
CC	of the monoclonal antibodies specifically binds to E6 proteins of at
CC	least three different oncogenic HPV strains. Also included are a
CC	diagnostic kit (for detecting an HPV E6 polypeptide in a sample,
CC	comprising the antibody composition above), a method of detecting an HPV
CC	E6 protein in a sample, a method of detecting the presence of an
CC	oncogenic HPV E6 protein in a sample and a system for detecting the
CC	presence of an oncogenic HPV E6 polypeptide in a sample (comprising a
CC	first and a second binding partner for an oncogenic HPV E6 polypeptide,
CC	where the first binding partner is a PDZ domain protein and the second
CC	binding partner is an antibody that specifically binds to the E6 proteins
CC	of at least three different oncogenic HPV strains). The antibody
CC	composition, kit, methods, and system are useful for diagnosing cancer,
CC	particularly cervical cancer. The present sequence is an HPV E6 protein.
XX	
SO	Sequence 148 AA:
	Query Match 58.7%; Score 487; DB 9; Length 148;
	Best Local Similarity 61.7%; Pred. No. 3.9e-46;
	Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0
Oy	1 MFQDQDERPKLPOLCTELQTTIHDIIECYVCKQQLRREYDFAFDLCIYRGNGPY 60
Db	1 MFEDATRPRTLHELCEVLAESVHEIRLQCVCKKELQRREYVKFLFTLRIRYRDNPY 60
Oy	61 AVXDCLFLFYSKISEYRHVCYVGTTEEQVKNKPLCDLLIRCTINQKPLCEPEKORHLD 120
Db	61 GVCIMCLAFSLKISSEYRHYSLYXKTLERKYPSETLTICITQTPLCPEKRRHYN 120
Oy	121 KKQRFHNIRGRWTGRCMSCCR 141
Db	121 ANKRPHNIMGKWTGRCSCECMR 141
	RESULT 66
	AEC98868
ID	AEC98868 standard; protein; 148 AA.
XX	
AC	AEC98868;
XX	
DT	01-DEC-2005 (first entry)
XX	
DE	HPV_52 Envelope protein E6.
XX	
KW	Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
XX	epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
OS	Human papillomavirus type 52.
XX	
PN	WO2005089164-A2.
XX	
PD	29-SEP-2005.
XX	
PF	03-JAN-2005; 2005WO-US000077.
XX	
PR	31-DEC-2003; 2003US-0533211P.
XX	
PR	02-JUL-2004; 2004US-0584652P.
XX	
PA	(EPIM-) EPIMUNE INC.

[illegible]

KM Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
KM epitope mapping; immune stimulation; cytotoxic T lymphocyte.
XX
OS Human papillomavirus type 52.
XX
PN WO2005089164-A2.
XX
XX 29-SEP-2005.
XX
PD 03-JAN-2005; 2005WO-US000077.
XX
PF 31-DEC-2003; 2003US-0533211P.
XX
PR 02-JUL-2004; 2004US-0584652P.
XX
XX (EPIM-) EPIMUNE INC.
PA (INNO-) INNOGENETICS NV.
PA (CHES/) CHESNUT R.
PA (NEMM/) NEMMAN M J.
PA (MOTH/) MOTH B.
PA (BAKE/) BAKER D.
PA (SOUT/) SOUTWOOD S.
PA (BABE/) BABE L M.
PA (CHEN/) CHEN Y.
PA (DEYO/) DEYOUNG L M.
PA (HUAN/) HUANG M T F.
PA (POME/) POWER S D.
XX
P1 Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;
P1 Chen Y, Deyoung LM, Huang MTF, Power SD;
XX
XX WPI; 2005-658982/67.
XX
DR New polynucleotide comprises a multi-epitope construct comprising nucleic
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
PT (CTL) epitopes, useful in preparing a vaccine against HPV.
XX
XX Disclosure; Page 64; 518pp; English.
XX
XX The invention relates to a new polynucleotide comprising a multi-epitope
CC construct comprising nucleic acids encoding the human papillomavirus
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that
CC are directly or indirectly joined to one another in the same reading
CC frame, a vaccine minigene. Also included are a vector comprising the
CC multi-epitope construct, a polypeptide comprising an amino acid sequence
CC encoded by the polynucleotide, a composition (comprising the
CC polynucleotide, vector and/or polypeptide and a carrier), a cell
CC (comprising the polynucleotide, vector or polypeptide), inducing an
CC immune response against human papillomavirus virus (HPV) and making the
CC polynucleotide, vector or polypeptide. The epitopes are derived from
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
CC epitopes may be linked via a gp-anchor/spacer peptide. The order of the
CC epitopes in the vaccine protein are disclosed in the tables referred to
CC in the claims of the specification. The polynucleotide, vector or
CC polypeptide is useful in preparing a composition for inducing an immune
CC response against human papillomavirus virus (HPV) and thus providing a
CC defence against HPV infection and HPV-related cancers. The present
CC sequence is an HPV protein used to derive epitopes for the vaccine of the
CC invention.
XX
XX Sequence 148 AA;
SQ

Query Match 58.7%; Score 487; DB 9; Length 148;
Best Local Similarity 61.7%; Pred. No. 3.9e-46;
Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECVYKQOQLRREYVDFAPFDLCIVYRDGNPY 60
DB 1 MFEDPATRPTLHCEVLSESVHRIHQCVQCKELQRRVYKRLFTDLRLVYDNNPY 60
QY 61 AVXDKCLKFKYSKISRYHYCSVYGTTLBQOYNKRLCDLLRCINXKXKPLCEEKORHLD 120
DB 61 GVCIMCLFRLSKISRYHYCSVYGTTLBQOYNKRLCDLLRCINXKXKPLCEEKORHLD 120

QY 121 KQRFHNIRGRWTCRMSCCR 141
DB 121 ANKRFHNIRGRWTCRMSCCR 141

RESULT 68
AEA98878
ID AEA98878 standard; protein, 148 AA.
XX
AC AEA98878;
XX
DT 08-SEP-2005 (first entry)
XX
DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 359.
XX
KM Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;
KM cancer; cervix tumor; cytostatic.
XX
OS Human papillomavirus; strain 34.
XX
PN US2005142541-A1.
XX
PD 30-JUN-2005.
XX
PP 23-DEC-2004; 2004US-00021949.
XX
PR 23-DEC-2003; 2003US-0532373P.
XX
PA (ARBO-) ARBOR VITA CORP.
XX
P1 Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;
XX
XX WPI; 2005-457781/46.
XX
DR New antibody composition comprising a mixture of monoclonal antibodies
PT for oncogenic strains of human papilloma virus, useful for diagnosing
PT cancer.
XX
XX Disclosure; SEQ ID NO 359; 161pp; English.
XX
XX The invention relates to an antibody composition comprising a mixture of
CC monoclonal antibodies that specifically bind to E6 proteins of human
CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one
CC of the monoclonal antibodies specifically binds to E6 proteins of at
CC least three different oncogenic HPV strains. Also included are a
CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,
CC comprising the antibody composition above), a method of detecting an HPV
CC E6 protein in a sample, a method of detecting the presence of an
CC oncogenic HPV E6 protein in a sample and a system for detecting the
CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a
CC first and a second binding partner for an oncogenic HPV E6 polypeptide,
CC where the first binding partner is a PD2 domain protein and the second
CC binding partner is an antibody that specifically binds to the E6 proteins
CC of at least three different oncogenic HPV strains). The antibody
CC composition, kit, methods, and system are useful for diagnosing cancer,
CC particularly cervical cancer. The present sequence is an HPV E6 protein.
XX
XX Sequence 148 AA;
SQ

Query Match 58.3%; Score 484; DB 9; Length 148;
Best Local Similarity 60.4%; Pred. No. 8.4e-46;
Matches 87; Conservative 17; Mismatches 40; Indels 0; Gaps 0;

QY 2 FQDQERPRKLPOLCTELQTTIHDIIECVYKQOQLRREYVDFAPFDLCIVYRDGNPY 61
DB 3 FPNDEERPRKLPALCEEVNISIHIEIDCVYCEQRLVCEYDFIFDLCIVYRKXKPLG 62
QY 62 VXDCKLKFYSKISRYHYCSVYGTTLBQOYNKRLCDLLRCINXKXKPLCEEKORHLD 121
DB 63 VQDPLLFYSKVRRYRRNOSVYGTTLBQOYNKRLCDLLRCINXKXKPLCEEKORHLD 122
QY 122 KQRFHNIRGRWTCRMSCCR 145

XX DE Amino acid sequence of the E6 polypeptide of HPV68.
XX KM E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;
XX KW cervical cancer; immune response; lower gastrointestinal tract cancer;
XX KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
XX OS Human papillomavirus type 68.
XX PN WO2004030636-A2.
XX PD 15-APR-2004.
XX PF 02-OCT-2003; 2003WO-US031726.
XX PR 03-OCT-2002; 2002US-0415929P.
XX PA (AMHP) WYETH HOLDINGS CORP.
XX PI Smith L, Cassetti MC;
XX DR WPI; 2004-316328/29.
XX DR N-PSDB; ADO44112.
XX PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
XX PT useful for treating or preventing human papillomavirus (HPV)-associated
XX PT cancers, e.g. cervical cancer.
XX PS Disclosure; Page 85-86; 101pp; English.
XX PS ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.
XX CC ADO44098 is the consensus sequence derived from these polypeptides. The
XX CC specification describes human papillomavirus E6 and E7 polypeptides,
XX CC where the E7 polypeptide has mutations at any one or more of the amino
XX CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
XX CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
XX CC one or more of the amino acids corresponding to amino acids 63 or 106 of
XX CC the sequence given in ADO44072. The polypeptides of the invention are
XX CC useful for treating or preventing human papillomavirus (HPV)-associated
XX CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
XX CC encoding the fusion proteins are useful for generating immune responses
XX CC against HPV. They are also useful for treating lower gastrointestinal
XX CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
XX CC system, including penile and vulvar cancer.
XX SQ Sequence 158 AA:
SQ Query Match 56.4%; Score 468.5; DB 8; Length 158;
Best Local Similarity 55.1%; Pred. No. 5e-44;
Matches 86; Conservative 23; Mismatches 42; Indels 5; Gaps 1;
QY 1 MFQDPQRRPKLPOLCTSLQTTIHDIIECYCKQQLRREYVDFAFDLCIVYRDGNPY 60
DB 3 LFHPPEERPYKLPDLCTLDITLHDVTCVCRQLOQTEVEYEFADLQVYRDGVF 62
QY 61 AVXKCKEYKISEYRYHCYVGTLEQONKPLCDLLRCINXOKPLCPBEKQRLD 120
DB 63 AACGSCIFFAKINBLRYSSVATYLTITNTKLVLLRCMSCLKPLCPAEKLRHLT 122
QY 121 KQQRPHNIRGWTGRCMSCCRSS-----RTRRETQL 151
DB 123 TKRLHKIAGNFTGQCRHCHWTSKREDRRIRRETQV 158
RESULT 72
AEA98880
ID AEA98880 standard; protein; 158 AA.
XX AC AEA98880;
XX DT 08-SEP-2005 (first entry)
XX XX HPV (oncogenic strain) E6 amino acid sequence SEQ ID 361.

XX KM Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;
XX KW cancer; cervix tumor; cytostatic.
XX OS Human papillomavirus; strain 70.
XX PN US2005142541-A1.
XX PD 30-JUN-2005.
XX PF 23-DEC-2004; 2004US-00021949.
XX PR 23-DEC-2003; 2003US-0532373P.
XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;
XX DR WPI; 2005-457781/46.
XX PT New antibody composition comprising a mixture of monoclonal antibodies
XX PT for oncogenic strains of human papilloma virus, useful for diagnosing
XX PT cancer.
XX PS Disclosure; SEQ ID NO 361; 161pp; English.
XX CC The invention relates to an antibody composition comprising a mixture of
XX CC monoclonal antibodies that specifically bind to E6 proteins of human
XX CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one
XX CC of the monoclonal antibodies specifically binds to E6 proteins of at
XX CC least three different oncogenic HPV strains. Also included are a
XX CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,
XX CC comprising the antibody composition above), a method of detecting an HPV
XX CC E6 protein in a sample, a method of detecting the presence of an
XX CC oncogenic HPV E6 protein in a sample and a system for detecting the
XX CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a
XX CC first and a second binding partner for an oncogenic HPV E6 polypeptide,
XX CC where the first binding partner is a PDZ domain protein and the second
XX CC binding partner is an antibody that specifically binds to the E6 proteins
XX CC of at least three different oncogenic HPV strains). The antibody
XX CC composition, kit, methods, and system are useful for diagnosing cancer,
XX CC particularly cervical cancer. The present sequence is an HPV E6 protein.
XX SQ Sequence 158 AA:
SQ Query Match 56.4%; Score 468.5; DB 9; Length 158;
Best Local Similarity 56.8%; Pred. No. 5e-44;
Matches 88; Conservative 21; Mismatches 41; Indels 5; Gaps 1;
QY 2 FQDPQRRPKLPOLCTSLQTTIHDIIECYCKQQLRREYVDFAFDLCIVYRDGNPY 61
DB 4 FPNPAERPYKLPDLCTLDITLHDITIDCVCKTLOOTEVEYEFADLQVYRDGVF 63
QY 62 VXDCKLFYSKISEYRYHCYVGTLEQONKPLCDLLRCINXOKPLCPBEKQRLD 121
DB 64 ACQKCIFFHAKVRLRYNSVATYLTITNTKLVLLRCMSCLKPLCPAEKLRHVT 123
QY 122 KQQRPHNIRGWTGRCMSCCRSS-----RTRRETQL 151
DB 124 KRFPHQIAGSYTQCRHCHWTSNREDRRIRRETQV 158
RESULT 73
AAR97562
ID AAR97562 standard; protein; 172 AA.
XX AC AAR97562;
XX DT 27-AUG-2003 (revised)
XX DT 11-JAN-1997 (first entry)
XX XX Human papilloma virus E6/E7 protein variant.

KM Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;
 KM humoral immune response; cellular immune response; vaccine.
 XX
 OS Human papillomavirus.
 XX
 PN MO9619496-A1.
 XX
 PD 27-JUN-1996.
 XX
 PF 20-DEC-1995; 95WO-AU000868.
 XX
 PR 20-DEC-1994; 94AU-00000157.
 XX
 PA (CSLC-) CSL LTD.
 XX (UYOU) UNIV QUEENSLAND.
 XX
 PI Edwards SJ, Cox J, Webb EA, Frazer I;
 XX
 DR WPI; 1996-309518/31.
 DR N-PSDB; AAT31834.
 XX
 PT Vaccine variants of human papilloma virus antigens - contain variants of
 PT E6 and/or E7 protein, pref. deletion mutants, and are used to treat or
 PT prevent HPV infection.
 XX
 PS Example 3; Page 17; 37pp; English.
 XX
 CC A variant of the human papilloma virus (HPV) E6 or E7 protein which
 CC elicits a humoral and/or cellular immune response against HPV can be used
 CC in vaccines against HPV or to treat HPV infection. The variant is
 CC preferably a deletion mutant comprising at least half, and preferably two
 CC thirds of full length E6 or E7 protein starting from the N- or C-
 CC terminal, or is a full length E6 moiety fused to a full length E7 moiety.
 CC The variant optionally has a linkage moiety and a foreign protein or
 CC peptide which functionally has a linkage moiety and a foreign protein or
 CC immunogenicity of the fusion protein. This is a fusion protein of the C-
 CC terminal end of E6 and the N-terminal end of E7. The protein is also a
 CC deletion mutant generated from the sequence described in AAT31833.
 CC (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 172 AA;
 XX
 Query Match 56.4%; Score 468; DB 2; Length 172;
 Best Local Similarity 86.1%; Pred. No. 6.3e-44;
 Matches 87; Conservative 1; Mismatches 1; Indels 12; Gaps 2;
 QY 57 GNPVAVXDKCLFYSKISEVRHYCVSGTTLTLEQQ-----YMKPLCDLLIRCNXQKPL 110
 DB 2 GNPVAVXDKCLFYSKISEVRHYCVSGTTLTLEQQINCKPKNKPLCDLLIR-----L 55
 QY 111 CPEEKQRHLDDKQRFNIRGRWTCGMSCCRSSRTRRETOL 151
 DB 56 CPEEKQRHLDDKQRFNIRGRWTCGMSCCRSSRTRRETOL 96
 XX
 RESULT 74
 ADO44080
 ID ADO44080 standard; protein; 151 AA.
 XX
 AC ADO44080;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Amino acid sequence of the E6 polypeptide of HPV51.
 XX
 KM E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
 XX
 OS Human papillomavirus type 51.
 XX
 PN MO2004030636-A2.
 XX

PD 15-APR-2004.
 XX
 XX 02-OCT-2003; 2003WO-US031726.
 PF
 XX 03-OCT-2002; 2002US-0415929P.
 PR
 XX (AMHP) WYETH HOLDINGS CORP.
 PA
 XX Smith L, Cassetti MC;
 XX
 PI WPI; 2004-316328/29.
 XX
 DR N-PSDB; ADO44107.
 XX
 PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.
 XX
 PS Disclosure; Page 82; 101pp; English.
 XX
 CC ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.
 CC ADO44098 is the consensus sequence derived from these polypeptides. The
 CC specification describes human papillomavirus E6 and E7 polypeptides.
 CC where the E7 polypeptide has mutations at any one or more of the amino
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of
 CC there sequence given in ADO44072. The polypeptides of the invention are
 CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.
 CC
 SQ Sequence 151 AA;
 XX
 Query Match 55.4%; Score 460; DB 8; Length 151;
 Best Local Similarity 57.0%; Pred. No. 4.2e-43;
 Matches 86; Conservative 24; Mismatches 41; Indels 0; Gaps 0;
 QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDAFQDLCTVYRDSNPY 60
 DB 1 MFEDKREPRRTLHELCEALNVSMHNIQVAVCYCKELCRADYVNAFTEIKTVYRDNPPY 60
 QY 61 AYXDKCLFYSKISEVRHYCVSGTTLTLEQQYNKPLCDLLIRCNXQKPLCPEEKQRHL 120
 DB 61 AYXDKCLFYSKISEVRHYCVSGTTLTLEQQYNKPLCDLLIRCNXQKPLCPEEKQRHL 120
 QY 121 KKQRFNIRGRWTCGMSCCRSSRTRRETOL 151
 DB 121 KKQRFNIRGRWTCGMSCCRSSRTRRETOL 151
 QY 121 EKKRHEIAGRWTGCGANCWQRTRORETQV 151
 DB
 XX
 RESULT 75
 AEA98543
 ID AEA98543 standard; protein; 151 AA.
 XX
 AC AEA98543;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 24.
 XX
 KM Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;
 KM cancer; cervix tumor; cytostatic.
 XX
 OS Human papillomavirus; strain 51.
 XX
 PN US2005142541-A1.
 XX
 PD 30-JUN-2005.
 XX
 PF 23-DEC-2004; 2004US-00021949.
 XX

XX 23-DEC-2003; 2003US-0532373P.
PR (ARBO-) ARBOR VITA CORP.
XX
XX Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;
XX WPI, 2005-457781/46.
DR
XX New antibody composition comprising a mixture of monoclonal antibodies
PT for oncogenic strains of human papilloma virus, useful for diagnosing
PT cancer.
XX
XX Disclosure: SEQ ID NO 24; 161pp; English.
XX
XX The invention relates to an antibody composition comprising a mixture of
CC monoclonal antibodies that specifically bind to E6 proteins of human
CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one
CC of the monoclonal antibodies specifically binds to E6 proteins of at
CC least three different oncogenic HPV strains. Also included are a
CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,
CC comprising the antibody composition above), a method of detecting an HPV
CC E6 protein in a sample, a method of detecting the presence of an
CC oncogenic HPV E6 protein in a sample and a system for detecting the
CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a
CC first and a second binding partner for an oncogenic HPV E6 polypeptide,
CC where the first binding partner is a PDZ domain protein and the second
CC binding partner is an antibody that specifically binds to the E6 proteins
CC of at least three different oncogenic HPV strains). The antibody
CC composition, kit, methods, and system are useful for diagnosing cancer,
CC particularly cervical cancer. The present sequence is an HPV E6 protein.
XX
SQ Sequence 151 AA;

Query Match 55.4%; Score 460; DB 9; Length 151;
Best Local Similarity 57.0%; Pred. No. 4.2e-43;
Matches 86; Conservative 24; Mismatches 41; Indels 0; Gaps 0;
QY 1 MFQDPERPRKLPOLCTELQTTIHIIIECVYCKQQLREYVDPAFRDLCTVYRDGNPY 60
DB 1 MFEDRREPRRTLHEICELANVSMHNIQVVCYCKKELRADVYVAFTKIKIVYDNNPY 60
QY 61 AVXDKLKFYSKISEYRHVYCSVGTLEQQYNKPLCDLLIRICINXOKPLCEPEKQRHLD 120
DB 61 AVXCKQLFYSKIRYRYSVYGTTLBATTKKSLVPLSLRCHACQKPLGPEEKQLVD 120
QY 121 KKQRFNIRGRWTCRCMCCRSSRTRETOL 151
DB 121 EKRFHEIAGRWTCGANCWCQRTRORETQV 151

RESULT 76
ADO44079
ID ADO44079 standard; protein; 158 AA.
XX
XX ADO44079;
XX
XX 15-JUL-2004 (first entry)
XX
XX Amino acid sequence of the E6 polypeptide of HPV45.
XX
XX E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;
KW cervical cancer; immune response; lower gastrointestinal tract cancer;
KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
XX
XX Human papillomavirus type 45.
XX
XX MO2004030636-A2.
XX
XX 15-APR-2004.
XX
XX 02-OCT-2003; 2003WO-US0311726.
XX
XX

PR 03-OCT-2002; 2002US-0415929P.
XX (AMHP) WYETH HOLDINGS CORP.
XX
XX Smith L, Casasetti MC;
XX
XX WPI: 2004-316328/29.
DR N-PsDB; ADO44106.
XX
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.
XX
XX Disclosure: Page 81-82; 101pp; English.
XX
XX ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.
CC ADO44098 is the consensus sequence derived from these polypeptides. The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.
XX
SQ Sequence 158 AA;

Query Match 55.4%; Score 459.5; DB 8; Length 158;
Best Local Similarity 56.1%; Pred. No. 5.1e-43;
Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;
QY 2 FQDPERPRKLPOLCTELQTTIHIIIECVYCKQQLREYVDPAFRDLCTVYRDGNPYA 61
DB 4 FDDKQRPYKLPDLCTELNTSLQDVSTACVCKATLETEYVQFAPKDLCTVYRDCIAYA 63
QY 62 VXDCKLKFYSKISEYRHVYCSVGTLEQQYNKPLCDLLIRICINXOKPLCEPEKQRHLD 121
DB 64 ACHKCIDYSHIRRELRYNSVYGTLEKINTTELVLNLIICLRQKPLPAEKSRHLD 123
QY 122 KQRFNIRGRWTCRCMCCRSS-----FTRRETOL 151
DB 124 KRFHSINGQYRGQCNCTCCDQARQERLRRTRETQV 158

RESULT 77
AEA98548
ID AEA98548 standard; protein; 158 AA.
XX
XX AEA98548;
XX
XX 08-SEP-2005 (first entry)
XX
XX HPV (oncogenic strain) E6 amino acid sequence SEQ ID 29.
XX
XX Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;
KW cancer; cervix tumor; cytostatic.
XX
XX Human papillomavirus; strain 45.
XX
XX US2005142541-A1.
XX
XX 30-JUN-2005.
XX
XX 23-DEC-2004; 2004US-00021949.
XX
XX 23-DEC-2003; 2003US-0532373P.
XX
XX (ARBO-) ARBOR VITA CORP.
XX
XX

XX PI Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;
 XX DR WPI, 2005-457781/46.
 XX PT New antibody composition comprising a mixture of monoclonal antibodies
 PT for oncogenic strains of human papilloma virus, useful for diagnosing
 PT cancer.
 XX PS Disclosure; SEQ ID NO 29; 161pp; English.
 XX CC The invention relates to an antibody composition comprising a mixture of
 CC monoclonal antibodies that specifically bind to E6 proteins of human
 CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one
 CC of the monoclonal antibodies specifically binds to E6 proteins of at
 CC least three different oncogenic HPV strains. Also included are a
 CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,
 CC comprising the antibody composition above), a method of detecting an HPV
 CC E6 protein in a sample, a method of detecting the presence of an
 CC oncogenic HPV E6 protein in a sample and a system for detecting the
 CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a
 CC first and a second binding partner for an oncogenic HPV E6 polypeptide,
 CC where the first binding partner is a PDZ domain protein and the second
 CC binding partner is an antibody that specifically binds to the E6 proteins
 CC of at least three different oncogenic HPV strains). The antibody
 CC composition, kit, methods, and system are useful for diagnosing cancer,
 CC particularly cervical cancer. The present sequence is an HPV E6 protein.
 CC
 SQ Sequence 158 AA;
 Query Match 55.4%; Score 459.5; DB 9; Length 158;
 Best Local Similarity 56.1%; Pred. No. 5.1e-43;
 Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;
 QY 2 FDDPQRPRLPOLCTELQTHIDILLCVCKQQLRREYVDFAFRDLCTIVYRDGNPYA 61
 DB 4 FDDPQRPRLPOLCTELQTHIDILLCVCKQQLRREYVDFAFRDLCTIVYRDGNPYA 63
 QY 62 VXDCKLKFYSKISEVHYHCYSYVGTTLLEQYNNKPLCDLLIRCNKQKPLCPBEKQRLHDK 121
 DB 64 ACHKCIDFYSRIRELRYNSVYGETLEKITETELYNLLIRLCQKPLNPAEKRRHLDK 123
 QY 122 KORFNIRGRMTGRMCCRSS-----RRRETQL 151
 DB 124 KRFFSHIAGQYRGQCNTCCDQARQERLRRRRRTQV 158
 RESULT 78
 AEC98867 standard; protein; 158 AA.
 AC AEC98867;
 XX 01-DEC-2005 (first entry)
 XX HPV_45 Envelope protein E6.
 DB Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
 KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
 XX Human papillomavirus type 45.
 OS WO2005089164-A2.
 XX 29-SEP-2005.
 PD 03-JAN-2005; 2005MO-US000077.
 PF 31-DEC-2003; 2003US-0533211P.
 PR 02-JUL-2004; 2004US-0584652P.
 XX (EPIIM-) EPIIMUNE INC.
 PA (INNO-) INNOGENETICS NV.
 PA

PA (CHES/) CHESNUT R.
 PA (NEWM/) NEWMAN M J.
 PA (MOTH/) MOTH B.
 PA (BAKE/) BAKER D.
 PA (SOUT/) SOUTHWOOD S.
 PA (BABE/) BABE L M.
 PA (CHEN/) CHEN Y.
 PA (DEYO/) DEYO L M.
 PA (HDAN/) HUANG M T F.
 PA (POWE/) POWER S D.
 XX
 PI Chen R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;
 PI Chen Y, Deyong LM, Huang MTF, Power SD;
 DR WPI, 2005-658982/67.
 XX New polynucleotide comprises a multi-epitope construct comprising nucleic
 PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
 PT (CTL) epitopes, useful in preparing a vaccine against HPV.
 XX Example 10; Page 349; 518pp; English.
 PS
 XX The invention relates to a new polynucleotide comprising a multi-epitope
 CC construct comprising nucleic acids encoding the human papillomavirus
 CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that
 CC are directly or indirectly joined to one another in the same reading
 CC frame, a vaccine minigene. Also included are a vector comprising the
 CC multi-epitope construct, a polypeptide comprising an amino acid sequence
 CC encoded by the polynucleotide, a composition (comprising the
 CC polynucleotide, vector and/or polypeptide and a carrier), a cell
 CC (comprising the polynucleotide, vector or polypeptide and making the
 CC immune response against human papillomavirus virus (HPV) and making the
 CC polynucleotide, vector or polypeptide. The epitopes are derived from
 CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
 CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the
 CC epitopes in the vaccine protein are disclosed in the tables referred to
 CC in the claims of the specification. The polynucleotide, vector or
 CC polypeptide is useful in preparing a composition for inducing an immune
 CC response against human papillomavirus virus (HPV) and thus providing a
 CC defense against HPV infection and HPV-related cancers. The present
 CC sequence is an HPV protein used to derive epitopes for the vaccine of the
 CC invention.
 XX
 SQ Sequence 158 AA;
 Query Match 55.4%; Score 459.5; DB 9; Length 158;
 Best Local Similarity 56.1%; Pred. No. 5.1e-43;
 Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;
 QY 2 FDDPQRPRLPOLCTELQTHIDILLCVCKQQLRREYVDFAFRDLCTIVYRDGNPYA 61
 DB 4 FDDPQRPRLPOLCTELQTHIDILLCVCKQQLRREYVDFAFRDLCTIVYRDGNPYA 63
 QY 62 VXDCKLKFYSKISEVHYHCYSYVGTTLLEQYNNKPLCDLLIRCNKQKPLCPBEKQRLHDK 121
 DB 64 ACHKCIDFYSRIRELRYNSVYGETLEKITETELYNLLIRLCQKPLNPAEKRRHLDK 123
 QY 122 KORFNIRGRMTGRMCCRSS-----RRRETQL 151
 DB 124 KRFFSHIAGQYRGQCNTCCDQARQERLRRRRRTQV 158
 RESULT 79
 AAR63866 standard; protein; 158 AA.
 ID AAR63866;
 XX 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-JUN-1995 (first entry)
 XX HPV18 E6/E7 proteins.
 DE

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XX  HPV, HPV18, E6 protein, E7 protein; diagnosis; cervical dysplasia;
KM  cervix cancer.
XX
XX  Human papillomavirus; strain 18.
OS
XX  MO9426934-A2.
PN
XX  24-NOV-1994.
PD
XX  06-MAY-1994; 94MO-US005085.
PF
XX  06-MAY-1993; 93US-00058920.
PR
XX  (BAXT ) BAXTER DIAGNOSTICS INC.
PA
XX  Brown JT;
PI
XX  WPI; 1995-006821/01.
PS  P-PSDB; AAQ75471.
PT  Human papilloma virus detection assay - by amplification using self
PR  sustained sequence replication and hybridisation with a detector probe.
XX
XX  Disclosure; Page 27-28; 79pp; English.
PS
XX  The sequences of the E6 and E7 polypeptide-encoding regions of human
CC  papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded
CC  proteins in AAR63865-66, respectively. Probes and primers based on these
CC  sequences were used for HPV infection diagnosis; expression of E6 and E7
CC  is diagnostic for cervical cancer or pre-malignant states. (Updated on
CC  25-MAR-2003 to correct FN field.) (Updated on 16-OCT-2003 to standardise
CC  OS field)
XX
SQ  Sequence 158 AA;

Query Match          54.9%; Score 455.5; DB 2; Length 158;
Best Local Similarity 56.1%; Pred. No. 1.4e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY  2 FODPERPRKLPOLCTELQTTIHDIIECVCKQQLREYVDFAPRDLCIYVRDGNPYA 61
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  4 FEDPTRRYPYKLPDLCTELNTSLQDIEITCVCKTVLETFEFAFKDLFVYRDSIPHA 63
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  62 VXDKCLKYKSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRNCINXOKPLCPBEKORHDK 121
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  64 ACHKCIDYFSRIRRELRHYSDSVYGTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRLHNE 123
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  122 KORFNINRGWTRGCMSCCRSSR-----TRRETOL 151
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  124 KRFFHNIAGHYRGQCHSCCNRAEROERLORRRETQV 158
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 80
AAR79656
ID  AAR79656 standard; protein; 158 AA.
XX
XX  AAR79656;
AC
XX  25-MAR-2003 (revised)
DT  06-DEC-1995 (first entry)
XX
XX  HPV-18 E6 protein.
DE
XX  Ubiquitin-conjugating enzyme; HPV-18 E6 protein; cell cycle;
KM  cell proliferation; cancer; psoriasis; fibrosis.
XX
OS  Homo sapiens.
XX
XX  MO9518974-A2.
PN
XX  13-JUL-1995.
PD
XX

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PF  04-JAN-1995; 95MO-US000164.
XX
XX  04-JAN-1994; 94US-00176937.
PR  23-MAY-1994; 94US-00247904.
XX  27-MAY-1994; 94US-00250795.
PR  13-SEP-1994; 94US-00305520.
XX
XX  (MITO-) MITOTIX INC.
PA
XX  Draetta G, Rolfe M, Eckstein JW, Cottarel G, Gyuris J;
PI
XX  WPI; 1995-255137/33.
DR  N-PSDB; AAQ97848.
XX
XX  Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle
PT  regulatory proteins - also new ubiquitin conjugating enzymes, their
PR  related nucleic acid, vectors, antibodies etc., useful for regulating
PT  e.g. cell proliferation.
XX
XX  Disclosure; Page 100-101; 157pp; English.
PS
XX  HPV-18 E6 cDNA (given in AAQ97848) was amplified from a HeLa cell cDNA
CC  library using the primers given in AAQ97846-47. The gene was subcloned
CC  into a baculovirus vector for expression of recombinant E6 in Sf9 insect
CC  cells for use as a component of an in vitro ubiquitin conjugating system.
CC  (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ  Sequence 158 AA;

Query Match          54.9%; Score 455.5; DB 2; Length 158;
Best Local Similarity 56.1%; Pred. No. 1.4e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY  2 FODPERPRKLPOLCTELQTTIHDIIECVCKQQLREYVDFAPRDLCIYVRDGNPYA 61
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  4 FEDPTRRYPYKLPDLCTELNTSLQDIEITCVCKTVLETFEFAFKDLFVYRDSIPHA 63
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  62 VXDKCLKYKSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRNCINXOKPLCPBEKORHDK 121
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  64 ACHKCIDYFSRIRRELRHYSDSVYGTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRLHNE 123
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  122 KORFNINRGWTRGCMSCCRSSR-----TRRETOL 151
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  124 KRFFHNIAGHYRGQCHSCCNRAEROERLORRRETQV 158
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 81
AAV39968
ID  AAV39968 standard; protein; 158 AA.
XX
XX  AAV39968;
AC
XX  15-DEC-1999 (first entry)
DT
XX
XX  HPV-18 E6 protein sequence.
DE
XX  Ubiquitin conjugating enzyme; UbCE; ubiquitin-mediated proteolysis;
KM  cell-cycle regulatory protein; ubiquitination inhibitor; atherosclerosis;
KM  proliferative disorder; cancer; restenosis; tissue connective disorder;
KM  wound healing; fibrosis disorder; rheumatoid arthritis; scleroderma;
KM  insulin dependent diabetes mellitus; glomerulonephritis; cirrhosis;
KM  diagnosis; therapy; E6.
XX
XX  Human papillomavirus.
OS
XX  US5968761-A.
XX  19-OCT-1999.
PD
XX  07-JUN-1995; 95US-00486663.
XX
XX  04-JAN-1994; 94US-00176937.
PR  23-MAY-1994; 94US-00247904.
XX

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PR 27-MAY-1994; 94US-00250795.
 PR 13-SEP-1994; 94US-00305520.
 PA (MITO-) MITOTIX INC.
 PI Chiu MI, Cottarel G, Berlin V, Damagnez V, Draetta G, Rolfe M;
 XX WPI, 1999-590402/50.
 DR N-PSDB; AA227568.
 XX
 PT Identifying ubiquitination inhibitors using novel ubiquitin conjugating
 PT enzymes.
 XX
 PS Example 2; Col 89-92; 61pp; English.
 XX
 CC This sequence is the human papillomavirus E6 protein. The invention
 CC relates to assays for identifying an inhibitor of ubiquitin-mediated
 CC proteolysis of a cell-cycle regulatory protein comprising contacting a
 CC candidate agent with an ubiquitin-conjugating system and measuring the
 CC level of ubiquitination. The ubiquitin-conjugating system comprises: (a)
 CC a reconstituted protein mixture including a ubiquitin conjugating enzyme
 CC (UBCE) produced by the expression of a nucleic acid which hybridizes
 CC under high stringency conditions to human UBCE, Candida albicans UBCE, or
 CC Schizosaccharomyces pombe UBCE coding sequences; (b) a regulatory protein
 CC, and (c) ubiquitin. The polynucleotides are useful for identifying
 CC ubiquitination inhibitors. The polynucleotides, polypeptides, antisense
 CC compounds and antibodies against them may also be useful for the
 CC treatment and/or diagnosis of proliferative disorders (e.g. cancer,
 CC atherosclerosis, or restenosis), tissue connective disorders, controlling
 CC wound healing, and disorders characterized by fibrosis (e.g. rheumatoid
 CC arthritis, insulin dependent diabetes mellitus, glomerulonephritis,
 CC cirrhosis, and scleroderma)
 CC
 XX
 SQ Sequence 158 AA;

Query Match 54.9%; Score 455.5; DB 2; Length 158;
 Best Local Similarity 56.1%; Pred. No. 1.4e-42;
 Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY 2 FODPQPRPKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFPARDLCIYRDGNPYA 61
 DB 4 FEPDTRRPYKLPDLCTELMTSLQDIEITVCYKTVLETFEVPFADKLFVYRRDSIPRA 63
 QY 62 VADKCLKFSKISSEVYHVCYVGTTLLEQOYKPKLDDLIRCNXQKPLCPPEKORHLDK 121
 DB 64 ACHKCIDFYSRIRELRLHSDSVYGDPLEKLTWGLYNLIRLCRCQKPLNPAEKLRLHNE 123
 QY 122 KORFNIRGRWTCRCMSCSSSR-----TRRETQL 151
 DB 124 KRFFHNIAGHYRGQCHSCCNRRARQERLQRRRETQV 158

RESULT 82
 AAB03176
 ID AAB03176 standard; protein; 158 AA.
 XX
 AC AAB03176;
 XX
 DT 12-SEP-2003 (revised)
 DT 23-OCT-2000 (first entry)
 XX
 DE HPV-18 E6 protein.
 XX
 KW HPV-18 E6; ubiquitin mediated proteolysis; human;
 KW cellular protein half life; ubiquitination inhibitor; p53; cyclin;
 KW cell cycle regulator; myc deregulation; human papillomavirus;
 KW HPV-18 E6 protein; cervical cancer; skin cancer; epidermal hyperplasia;
 KW epidermal neoplasia; psoriasis; connective tissue disorder;
 KW wound healing; cytostatic; antiproliferative; anticancer; antipsoriatic.
 XX
 OS Human papillomavirus; 18.
 OS
 XX
 PN US6068982-A.

XX 30-MAY-2000.
 PD
 XX
 PF 17-DEC-1996; 96US-00767942.
 XX
 PR 04-JAN-1994; 94US-00176937.
 PR 23-MAY-1994; 94US-00247904.
 PR 27-MAY-1994; 94US-00250795.
 PR 13-SEP-1994; 94US-00305520.
 PR 07-JUN-1995; 95US-00486663.
 XX
 PA (MITO-) MITOTIX INC.
 XX
 PI Chiu MI, Cottarel G, Berlin V, Draetta G, Damagnez V, Rolfe M;
 XX WPI, 2000-410854/35.
 DR N-PSDB; AAA61623.
 XX
 PT Identifying an inhibitor of ubiquitin mediated proteolysis of regulatory
 PT protein for treating cancers involves measuring ubiquitination levels of
 PT the protein in the presence of candidate agent in an eukaryotic cell.
 XX
 PS Example 2; Col 97-100; 73pp; English.

CC The invention relates to a method of identifying an inhibitor of
 CC ubiquitin-mediated proteolysis of a cell cycle regulatory protein
 CC comprising contacting an engineered eukaryotic cell with a candidate
 CC agent. The eukaryotic cells is engineered to express a recombinant human,
 CC Candida albicans or Schizosaccharomyces pombe ubiquitin-conjugating
 CC enzyme (AAB03169-B03171), a cell cycle regulatory protein (such as p53)
 CC and ubiquitin. The specification also discloses novel Candida albicans
 CC and Schizosaccharomyces pombe ubiquitin-conjugating enzymes, caubCE and
 CC spUBCE (AAB03170, AAB03171), and two novel human ubiquitin-conjugating
 CC enzymes, hUBCE and rapUBC (AAB03169, AAB03173). The ubiquitin-mediated
 CC proteolysis system is the major pathway for the selective, controlled
 CC degradation of intracellular proteins in eukaryotic cells, and is
 CC this system controls the half-lives of cellular proteins, in particular,
 CC important in controlling the levels of proteins involved in cell cycle
 CC progression. Alterations in the ubiquitination of these proteins may
 CC therefore play a role in the development of cancer. For example, human
 CC papillomaviruses such as HPV-18 encode a transforming protein, E6 (E6-AP;
 CC AAB03177), which combines with a cellular E6-associated protein (E6-AP;
 CC AAB03177) to stimulate the ubiquitination of p53, thus targeting it for
 CC degradation. The ubiquitination inhibitors identified according to the
 CC method of the invention are useful for treatment of cervical cancers and
 CC connective tissue disorders and for controlling the wound healing
 CC process. They are also useful in treatment of hyperplastic epidermal
 CC conditions such as psoriasis, neoplastic epidermal conditions, skin
 CC cancers e.g., basal cell carcinomas, squamous cell carcinomas. The
 CC inhibitors are useful for deregulating myc expression and rendering the
 CC cells sensitive to chemotherapeutic treatment or to upset the balance of
 CC transformed cells and cause apoptosis to occur. Inhibitors of ubiquitin-
 CC mediated degradation of cyclins are useful as antiproliferative agents.
 CC The present sequence represents HPV-18 E6 protein. (Updated on 12-SEP-
 CC 2003 to standardise OS field)
 XX
 SQ Sequence 158 AA;

Query Match 54.9%; Score 455.5; DB 3; Length 158;
 Best Local Similarity 56.1%; Pred. No. 1.4e-42;
 Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY 2 FODPQPRPKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFPARDLCIYRDGNPYA 61
 DB 4 FEPDTRRPYKLPDLCTELMTSLQDIEITVCYKTVLETFEVPFADKLFVYRRDSIPRA 63
 QY 62 VADKCLKFSKISSEVYHVCYVGTTLLEQOYKPKLDDLIRCNXQKPLCPPEKORHLDK 121
 DB 64 ACHKCIDFYSRIRELRLHSDSVYGDPLEKLTWGLYNLIRLCRCQKPLNPAEKLRLHNE 123
 QY 122 KORFNIRGRWTCRCMSCSSSR-----TRRETQL 151
 DB 124 KRFFHNIAGHYRGQCHSCCNRRARQERLQRRRETQV 158

RESULT 83
ID AAB98427 standard; protein; 158 AA.
XX
AC AAB98427;
XX
DT 22-AUG-2001 (first entry)
XX
DE Human papillomavirus protein HPV18 E6.
XX
KW Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
KM epitope; T cell; identification; vaccine; infection; genital wart;
KM neoplastic growth; antiviral.
XX
OS Human papillomavirus.
XX
PN WO200141799-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033549.
XX
PR 10-DEC-1999; 99US-0172705P.
PR 15-AUG-2000; 2000US-00641528.
XX
PA (EPI-M-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
XX WPI; 2001-381497/40.
DR
XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT treating HPV infections.
PT
XX
PS Disclosure; Page 22; 756bp; English.
XX
CC The present invention describes an isolated prepared human papillomavirus
CC (HPV) epitope (I). (1) has antiviral activity, and can be used in vaccine
CC production. Peptides and corresponding nucleic acid compositions from the
CC present invention are useful for stimulating an immune response to HPV by
CC stimulating the production of CTL or HTL responses, specifically in the
CC treatment or prophylaxis of HPV infection, in persons who have not
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
CC can also be used in a tetramer staining assay to assess peripheral blood
CC mononuclear cells for the presence of antigen-specific CTLs following
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune
CC recall responses or evaluate the efficacy of a vaccine. The vaccine
CC compositions are useful for removing warts or treating HPV infections.
CC The epitopes for inclusion in an epitope-base vaccine may be selected
CC from conserved regions of viral or tumour-associated antigens, which
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
CC that may be present in whole antigens can be avoided with the use of
CC epitope-base vaccines. An additional advantage is the ability to combine
CC selected epitopes (CTL and HTL) and to modify the composition of the
CC epitopes achieving enhanced immunogenicity, the major benefit of the
CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
CC polypeptide sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 158 AA;
Query Match 54.9%; Score 455.5; DB 4; Length 158;
Best Local Similarity 56.1%; Pred. No. 1.4e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;
QY 2 FODDERPRKLPOLCTELTTHDIIIECVCKQQLAREVYDPAFRDLCTIVYDGNPFA 61
DB 4 FEDPRRRPKLPDLCTELTNTSLQDIEITVCYCKVLELTVFEPFADLFVYVDSITHA 63
QY 62 VXDCKLKFYSKISEYRHVCYSVYGTTLLEQVYKPKDLLIRICINXQKPLCEBEKORHLDK 121
DB 64 ACHKCIDFYSKIRIRLHYSDSVYGTLEKLTNTGIVNLLIRCLRCQKPLNPAEKRLHINE 123

DB 64 ACHKCIDFYSKIRIRLHYSDSVYGTLEKLTNTGIVNLLIRCLRCQKPLNPAEKRLHINE 123
QY 122 KORFHNIRGWTGRCMSCCRSSR-----TRRETQI 151
DB 124 KRFHNIRAGHYGQCHSCCNRAQERLORRRETQV 158
RESULT 84
ID ADO44074 standard; protein; 158 AA.
XX
AC ADO44074;
XX
DT 15-JUL-2004 (first entry)
XX
DE Amino acid sequence of the E6 polypeptide of HPV18.
XX
KW E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
XX
OS Human papillomavirus type 18.
XX
PN WO2004030636-A2.
XX
PD 15-APR-2004.
XX
PF 02-OCT-2003; 2003WO-US0311726.
XX
PR 03-OCT-2002; 2002US-0415922P.
XX
PA (AMHP) WYETH HOLDINGS CORP.
XX
PI Smith L, Cassetti MC;
XX WPI; 2004-316328/29.
DR
XX N-PEDB; ADO44101.
XX
PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.
XX
PS Disclosure; Page 78; 101bp; English.
XX
CC ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.
CC ADO44098 is the consensus sequence derived from these polypeptides. The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.
XX
SQ Sequence 158 AA;
Query Match 54.9%; Score 455.5; DB 8; Length 158;
Best Local Similarity 56.1%; Pred. No. 1.4e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;
QY 2 FODDERPRKLPOLCTELTTHDIIIECVCKQQLAREVYDPAFRDLCTIVYDGNPFA 61
DB 4 FEDPRRRPKLPDLCTELTNTSLQDIEITVCYCKVLELTVFEPFADLFVYVDSITHA 63
QY 62 VXDCKLKFYSKISEYRHVCYSVYGTTLLEQVYKPKDLLIRICINXQKPLCEBEKORHLDK 121
DB 64 ACHKCIDFYSKIRIRLHYSDSVYGTLEKLTNTGIVNLLIRCLRCQKPLNPAEKRLHINE 123

CY		122	KORFENIRGRWTCMCCSCSSR-----TRRETQL	151
			: : : :	
DQ		124	KORFENIAGHTRGQCSCCNRAKROERLQRRETOV	158
RESULT 97				
AEC98864				
ID	AEC98864	standard; protein; 158 AA.		
XX				
AC	AEC98864;			
XX				
DT	01-DEC-2005	(first entry)		
XX				
DE	HPV_18 Envelope protein E6.			
KM	Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;			
KW	epitope mapping; immune stimulation; cytotoxic T-lymphocyte.			
OS	Human papillomavirus type 18.			
XX				
PN	MO2005089164-A2.			
XX				
PD	29-SEP-2005.			
XX				
PE	03-JAN-2005; 2005WO-US000077.			
PR	31-DEC-2003; 2003US-0533211P.			
PP	02-JUL-2004; 2004US-0584652P.			
XX				
XX				
PA	(EPI-M-) EPIMUNE INC.			
PA	(INNO-) INNOGENETICS NV.			
PA	(CHES/) CHESNUT R.			
PA	(NEWM/) NEWMAN M J.			
PA	(MOTH/) MOTHE B.			
PA	(BAKE/) BAKER D.			
PA	(SOUT/) SOUTWOOD S.			
PA	(BABE/) BABE L M.			
PA	(CHEN/) CHEN Y.			
PA	(DEYO/) DEYOUNG L M.			
PA	(HUAN/) HUANG M T F.			
XX	(POWE/) POWER S D.			
PI	Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;			
PI	Chen Y, Deyoung LM, Huang MT, Power SD;			
XX				
DR	WI; 2005-658982/67.			
PT	New polynucleotide comprises a multi-epitope construct comprising nucleic			
PT	acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte			
PT	(CTL) epitopes, useful in preparing a vaccine against HPV.			
XX				
PS	Example 10; Page 349; 518pp; English.			
XX				
XX	The invention relates to a new polynucleotide comprising a multi-epitope			
XX	construct comprising nucleic acids encoding the human papillomavirus			
CC	(HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that			
CC	are directly or indirectly joined to one another in the same reading			
CC	frame, a vaccine minigene. Also included are a vector comprising the			
CC	multi-epitope construct, a polypeptide comprising an amino acid sequence			
CC	encoded by the polynucleotide, a composition (comprising the			
CC	polynucleotide, vector and/or polypeptide and a carrier), a cell			
CC	(comprising the polynucleotide, vector or polypeptide), inducing an			
CC	immune response against human papillomavirus virus (HPV) and making the			
CC	polynucleotide, vector or polypeptide. The epitopes are derived from			
CC	different strains of HPV and are from the E1, E2, E6 and E7 proteins. The			
CC	epitopes may be linked via a GP-anchor/spacer peptide. The order of the			
CC	epitopes in the vaccine protein are disclosed in the tables referred to			
CC	in the claims of the specification. The polynucleotide, vector or			
CC	polypeptide is useful in preparing a composition for inducing an immune			
CC	response against human papillomavirus virus (HPV) and thus providing a			
CC	defense against HPV infection and HPV-related cancers. The present			
CC	sequence is an HPV protein used to derive epitopes for the vaccine of the			
CC	invention.			

Seq	Sequence	158 AA
Query	Match	54.9%; Score 455.5; DB 9; Length 158;
	Best Local Similarity	56.1%; Pred. No. 1.4e-42;
	Matches	87; Conservative 21; Mismatches 42; Indels 5; Gaps 1
Db		
Qy	2 FODPERRRLPOLCTELHQTTHIDILIECVCKKQOLLRREYVDFAPRLDICYRDGNPYA 61	
	4 FEDPRRRRYKLPDLCTELNTSLQDIETICVCKTYLTELTEVRFPAFKDLFVYRDSIPHA 63	
Db	62 VXDCKLFYSKISEYRHYCVSYGTTLEQQYNKPLCDLLIRICINXQKPLCPREKQRLDK 121	
	64 ACHKIDFYSRIRELRYHSDSVYGDTLERKLTNTGTYNLLIRLCRCQKPLNPAKRLHLNE 123	
Qy	122 KQRFNIRGRWTRGRCMCCRSR-----TRRETOL 151	
	124 KRPFNINAGHYRGQCHSCCNPAROERLORRRRTQV 158	
Db		
RESULT 88		
AEC96398		
ID	AEC96398 standard; protein; 158 AA.	
XX		
AC	AEC96398;	
XX		
DT	01-DEC-2005 (first entry)	
XX		
DE	HPV protein E6 from HPV18.	
XX		
KM	Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;	
XX	epitope mapping; immune stimulation; cytotoxic T-lymphocyte.	
XX		
OS	Human papillomavirus type 18.	
XX		
PN	WO200508164-A2.	
XX		
PD	29-SEP-2005.	
XX		
PF	03-JAN-2005; 2005WO-US000077.	
XX		
PR	31-DEC-2003; 2003US-053211P.	
PR	02-JUL-2004; 2004US-0584652P.	
XX		
PA	(EPIM-) EPIIMUNE INC.	
PA	(INNO-) INNOGENETICS NV.	
PA	(CHES-) CHESNUT R.	
PA	(NEMM-) NEMMAN M. J.	
PA	(MOTH-) MOTHER B.	
PA	(BAKE-) BAKER D.	
PA	(SOUT-) SOUTWOOD S.	
PA	(BABE-) BABE L. M.	
PA	(CHEN-) CHEN Y.	
PA	(DEYO-) DEYOUNG L. M.	
PA	(HUAN-) HUANG M. T. F.	
PA	(POME-) POWER S. D.	
XX		
PI	Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;	
XX	Chen Y, Deyoung LM, Huang MTF, Power SD;	
XX		
DR	WPI; 2005-658982/67.	
XX		
PT	New polynucleotide comprises a multi-epitope construct comprising nucleic	
XX	acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte	
PT	(CTL) epitopes, useful in preparing a vaccine against HPV.	
XX		
PS	Disclosure; Page 57; 518pp; English.	
CC		
CC	The invention relates to a new polynucleotide comprising a multi-epitope	
CC	construct comprising nucleic acids encoding the human papillomavirus	
CC	(HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that	
CC	are directly or indirectly joined to one another in the same reading	
CC	frame, a vaccine minigene. Also included are a vector comprising the	

CC multi-epitope construct, a polypeptide comprising an amino acid sequence
CC encoded by the polynucleotide, a composition (comprising the
CC polynucleotide, vector and/or polypeptide and a carrier), a cell
CC (comprising the polynucleotide, vector or polypeptide), inducing an
CC immune response against human papillomavirus virus (HPV) and making the
CC polynucleotide, vector or polypeptide. The epitopes are derived from
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the
CC epitopes in the vaccine protein are disclosed in the tables referred to
CC in the claims of the specification. The polynucleotide, vector or
CC polypeptide is useful in preparing a composition for inducing an immune
CC response against human papillomavirus virus (HPV) and thus providing a
CC defense against HPV infection and HPV-related cancers. The present
CC sequence is an HPV protein used to derive epitopes for the vaccine of the
CC invention.

XX S0 Sequence 158 AA;

Query Match 54.9%; Score 455.5; DB 9; Length 158;
Best Local Similarity 56.1%; Pred. No. 1.4e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY 2 FDDPQRPRLPOLCTELQTTIHDIILCYCKQQLRREYDPAFRLCTIVRDGNPYA 61
DB 4 FEDPTRRPPYKLPDLCTELNTSLQDIEITCYCKTVLELVEPFAFKDLFVYRDSIPHA 63
QY 62 VADKCLKPYSKISEYRHYCYSVYGTLEQYNNKPLCDLIRCTINXOKPLCPREKORHLDK 121
DB 64 ACHKCIDFYSRIRLELHYSDSYGDTLEKLTGTGLYNLIRCLRCQKPLNPAKLRHNE 123

QY 122 KORFNINRGMTGRCMSCCRSSR-----TRRETOL 151
DB 124 KRFRNIAGHYRGQCHSCCNRAQRERLQRRRETQV 158

RESULT 89
AA022924
ID AA022924 standard; protein; 172 AA.
XX
XX AA022924;
AC
XX 12-DEC-2002 (first entry)
DT
XX
XX Human papillomavirus-18 (HPV18) E6E7-protein sequence.
DE
XX
XX Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;
KM fusion partner; immunogenicity; HPV infection; neoplasia; HPV18;
KM human papillomavirus-18; E6E7-sequence.
XX
XX Human papillomavirus.
OS
XX
XX EP1243655-A1.
PN
XX
XX 25-SEP-2002.
PD
XX
XX 23-MAR-2001; 2001EP-00107271.
PF
XX
XX 23-MAR-2001; 2001EP-00107271.
PR
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
XX
XX Cid-Arregui A, Zur Hausen H;
PI
XX
XX WPI; 2002-724952/79.
DR
XX
XX N-PSDB; AAL53422.
PT
XX
XX A new DNA sequence encoding a fusion protein comprising a mutagenized HPV
PT (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a
PT highly immunogenic fusion partner is useful to vaccinate against HPV
XX infection.
PS
XX
XX Disclosure; Fig 4; 34pp; English.
XX

CC The invention relates to a new DNA sequence encodes an E6 or E7 fusion
CC protein of HPV, where at least 20% of the original codons are replaced by
CC codons which lead to enhanced translation of a mammalian cell, containing
CC a mutation which results in production of a truncated non-functional
CC protein, and encoding a highly immunogenic polypeptide fusion partner
CC capable of enhancing immunogenicity of the E6 or E7 protein in the
CC mammalian host. The invention is used as a vaccine for the prevention or
CC treatment of an HPV infection or a neoplasm associated with HPV
CC infection. This sequence represents the human papillomavirus-18 (HPV18)
CC E6E7-protein sequence of the invention

XX S0 Sequence 172 AA;

Query Match 54.9%; Score 455.5; DB 5; Length 172;
Best Local Similarity 56.1%; Pred. No. 1.6e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

QY 2 FDDPQRPRLPOLCTELQTTIHDIILCYCKQQLRREYDPAFRLCTIVRDGNPYA 61
DB 10 FEDPTRRPPYKLPDLCTELNTSLQDIEITCYCKTVLELVEPFAFKDLFVYRDSIPHA 69
QY 62 VADKCLKPYSKISEYRHYCYSVYGTLEQYNNKPLCDLIRCTINXOKPLCPREKORHLDK 121
DB 70 ACHKCIDFYSRIRLELHYSDSYGDTLEKLTGTGLYNLIRCLRCQKPLNPAKLRHNE 129
QY 122 KORFNINRGMTGRCMSCCRSSR-----TRRETOL 151
DB 130 KRFRNIAGHYRGQCHSCCNRAQRERLQRRRETQV 164

RESULT 90
AAR27728
ID AAR27728 standard; protein; 271 AA.
XX
XX AAR27728;
AC
XX
XX 24-OCT-2003 (revised)
DT
XX
XX 25-MAR-2003 (revised)
DT
XX
XX 09-MAR-1993 (first entry)
DT
XX
XX HPV 18 E6 protein fragment.
DE
XX
XX Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;
KM immunotherapeutic.
KM
XX
XX Human papillomavirus; 18.
OS
XX
XX Key Location/Qualifiers
FH
XX
XX Peptide 2..259
FT
XX
XX /note="HPV-18 E6 protein"
FT
XX
XX WO9216636-A1.
PN
XX
XX 01-OCT-1992.
PD
XX
XX 10-MAR-1992; 92WO-GB000424.
PF
XX
XX 14-MAR-1991; 91GB-00005383.
PR
XX
XX (IMMU) IMMUNOLOGY LTD.
PA
XX
XX Boursnell MEG, Inglis SC, Munro AJ;
PI
XX
XX WPI; 1992-349219/42.
DR
XX
XX N-PSDB; AAO29390.
PT
XX
XX Recombinant virus vectors encoding human papillomavirus proteins - for
PT treating and vaccinating against HPV infections and conditions caused by
PT them, such as cervical cancer.
XX
XX
XX Disclosure; Fig 1b; 83pp; English.
PS
XX
XX The fragment of DNA contg. the HPV-18 E6/E7 coding region was prepd. by
CC


```

Query Match          54.9%; Score 455.5; DB 2; Length 278;
Best Local Similarity 56.1%; Pred. No. 2.8e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

OY 2 FODPBRPKLPOLCTELQTTIHDIILCEVCYCKOQLLRREVYDFAFRDLCTIYRDGNPYA 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 115 FEDPTRRPYKLPDLCTELNTSLQDIETICVCKTVLELVEFEPAFKDLFVYVRSIPHA 174
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 62 VXDCKLKFYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRICINXQKPLCEBKORHLDK 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 175 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKURLHNE 234
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 122 KORFNINRGWTRGCMSCCRSSR-----TRRETOL 151
DB 235 KRPFNINAGHYRGQCHSCCNRAEROERLORRRETQV 269

RESULT 93
AED52653
ID AED52653 standard; protein; 278 AA.
XX
XX AED52653;
AC
XX
XX 29-DEC-2005 (first entry)
DT
XX
XX Fusion protein D1/3-E6-His(HPV18).
DE
XX
XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KM viricide; uterine cervix tumor; E6; D protein.
XX
XX Haemophilus influenzae; strain 772.
OS
OS Human papillomavirus type 18.
OS Synthetic.
OS Chimeric.
XX
XX IN9801903-14.
XX
XX PD 04-MAR-2005.
XX
XX PF 24-AUG-1998; 98IN-CH001903.
XX
XX PR 22-AUG-1997; 97EP-00179535.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX PI Tyrrell AMR;
XX
XX DR WPI; 2005-557648/57.
XX
XX DR N-PSDB; AED52652.
XX
XX PT Vaccine.
XX
XX PS Example 16; Fig 22; 96pp; English.
XX
XX CC The invention relates to human Papilloma virus (HPV) fusion proteins,
CC linked to an immunological fusion partner that provides T helper epitopes
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC are useful in the treatment or prophylaxis of HPV induced lesions
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
CC Haemophilus influenzae D protein (20-127), the C-terminus of
CC Streptococcus pneumoniae type 1 protein (clysA) or thioredoxin. The present
CC sequence represents an HPV-H. influenzae D protein, fusion protein of the
CC invention.
XX
XX SQ Sequence 278 AA;

Query Match          54.9%; Score 455.5; DB 9; Length 278;
Best Local Similarity 56.1%; Pred. No. 2.8e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

OY 2 FODPBRPKLPOLCTELQTTIHDIILCEVCYCKOQLLRREVYDFAFRDLCTIYRDGNPYA 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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```

DB 115 FEDPTRRPYKLPDLCTELNTSLQDIETICVCKTVLELVEFEPAFKDLFVYVRSIPHA 174
OY 62 VXDCKLKFYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRICINXQKPLCEBKORHLDK 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 175 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKURLHNE 234
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 122 KORFNINRGWTRGCMSCCRSSR-----TRRETOL 151
DB 235 KRPFNINAGHYRGQCHSCCNRAEROERLORRRETQV 269

RESULT 94
AAV25386
ID AAV25386 standard; protein; 383 AA.
XX
XX AAV25386;
AC
XX
XX 06-SEP-1999 (first entry)
DT
XX
XX HPV fusion protein D1/3-E6/E7-His/HPV18.
DE
XX
XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KM immunological fusion partner; CpG oligonucleotide; immune response;
KM HPV antigen; prevention; treatment.
XX
XX OS Synthetic.
OS Human papillomavirus.
XX
XX PN W09933868-A2.
XX
XX PD 08-JUL-1999.
XX
XX PF 18-DEC-1998; 98WO-EP008563.
XX
XX PR 24-DEC-1997; 97GB-00027262.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX PI Dalemans WJL; Gerard CMG;
XX
XX DR WPI; 1999-405485/34.
XX
XX DR N-PSDB; AAX78801.
XX
XX PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
XX induce immune response to HPV.
XX
XX PS Example XII; Page 61-62; 62pp; English.
XX
XX CC AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAV25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours
XX
XX SQ Sequence 383 AA;

Query Match          54.9%; Score 455.5; DB 2; Length 383;
Best Local Similarity 56.1%; Pred. No. 4.1e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

OY 2 FODPBRPKLPOLCTELQTTIHDIILCEVCYCKOQLLRREVYDFAFRDLCTIYRDGNPYA 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 115 FEDPTRRPYKLPDLCTELNTSLQDIETICVCKTVLELVEFEPAFKDLFVYVRSIPHA 174
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 62 VXDCKLKFYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRICINXQKPLCEBKORHLDK 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 175 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKURLHNE 234
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 122 KORFNINRGWTRGCMSCCRSSR-----TRRETOL 151
DB 235 KRPFNINAGHYRGQCHSCCNRAEROERLORRRETQV 269

```

```

RESULT 95
ID AAY02642 standard; protein; 383 AA.
XX
AC AAY02642;
XX
XX 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)
XX
DE Prot.D1/3-E6-E7-His/HPV18 protein.
XX
KM Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KM tumour; lesion; benign; malignant; virus; infection.
XX
OS Human papillomavirus.
OS Haemophilus influenzae.
OS Chimeric.
XX
XX WO9910375-A2.
XX
XX 04-MAR-1999.
XX
XX 17-AUG-1998; 98WO-EP005285.
XX
XX 22-AUG-1997; 97GB-00017953.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
XX Lombardo-Bencheikh A;
XX
XX WPI; 1999-190587/16.
XX
XX N-PSDB; AAX29790.
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX treatment or prophylaxis of HPV induced lesions.
XX
XX Disclousure; Fig 25; 95pp; English.
XX
XX This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
XX protein from Human papillomavirus (HPV) linked to an immunological fusion
XX partner, in this case, a fragment of the Haemophilus influenzae B protein
XX D. The sequence also contains a histidine tag at the C-terminus of the
XX encoded protein. The protein can be used in a vaccine, for immuno-
XX therapeutically treating HPV induced tumour lesions (benign or malignant)
XX and preventing HPV viral infection. (Updated on 17-Oct-2003 to
XX standardise OS field)
XX
XX Sequence 383 AA;
XX
Query Match 54.9%; Score 455.5; DB 2; Length 383;
Best Local Similarity 56.1%; Pred. No. 4.1e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;
QY 2 FODQERPRKLPQLCTELQTTIHDIILFCVYCKQQLRREYVDFAFRDLCTIYRDGNPYA 61
DB 115 FEDPFRPRYKLPDLCTELINTSLQDIEITCVYCKTVLETFEVEFAFKDLFVYVRDSIPHA 174
QY 62 VXDCKLKYSKISEYRHYCVSYGTTLEQYNNKPLCDLILRCINXOKPLCEBEKORHDK 121
DB 175 ACHKCTIDYSRIRELRHYSDSVYGDTLEKLTNTGLYNLIRLCRCQKPLNPAEKURLHNE 234
QY 122 KORFNINRGWTRGCMSCCRSSR-----TRRETOL 151
DB 235 KRRFNNINGHYRGQCHSCCNBARQERLQRRRETQV 269
XX
RESULT 96
ID AED52657 standard; protein; 383 AA.
XX

```

```

AC AED52657;
XX
XX 29-DEC-2005 (first entry)
DT
XX
XX Fusion protein D1/3-E6-E7-His/HPV18.
XX
XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
XX virucide; uterine cervix tumor; E7; E6; D protein.
XX
XX Haemophilus influenzae; strain 772.
XX
XX Human papillomavirus type 18.
XX
XX Synthetic.
XX
XX Chimeric.
XX
XX IN9801903-14.
XX
XX 04-MAR-2005.
XX
XX 24-AUG-1998; 98IN-CH001903.
XX
XX 22-AUG-1997; 97EP-00179535.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Tytrell AMR;
XX
XX WPI; 2005-557648/57.
XX
XX N-PSDB; AED52656.
XX
XX Vaccine.
XX
XX Example 17; Fig 25; 96pp; English.
XX
XX The invention relates to human Papilloma virus (HPV) fusion proteins,
XX linked to an immunological fusion partner that provides T helper epitopes
XX to the HPV antigen. Vaccine formulations comprising the fusion proteins
XX are useful in the treatment or prophylaxis of HPV induced lesions
XX (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
XX proteins (singly, as an E6-E7 fusion or mutated) were fused to either
XX Haemophilus influenzae D protein (20-127), the C-terminus of
XX Streptococcus pneumoniae LytA protein (cLytA) or chloroixin. The present
XX sequence represents an HPV-H. influenzae D protein, fusion protein of the
XX invention.
XX
XX Sequence 383 AA;
XX
Query Match 54.9%; Score 455.5; DB 9; Length 383;
Best Local Similarity 56.1%; Pred. No. 4.1e-42;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;
QY 2 FODQERPRKLPQLCTELQTTIHDIILFCVYCKQQLRREYVDFAFRDLCTIYRDGNPYA 61
DB 115 FEDPFRPRYKLPDLCTELINTSLQDIEITCVYCKTVLETFEVEFAFKDLFVYVRDSIPHA 174
QY 62 VXDCKLKYSKISEYRHYCVSYGTTLEQYNNKPLCDLILRCINXOKPLCEBEKORHDK 121
DB 175 ACHKCTIDYSRIRELRHYSDSVYGDTLEKLTNTGLYNLIRLCRCQKPLNPAEKURLHNE 234
QY 122 KORFNINRGWTRGCMSCCRSSR-----TRRETOL 151
DB 235 KRRFNNINGHYRGQCHSCCNBARQERLQRRRETQV 269
XX
RESULT 97
ID AEA98550 standard; protein; 162 AA.
XX
XX AEA98550;
XX
XX 08-SEP-2005 (first entry)
DT
XX
XX HPV (oncogenic strain) E6 amino acid sequence SEQ ID 31.
XX

```

KM	Papillomavirus infection; viruicide; E6 protein; diagnosis; antibody;
KM	Cancer; cervix tumor; cytostatic.
XX	
OS	Human papillomavirus; strain 68.
XX	
FN	US2005142541-A1.
XX	
PD	30-JUN-2005.
XX	
PF	23-DEC-2004; 2004US-00021949.
XX	
PR	23-DEC-2003; 2003US-0532373P.
XX	
PA	(ARB0-) ARBOR VITA CORP.
XX	
PI	Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;
XX	
DR	WPI; 2005-457781/46.
XX	
PT	New antibody composition comprising a mixture of monoclonal antibodies
PT	for oncogenic strains of human papilloma virus, useful for diagnosing
PT	cancer.
XX	
XX	Disclosure; SEQ ID NO 31, 161pp; English.

CC The invention relates to an antibody composition comprising a mixture of
 CC monoclonal antibodies that specifically bind to E6 proteins of human
 CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one
 CC of the monoclonal antibodies specifically binds to E6 proteins of at
 CC least three different oncogenic HPV strains. Also included are a
 CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,
 CC comprising the antibody composition above), a method of detecting an HPV
 CC E6 protein in a sample, a method of detecting the presence of an
 CC oncogenic HPV E6 protein in a sample and a system for detecting the
 CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a
 CC first and a second binding partner for an oncogenic HPV E6 polypeptide,
 CC where the first binding partner is a PDZ domain protein and the second
 CC binding partner is an antibody that specifically binds to the E6 proteins
 CC of at least three different oncogenic HPV strains). The antibody
 CC composition, kit, methods, and system are useful for diagnosing cancer,
 CC particularly cervical cancer. The present sequence is an HPV E6 protein.
 XX

Query Match	54.4%	Score 451.5	DB 9	Length 162
Best Local Similarity	55.1%	Pred. No. 4,1e-42		
Matches 86; Conservative	21	Mismatches 44	Indels 5	Gaps 1

```

QY      1 MFOQDQERRRKPOLCTBELQTTIHDIILEVYVKKOOLLREVYDPAFRODCIYVRGNPY 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      7 LFHNPEERYKLPDLCTRTDITTLHDVTIDCVYCRDLORTVEYEFAGDINVYRGVPL 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61 AXDXCLKRYKSISEYRHCVSYVGTTLDEQVYKPKCDLILRCINQKPLCPBEKORHLD 120
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      67 AACQSIKRYAKIRELRYSESAYATLTETITNTKYDISIRWCCLKPLSPAEKRHLN 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      121 KQRFENINGRMTRGMSCCRSS-----RTREPTOL 151
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      127 SRRRFPAKLAGNFTGQCRHCWTISRREDRRRRRTQYOV 162
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 98
ADL90077
ID ADL90077 standard; protein: 158 AA.

ADL90077;
XX
AC
XX
DT 17-JUN-2004 (first entry)

Human papillomavirus 18-E6 protein, SEQ ID 17.

OS Human papillomavirus.
XX
XX WO2004027049-A2.
XX
XX PD 01-APR-2004.
XX
XX PF 18-SEP-2003; 2003WO-US030188.
XX
XX PR 20-SEP-2002; 2002US-0412219P.
PR 14-MAR-2003; 2003WO-US007995.
XX
XX PA (ASTR-) ASTRAL INC.
XX
XX PI Bot A, Wang L, Smith D, Phillips B;
XX
XX DR WPI; 2004-295415/27.
XX
XX PT Generating an immune response to an antigen, useful for generating
PT desired T cell responses comprises administering an immunoglobulin having
PT one peptide epitope of the antigen attached to the immunoglobulin.
XX
XX PS Disclosure; Fig 1G; 154pp; English.

CC The present invention relates to a method for generating an immune
CC response to an antigen in a patient. The method comprises administering
CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at
CC least one peptide epitope of the antigen attached to the Ig or its
CC portion and administering the immunoglobulin or its portion in
CC conjunction with a RNA segment. The present sequence is an antigen
CC sequence, used to illustrate the invention.

SQ Sequence 158 AA;

Query Match	54.2%	Score 449.5	DB 8	Length 158
Best Local Similarity	55.5%	Pred. No. 6	7e-42	
Matches 86	Conservative 21	Mismatches 43	Indels 5	Gaps 1

QY	2	FODDERPRKLPOLCTELQTTIHIIILECYCCKOQLRREYVDAFPFDLCIVADGNPA	61
Dd	4	FEDFRRRYPKLPDCTELNISTLODIETVCYCCKVLBLEVEEPAFDOLFVWYDSIPHA	63
QY	62	VXDKCLKYSKISIEVRHCYCVGTTLBEOQNNKLCDLLTRCINXOKPLCBEEKQRHLKD	121
Dd	64	ACHKIDFSIRIRELRHSDSVYDDTLEKLTNTGLYNLLIRCLRCQRPKNPAXEKLRLNE	123
QY	122	KQRFHNIRGRWTGCMSCCRSSR-----TRRETOL	151
Dd	124	KRFPHKIAGHYRGQCHSCCNBARERLORRREITVV	158

RESULT 99
ADO44078
ID ADO44078 standard; protein: 158 AA.

```

XX      ADO44078;
AC
XX      15-JUL-2004 (first entry)
DT

```

AA Amino acid sequence of the E6 polypeptide of HPV39.
DE
XX E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; KM

OS Human papillomavirus type 39.
 XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
 KW cervical cancer; immune response; lower genital tract cancer; prostate cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
 NM
 KW
 XX

AA WO2004030636-A2.
PN
XX
PD 15-APR-2004.

XX 02-OCT-2003; 2003WO-US031726.
PF
XX
PR 03-OCT-2002; 2002US-0415929P.

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:10:28 ; Search time 29.1084 Seconds
(without alignments)
499.124 Million cell updates/sec

Title: US-10-530-253-13ED
Perfect score: 830
Sequence: 1 MFQDDPQRPRKLPOLCTELO.....WTGRCHMSCCRSSRRRTQTQL 151

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 80:.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	823	99.2	158	1	protein B6 - human
2	578	69.6	149	1	B6 protein - human
3	523	63.0	149	1	B6 protein - human
4	520	62.7	149	1	B6 protein - human
5	496	59.8	149	1	B6 protein - human
6	487	58.7	148	2	B6 protein - human
7	484	58.3	148	2	B6 protein - human
8	460	55.4	151	1	B6 protein - human
9	459.5	55.4	158	2	B6 protein - human
10	455.5	54.9	158	1	B6 protein - human
11	451.5	54.4	158	1	B6 protein - human
12	449.5	54.2	158	1	B6 protein - human
13	438	52.8	191	1	B6 protein - human
14	436.5	52.6	150	2	B6 protein - human
15	436.5	51.4	155	1	B6 protein - human
16	426.5	46.4	153	2	B6 protein - human
17	385.5	45.7	154	2	B6 protein - human
18	379	45.7	154	2	B6 protein - human
19	372.5	44.9	155	2	B6 protein - human
20	326.5	39.3	155	1	B6 protein - human
21	304	36.6	150	1	B6 protein - human
22	303	36.5	153	1	B6 protein - human
23	301	36.3	150	1	B6 protein - human
24	297.5	35.8	159	1	B6 protein - human
25	294	35.4	150	1	B6 protein - human
26	292	35.2	159	2	B6 protein - human
27	290.5	35.0	154	2	B6 protein - human
28	288.5	34.8	154	2	B6 protein - human
29	288	34.7	150	1	B6 protein - human

30	283	34.1	142	2	S36509	B6 protein - human
31	273	32.9	150	1	M6WL13	B6 protein - human
32	268	32.3	150	1	M6WL42	B6 protein - human
33	239	28.8	148	2	S36532	B6 protein - human
34	231	27.8	152	2	S36550	B6 protein - human
35	154	18.6	138	2	S36567	B6 protein - human
36	143.5	17.3	141	2	S36479	B6 protein - human
37	137	16.5	156	1	M6WL41	B6 protein - human
38	136.5	16.4	140	1	M6WL	B6 protein - human
39	134.5	16.2	139	1	M6WL82	B6 protein - human
40	129.5	15.9	161	2	S36491	B6 protein - human
41	129.5	15.6	207	2	S28510	B6 protein - multi
42	128.5	15.5	141	2	S36473	B6 protein - human
43	127	15.3	57	2	IS6705	B6 protein - human
44	127	15.3	273	1	M6WL8B	B6 protein - human
45	123	14.8	157	2	S36538	B6 protein - human
46	123	14.8	166	2	S36485	B6 protein - human
47	121.5	14.6	148	2	S36590	B6 protein - human
48	119	14.3	137	1	M6WL8B	B6 protein - human
49	119	14.3	156	1	M6WL47	B6 protein - human
50	118	14.2	155	1	M6WL8	B6 protein - human
51	116	14.0	157	1	M6WL85	B6 protein - human
52	113	13.6	157	1	M6WL5	B6 protein - human
53	86	10.4	154	2	S28509	B6 protein - Old W
54	83.5	10.1	135	1	M6WLDP	B6 protein - deer
55	83	10.0	32	2	S19906	B6-II protein - h
56	83	10.0	35	2	S19909	B6-II protein - h
57	83	10.0	47	2	S23825	B6-I protein - hum
58	79.5	9.6	471	2	T02749	G1/S transifion co
59	77.5	9.3	135	1	M6WL8P	B6 protein - Euro
60	77.5	9.3	572	2	G02845	zyxin - human
61	77.5	9.3	1468	2	S11515	formin - mouse
62	77	9.3	699	2	T09483	Cys-rich protein R
63	76	9.2	400	2	S44810	outer dense fiber
64	75.5	9.1	250	2	S71522	hypothetical prote
65	75	9.0	303	2	T21125	outer dense fiber
66	74.5	9.0	262	2	S56100	alpha-fetoprotein
67	74.5	9.0	609	1	FPGO	alpha-fetoprotein
68	74.5	9.0	609	1	FPHU	alpha-fetoprotein
69	74.5	9.0	609	2	UC4258	hypothetical prote
70	74	8.9	524	2	F96784	hypothetical prote
71	71	8.9	1379	2	T45119	FIM protein (Impor
72	73.5	8.9	357	2	A72220	conserved hypothet
73	73.5	8.9	549	2	T17525	proline-rich prote
74	73	8.8	284	2	UC7686	activator of CAMP-
75	73	8.8	557	2	B55933	paxillin - human
76	73	8.8	559	2	B55933	G1/S transifion co
77	72.5	8.7	866	2	T01171	conserved hypothet
78	72	8.7	270	2	G82108	hypothetical prote
79	72	8.7	422	2	T21820	hypothetical prote
80	71.5	8.6	565	2	H86477	protein p1504.19 (
81	71.5	8.6	616	2	T11850	DNA primase (EC 2.
82	71	8.6	375	1	A23689	limulus clotting e
83	71	8.6	1630	2	T40217	hypothetical prote
84	71	8.6	1638	2	D87749	protein unc-73b (i
85	71	8.6	2488	2	T42739	guanine nucleotide
86	70.5	8.5	615	2	C97723	separate-trna lig
87	70	8.4	449	2	C86496	hypothetical prote
88	70	8.4	449	2	D72121	hypothetical prote
89	70	8.4	449	2	A81544	hypothetical prote
90	70	8.4	708	2	T23616	hypothetical prote
91	70	8.4	1436	2	B81704	conserved hypothet
92	69.5	8.4	314	2	T15519	hypothetical prote
93	69	8.3	298	2	B84474	hypothetical prote
94	69	8.3	327	2	T33884	cag island protein
95	69	8.3	1819	2	A71928	outer dense fiber
96	68.5	8.3	262	1	S56101	tumor necrosis fac
97	68.5	8.3	455	1	GQHUT1	hypothetical prote
98	68.5	8.3	519	2	T28250	sependily (ery h
99	68.5	8.3	868	2	A20817	skeletal muscle Li
100	68	8.2	280	2	G02741	

ALIGNMENTS

RESULT 1

M6WL35 protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

A:Accession: A03682; T10427

R:Seedorf, K.; Krammer, G.; Duret, M.; Suhai, S.; Roweckamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEB>

A:Cross-references: UNIPROT:P03126; UNIPARC:UPI000000138B; GB:K02718; NID:G333031; PIDN:

R.Kennedy, I.M.; Haddock, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: UNIPARC:UPI000000138B; EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PI

C:Genetics:

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 99.2%; Score 823; DB 1; Length 158;

Best Local Similarity 98.0%; Pred. No. 2.7e-71;

Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIYRDGPNY 60

DB 8 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIYRDGPNY 67

QY 61 AVXDCKLFYSKISEYRHVCYSVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

DB 68 AVXDCKLFYSKISEYRHVCYSVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 127

QY 121 KKQRFHNIRGRWTCSCSSSRTRETOL 151

DB 128 KKQRFHNIRGRWTCSCSSSRTRETOL 158

Query Match 63.0%; Score 523; DB 1; Length 149;

Best Local Similarity 64.9%; Pred. No. 9.9e-43;

Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;

QY 1 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIYRDGPNY 60

DB 1 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIYRDGPNY 60

QY 61 AVXDCKLFYSKISEYRHVCYSVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

DB 61 AVXDCKLFYSKISEYRHVCYSVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

QY 121 KKQRFHNIRGRWTCSCSSSRTRETOL 151

DB 121 KKQRFHNIRGRWTCSCSSSRTRETOL 151

Query Match 69.6%; Score 578; DB 1; Length 149;

Best Local Similarity 71.5%; Pred. No. 5.7e-48;

Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIYRDGPNY 60

DB 1 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIYRDGPNY 60

QY 61 AVXDCKLFYSKISEYRHVCYSVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

DB 61 AVXDCKLFYSKISEYRHVCYSVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

QY 121 KKQRFHNIRGRWTCSCSSSRTRETOL 151

DB 121 KKQRFHNIRGRWTCSCSSSRTRETOL 151

Query Match 69.6%; Score 578; DB 1; Length 149;

Best Local Similarity 71.5%; Pred. No. 5.7e-48;

Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIYRDGPNY 60

DB 1 MFODPOEPRRLPOLCTELQTTIHIIIECVYCKQQLRREYDPAFRLDCIYRDGPNY 60

QY 61 AVXDCKLFYSKISEYRHVCYSVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

DB 61 AVXDCKLFYSKISEYRHVCYSVGTTLBQYKNRPLCDLIRICINXQKPLCPBEKQRHLD 120

QY 121 KKQRFHNIRGRWTCSCSSSRTRETOL 151

DB 121 KKQRFHNIRGRWTCSCSSSRTRETOL 151

A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #ext_change 09-Jul-2004
C:Accession: C40509
R:Reuter, S.; Dellus, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A:Reference number: M40509; MUID:91374616; PMID:1716694
A:Accession: C40509
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <REU>
A:Cross-references: UNIPROT:P27962; UNIPARC:UPI000000082F; GB:M73258
C:Superfamily: Papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
P:32-68/Region: zinc finger CCCC motif
P:105-141/Region: zinc finger CCCC motif

Query Match	54.4%	Score	451.5	DB 1	Length	158			
Best Local Similarity	55.1%	Pred. No.	6	8e-36					
Matches	86	Conservative	21	Mismatches	44	Indels	5	Gaps	1
Qy	1	MFODPQERPRKL	POLCTELQTTIHDIILECVYCKQKOLLREVVYDPAFRDLCTIVYDGNPY	60					
Db	3	LFNHNEEPRYKLPDLCTRTIDTTLTLDVTTIDVCYCRQRLQRTVEYBEAFGDLNVVYRDGVL	62						
Qy	61	AVXDKCLFYSKLSISYRHYCYVYGTILEQVNNKRLCDLLIFCINAKQKPLCPEBQQRHD	120						
Db	63	AACOSCIFYAKIRLRLAYSESVAVTTLETINTKLVDLISIRCMCLKPLSPAERKLRLHN	122						
Qy	121	KKORFHNIRGRWTCRCMSCCRSS-----RTRRETL	151						
Db	123	SKRRPHKLAGNFTGCGRHCWTSKREDRRRTROETOV	158						

RESULT 13
W6WL39 E6 protein - human papillomavirus type 39
C:Species: human papillomavirus type 39
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A38502
R:Volpert, C.; Strecek, R.E.
Virology 181, 419-423, 1991
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A:Reference number: A38502; MUID:91135017; PMID:1847266
A:Accession: A38502
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <VOL>
A:Cross-references: UNIPROT:P24835; UNIPARC:UPI00003383D2; GB:M62849; EMBL:M38185; NID:G
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:/32-68/Region: zinc finger CCCC motif
F:/105-141/Region: zinc finger CCCC motif

[illegible]

RESULT 14

W6MRL1
E6 protein - rhesus papillomavirus (type 1)
C:Species: rhesus papillomavirus
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #ext_change 09-Jul-2004
C:Accession: A38503
R:Ostrow, R.S.; Labresh, K.V.; Farae, A.J.
Virology, 181, 424-429, 1991
A:Title: Characterization of the complete RHPV 1 genomic sequence and an integration loci
A:Reference number: A38503; MUID:91135018; PMID:1847267
A:Accession: A38503
A:Status: translation not shown
A:Residues: 1-191 <OST>
A:Molecule type: DNA
A:Cross-references: UNIPROT:P22159; UNIPARC:UP100001383EE; EMBL:M37717
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:60-96/Region: zinc finger CCCC motif
F:133-169/Region: zinc finger CCCC motif

	Query March	Similarity	52.8%; Score 438; DB 1;	Length 191;
	Best Local Matches	Conservative	82; Mismatches 40; Indels 2; Gaps 1;	Pred. No. 1.6e-34;
Oy	4 DPOERPRKLPOLCTELQTTIHDIILIECVYCKQOILRREVDFAFRDLICIVYRDGNPYAVX	63		
	: :			
Dd	34 EPNELPRTIHLHGQRESTLHELQECVYCKKELTRLEVVDFAWMDLTRVHROGKPVCYC	93		
Oy	64 DKCLFYSKISSEYHHYCYSVGTLLBEQQYNKPLCDLLIRCLNNQKPLCPBKKORHLDDKQ	123		
	: :			
Dd	94 PICLFYSKIRKYRYEYSIVGTLERTRKQLVEVLIRCCYCKPKLCPIEKORHVDOGQ	153		
Oy	124 RFNIRGWTCRCMSSCRSTRRETQ	150		
	: :			
Dd	154 RFNRDAGWTGRCLMCWRP--TVDETQ	178		

RESULT 15
S36544
B6 protein - human papillomavirus type 26
C.Species: human papillomavirus type 26
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C.Accession: S36544
R.Dellus, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A.Description: Primer-directed sequencing of human papillomavirus types.
A.Reference number: S36469
A.Accession: S36544
A.Molecule type: DNA
A.Residues: 1-150
A.Cross-references: UNIPROT:P36807; UNIPARC:UPI00001383C5; EMBL:X74472; NID:g396956; PIDD
C:Superfamily: papillomavirus B6 protein
C:Keywords: early protein; zinc finger

	Query Match	Similarity	Score	DB 2	Length
Beet	Local	52.6%	436.5	150	
Matches	83	Conservative	24	Mismatches	43
				Indels	1
				Gaps	1

	Query	DB	Score	DB 2	Length
1	MFODPQERPRKLPOLCTELQTTIHDIIDECYVCKQOOLLREYVDFAFRDLCTIVADGNDY	60			
2	MFEDPREPRITLHELCSLNTLQIQLQVQVYCKEKLQWADVYNFAICDLRVYRDSRSPY	60			
3	AVXDKCLFYSKISLRYRHCVSYVGTIIIEQGNKRLCDLILFICNIXQKRLCEBENQRHID	120			
4	AACKRCVIFYSKITETRYRRYTSVYATLEATPKSLCNLLIRCHRCOMPLGPEEKORIYD	120			
5	KKORFPHNIRGRWTCRCMCCRRSPRRRETOL	151			
6	EGRFPHETAGQWKGELCTINCWR-PRKQETQV	150			

RESULT 16
W6WL56
E6 protein - human papillomavirus type 56

C:Species: human papillomavirus type 56
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A33377; S36579
R:Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; McAllister, P.; Temple, G.F.
J. Gen. Virol. 70, 3099-3104, 1989
J. Title: Human papillomavirus type 56: a new virus detected in cervical cancers.
A:Reference number: A33377; PMID:90063558; PMID:2555440
A:Accession: A33377
A:Molecule type: DNA
A:Residues: 1-155 <LOE>
A:Cross-references: UNIPROT:P24836; UNIPARC:UPI00001383E0
R:Deinze, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36579
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-155 <DEU>
A:Cross-references: UNIPARC:UPI00001383E0; EMBL:X74483; NID:G397053; PIDN:CA52596.1; PI
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:33-69/Region: zinc finger CCCC motif
F:106-142/Region: zinc finger CCCC motif

Query Match 51.4%; Score 426.5; DB 1; Length 155;
Best Local Similarity 56.4%; Pred. No. 1.6e-33;
Matches 84; Conservative 17; Mismatches 47; Indels 1; Gaps 1;

Qy 2 FODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFARFDCIYVRDGNPY 61
Db 5 FNNPOERPRSLHNLSEVLLEPLDLRLSCVCKKELTAEVYNFACELKLVYRDPDFYA 64

Qy 62 VXDCKLKFYSKISEYHNYCYVGTTLLEQYNNKPLCDLLIRCIYNKQKPLCEBEKQRLHD 121
Db 65 VCRVCLLFYSKVRKRYDYVSGATLESITRKQKCDLLIRCYRCQSPLTPEBKQLHCDR 124

Qy 122 KORFHNIRGRWTGRCMSCCR--SSRTRET 149
Db 125 KRRFHLAHGWTGSLGCMWRQTSREPRRS 153

RESULT 17

S36503
E6 protein - human papillomavirus type 30
C:Species: human papillomavirus type 30
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36503
R:Deinze, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36503
A:Molecule type: DNA
A:Residues: 1-153 <DEU>
A:Cross-references: UNIPROT:P36809; UNIPARC:UPI00001383CA; EMBL:X74474; NID:G396973; PID
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 46.4%; Score 385.5; DB 2; Length 153;
Best Local Similarity 50.0%; Pred. No. 1.3e-29;
Matches 74; Conservative 26; Mismatches 47; Indels 1; Gaps 1;

Qy 2 FODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFARFDCIYVRDGNPY 61
Db 5 FENGERRRTVHHLCEVQSTLLELDQCVCKKLSSEVYNFAFKQLRLVYRDSFYA 64

Qy 62 VXDCKLKFYSKISEYHNYCYVGTTLLEQYNNKPLCDLLIRCIYNKQKPLCEBEKQRLHD 121
Db 65 VCNFCCLLFYSKVRKRYDYVSGATLESITRKQKCDLLIRCYRCQSPLTPEBKQLHCEY 124

Qy 122 KORFHNIRGRWTGRCMSCCRSSRTRET 149
Db 125 KRRFHLAHGWTGSLGCMWRQTSREPRRS 153

Db 125 KRRFHLAHGWTGSLGCMWRQTSREPRRS 151

RESULT 18

S36527
E6 protein - human papillomavirus type 53
C:Species: human papillomavirus type 53
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36527
R:Deinze, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36527
A:Molecule type: DNA
A:Residues: 1-154 <DEU>
A:Cross-references: UNIPROT:P36815; UNIPARC:UPI00001383DE; EMBL:X74482; NID:G397046; PIDN
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 45.7%; Score 379; DB 2; Length 154;
Best Local Similarity 51.1%; Pred. No. 5.4e-29;
Matches 72; Conservative 20; Mismatches 49; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFARFDCIYVRDGNPY 60
Db 5 LFENGERRPRSLHNLSEVLLEPLDLRLSCVCKKELTAEVYNFACELKLVYRDPDFYA 64

Qy 61 AVXDCKLKFYSKISEYHNYCYVGTTLLEQYNNKPLCDLLIRCIYNKQKPLCEBEKQRLHD 120
Db 65 GVCKRCLLFYSKVRKRYDYVSGATLESITRKQKCDLLIRCYRCQSPLTPEBKQLHCD 124

Qy 121 KORFHNIRGRWTGRCMSCCR 141
Db 125 YKRRFHLAHGWTGSLGCMWRQTSREPRRS 145

Qy 121 KORFHNIRGRWTGRCMSCCR 141
Db 125 YKRRFHLAHGWTGSLGCMWRQTSREPRRS 145

RESULT 19
A44890
E6 protein - human papillomavirus type 66
C:Species: human papillomavirus type 66
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C:Accession: A44890
R:Tawheed, A.R.; Beaudenon, S.; Favre, M.; Orth, G.
J. Clin. Microbiol. 29, 2656-2660, 1991
J. Title: Characterization of human papillomavirus type 66 from an invasive carcinoma of
A:Reference number: A44890; PMID:92128556; PMID:1663515
A:Accession: A44890
A:Molecule type: DNA
A:Residues: 1-155 <TAM>
A:Cross-references: UNIPROT:Q80955; UNIPARC:UPI00001383E6
A>Note: sequence extracted from NCBI backbone (NCBI:178637, NCBI:P:78638)
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:33-69/Region: zinc finger CCCC motif
F:106-142/Region: zinc finger CCCC motif

Query Match 44.9%; Score 372.5; DB 2; Length 155;
Best Local Similarity 50.7%; Pred. No. 2.2e-28;
Matches 76; Conservative 20; Mismatches 53; Indels 1; Gaps 1;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFARFDCIYVRDGNPY 60
Db 4 IFSTQGRPRSLHNLSEVLLEPLDLRLSCVCKKELTAEVYNFACELKLVYRNNMPY 63

Qy 61 AVXDCKLKFYSKISEYHNYCYVGTTLLEQYNNKPLCDLLIRCIYNKQKPLCEBEKQRLHD 120
Db 64 AVNCVCLLFYSKVRKRYDYVSGATLESITRKQKCDLLIRCYRCQSPLTPEBKQLHCEY 123

Qy 121 KORFHNIRGRWTGRCMSCCRSSRTRETQ 150
Db 124 HKRRFHLAHGWTGSLGCMWRQTSREPRRS 152

RESULT 24

S15614
E6 protein - human papillomavirus type 2a
C/Species: human papillomavirus type 2a
A/Note: host Homo sapiens (man)
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Accession: S15614
R/Hirsch-Benam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A/Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and
A/Reference number: S15614; MUID:91188699; PMID:1964523
A/Accession: S15614
A/Molecule type: DNA
A/Residues: 1-159 <HR>
A/Cross-references: UNIPROT:P25484; UNIPARC:UPI0000164A75; EMBL:X55964
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; transforming protein; zinc finger
F:35-71/Region: zinc finger CCCC motif
F:108-144/Region: zinc finger CCCC motif

Query Match 35.8%; Score 297.5; DB 1; Length 159;
Best Local Similarity 41.7%; Pred. No. 3.2e-21;
Matches 60; Conservative 23; Mismatches 54; Indels 7; Gaps 1;

QY 9 PRKLPOLCTELQTTIHDIIECYCKOQLRREYDFAFRDLCTVYRDGNPYAVXDKCLK 68
DB 14 PRNIFLLCKEYGLELDRLICVCRALSDADVAFAIKELSVWKRKGFPGACGKCLI 73
QY 69 FYSKISEYRHVCYVGTTLLEQOYNKPLCDLLIRICINXOKPLCEBKORHLDKQRFHNI 128
DB 74 AAGKLRLQYRHMVHSCYGDVETETGPIPLQLFMRICYCHKPLSWEKXKALLVGNKRPHNI 133
QY 129 RGRWTRGCMSCRS-----SRT 145
DB 134 SGRWTHGCMNCSSCTATDPASRT 157

RESULT 25

M6WU1
E6 protein - human papillomavirus type 11
C/Species: human papillomavirus type 11
C/Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C/Accession: A03684
R/Dartmann, K.; Schwarz, E.; Giesmann, L.; zur Hausen, H.
Virology 151, 124-130, 1986
A/Title: The nucleotide sequence and genome organization of human papilloma virus type 1
A/Reference number: A94338; MUID:86181601; PMID:3008427
A/Accession: A03684
A/Molecule type: DNA
A/Residues: 1-150 <DAR>
A/Cross-references: UNIPROT:P04019; UNIPARC:UPI00001383B7; GB:M14119; NID:G333026; PIDN:
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger
F:31-67/Region: zinc finger CCCC motif
F:104-140/Region: zinc finger CCCC motif

Query Match 35.4%; Score 294; DB 1; Length 150;
Best Local Similarity 35.8%; Pred. No. 6.6e-21;
Matches 49; Conservative 33; Mismatches 55; Indels 0; Gaps 0;

QY 3 QDPERPRKLPOLCTELQTTIHDIIECYCKOQLRREYDFAFRDLCTVYRDGNPYAV 62
DB 4 KDASTSATSIQOLCKTFPLSLHTIQICVFCRNALTTETIAYAVKMLKVVWRDNFPFA 63
QY 63 XDKCLFYSKISEYRHVCYVGTTLLEQOYNKPLCDLLIRICINXOKPLCEBKORHLDDK 122
DB 64 CACCLELQKINQYRHMVHSCYGDVETETGPIPLQLFMRICYCHKPLCEIEKLGHLGK 123
QY 123 QRFNINRGRWTRGCMSC 139
DB 124 ARFTKLNNQWGRCLHC 140

RESULT 26

S36497
E6 protein - human papillomavirus type 27
C/Species: human papillomavirus type 27
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36497
R/Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36497
A/Molecule type: DNA
A/Residues: 1-159
A/Cross-references: UNIPROT:P36808; UNIPARC:UPI00001383C6; EMBL:X74473; NID:G336964; PID:
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 35.2%; Score 292; DB 2; Length 159;
Best Local Similarity 42.7%; Pred. No. 1.1e-20;
Matches 56; Conservative 21; Mismatches 54; Indels 0; Gaps 0;

QY 9 PRKLPOLCTELQTTIHDIIECYCKOQLRREYDFAFRDLCTVYRDGNPYAVXDKCLK 68
DB 14 PRNIFLLCKOYGLELDRLICVCRALSDADVAFAIKELSVWKRKGFPGACGKCLI 73
QY 69 FYSKISEYRHVCYVGTTLLEQOYNKPLCDLLIRICINXOKPLCEBKORHLDKQRFHNI 128
DB 74 AAGKLRLQYRHMVHSCYGDVETETGPIPLQLFMRICYCHKPLSWEKXKALLVGNKRPHNI 133
QY 129 RGRWTRGCMSC 139
DB 134 SGRWTHGCMQC 144

RESULT 27

S36584
E6 protein - human papillomavirus type 7
C/Species: human papillomavirus type 7
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36584
R/Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36584
A/Molecule type: DNA
A/Residues: 1-154
A/Cross-references: UNIPROT:P36800; UNIPARC:UPI00001383B3; EMBL:X74463; NID:G3397060; PIDN:
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 35.0%; Score 290.5; DB 2; Length 154;
Best Local Similarity 37.1%; Pred. No. 1.5e-20;
Matches 53; Conservative 30; Mismatches 57; Indels 3; Gaps 1;

QY 10 RKLPLCTELQTTIHDIIECYCKOQLRREYDFAFRDLCTVYRDGNPYAVXDKCLK 69
DB 10 RTLELDCQCNITLPTQINICFNSILQTAEVAFRFLYVWRNDPFAACVCKLEF 69
QY 70 YSKISEYRHVCYVGTTLLEQOYNKPLCDLLIRICINXOKPLCEBKORHLDDKQRFHNI 129
DB 70 YGKVNQYRNPYAVAPVTEETGLTILEYRIRCCKCHKPLSPVEKTNHIVKTOFFRLQ 129
QY 130 GRWTRGCMSC--CRSSRTRET 149
DB 130 DSWTGYCLHCKMKCKEGRSSET 152

RESULT 28

S36555
E6 protein - human papillomavirus type 40

```

C:Species: human papillomavirus type 40
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36555
R:Delius, H.; Holmann, B.
A:Submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36555
A:Molecule type: DNA
A:Residues: 1-154 <DEL>
A:Cross-references: UNIPROT:P36812; UNIPARC:UPI00001383D3; EMBL:X74478; NID:g397014; PIR
C:Superfamily: Papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match          34.8%; Score 288.5; DB 2; Length 154;
Best Local Similarity 37.1%; Pred. No. 2.3e-20;
Matches 53; Conservative 29; Mismatches 58; Indels 3; Gaps 1;

Oy      10 RKLPOLCTELQTTIHDIILBCVYCKQOLLRREVDFAFRDLCIYYRDGNPYAVXDKCLKF 69
       11 :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      10 RTVLVELCDQCQNITPLTLDICVFCKTVKTAEVLAFARELIVYWRDDFPFAACPRCLD 69
       11 :|::||::||::||::||::||::||::||::||::||::||::||::||::||:

Oy      70 YSKISEYRHVCYSYGTTLEQQYNKPCLDLLIRCLNOKPCLCPBEKQRHLDKKORFNHR 129
       71 :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      70 HGKNQNYNRPYAVALPAVPVEETGTLTIQVIRCCCKHPSPVEKTNHVIKTKQPFRLK 129
       71 :|::||::||::||::||::||::||::||::||::||::||::||::||::||:

Oy      130 GRWTGRCMS---CRSRTRRRET 149
       131 |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      130 DSWTGTCYLCMKKKCKMEKGQRSET 152
       131 |||||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 29
W6M1C1
E6 protein - pygmy chimpanzee papillomavirus (type 1)
C:Species: pygmy chimpanzee papillomavirus
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jul-1999
C:Accession: A36818
R:van Ranst, M.; Fuse, A.; Filten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Odenakker, G.
A>Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compar
A:Reference number: A42955; MUID:92391075; PMID:1325697
A:Accession: A36818
A:Molecule type: DNA
A:Residues: 1-150 <VAN>
A:Cross-references: UNIPARC:UPI00001383BD; EMBL:X62844; NID:961010; PIDN:CAA4655.1; PIR
C:Superfamily: Papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:31-67/Region: zinc finger CCCC motif
F:104-140/Region: zinc finger CCCC motif

Query Match          34.7%; Score 288; DB 1; Length 150;
Best Local Similarity 38.3%; Pred. No. 2.5e-20;
Matches 51; Conservative 28; Mismatches 54; Indels 0; Gaps 0;

Oy      10 RKLPOLCTELQTTIHDIILBCVYCKQOLLRREVDFAFRDLCIYYRDGNPYAVXDKCLKF 69
       11 :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      11 KTIIDLCKECNLCHMSIQILCVFCRKLTSTREVAIFQKDINLYWGFFPAACACCLEI 70
       12 :|::||::||::||::||::||::||::||::||::||::||::||::||::||:

Oy      70 YSKISEYRHVCYSYGTTLEQQYNKPCLDLLIRCLNOKPCLCPBEKQRHLDKKORFNHR 129
       71 :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      71 QGKNQNYNRPYAVALPAVPVEEINKSPIDVAIRCYLCHKPLCDYEKRLHIIEKARFIKLN 130
       72 :|::||::||::||::||::||::||::||::||::||::||::||::||::||:

Oy      130 GRWTGRCMSCCRS 142
       131 |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      131 CEWKGRCFHCWTS 143
       131 |||||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 30
S36509
E6 protein - human papillomavirus type 32
C:Species: human papillomavirus type 32
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36509

```

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R.Dellus, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A.Description: Primer-directed sequencing of human papillomavirus types.  
A.Reference number: S36463  
A.Accession: S36509  
A.Molecule type: DNA  
A.Residues: 1-142 <DEL>  
A.Cross-references: UNIPROT:P36810; UNIPARC:UP100001383CC; EMBL:X74475; NID:g396981; PIDB:  
C.Superfamily: papillomavirus B6 protein  
C.Keywords: DNA binding; early protein; nucleus; zinc finger
```

Query Match 34.1%; Score 283; DB 2; Length 142;

Best Local Similarity 40.9%; Pred. No. 7e-20;

Matches 54; Conservative 22; Mismatches 56; Indels 0; Gaps 0;

```
Oy      8 RRRKLPOLCTELQTTIHDLILCEVCYCKOQLRREVDFAFRDLCIVRDGNPYAVXKCL 67  
       :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db     9 QSTLYOLCKDKGLTIRNLQICIWCKNHLTSAAVAHYMKDXLVVKKGFPPYAACFCL 68  
  
Oy    68 KFYSLSEAYRYHCYSVGVTLEEQYNKPPLCDLLIRCINMXKPLCPBEKHRLDKORFHNN 127  
       ::::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db   69 EFYSKVCALRHVRDSAFMTHTVEGETGILLLEEQTIFCALIQKPLSPSKDHIIYGRHRPRF 128  
  
Oy    128 ITRGWTCRCMSC 139  
       |||||||  
Db   129 ILNRWTCRCTQC 140
```

RESULT 31

KEMLI3

B6 protein - human papillomavirus type 13

C.Species: human papillomavirus type 13

A.Note: host Homo sapiens (man)

C.Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C.Accession: A42955

R.van Ranst M.; Fuse, A.; Filten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Odenakker, G.

Virology 190, 587-596, 1992

A>Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compar-

A.Reference number: A42955; MID:D:92391075; PMID:1325697

A.Accession: A42955

A.Molecule type: DNA

A.Residues: 1-150 <VAN>

A.Cross-references: UNIPROT:Q0Z269; UNIPARC:UPI00001383B9; EMBL:X62843; NID:g60295; PIDN:

C.Superfamily: papillomavirus B6 protein

C.Keywords: DNA binding; early protein; transforming protein; zinc finger

F.31-67/Region: zinc finger CCCC motif

F.104-140/Region: zinc finger CCCC motif

Query Match 32.9%; Score 273; DB 1; Length 150;

Best Local Similarity 36.8%; Pred. No. 6.e-19;

Matches 49; Conservative 29; Mismatches 55; Indels 0; Gaps 0;

```
Oy      10 RKLPOLCTELQTTIHDILIIECYCKOQLRREVDFARFDLCIVRDGNPYAVXDCLKLF 69  
       :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db     11 KIIDLCKECNMWSMLQILCVFCRKLTSTAETVARFQYKSLEYVMRGQPFPALACCILEI 70  
  
Oy    70 YKSISEYRYHCYSVGVTLEEQYNKPPLCDLLIRCINMXKPLCPBEKHRLDKORFHNNIR 129  
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db   71 QCKIKNQRFHFDDAGVFATVEDTKOSILDVLIRCYLCHKPICEVKLRHLQKRFTKLNN 130  
  
Oy    130 GRWTGCRCMSCCR 142  
       |||||||  
Db   131 SSWKGRCFHCWSS 143
```

RESULT 32

M6MIA2

B6 protein - human papillomavirus type 42

C.Species: human papillomavirus type 42

A>Note: host Homo sapiens (man)

C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C.Accession: E39451

R.Philipp, W.; Honore, N.; Sapp, M.; Cole, S.T.; Strebeck, R.E.


```

Qy      9 PRKLPLCTELQTTIHDIIECVYCKQQLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK 68
Db      24 PATTDLAALFIPDDCLVPCNFCGNFLTYLEIEFEPEKSLIMKYLTVYACCCCT 83
Qy      69 FYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKORHLDKQRFNI 128
Db      84 ATATFEFNEFESYVTGRIEDVTGKSIFFDIDVRQCTCMKTLDAIEKLDICORRRPFLTV 143
Qy      129 RGRWTRGCMSC 139
Db      144 RGSWKGICRLC 154

RESULT 41
S28510
E6 protein - multimammate rat papillomavirus (fragment)
C/Species: multimammate rat papillomavirus
C/Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C/Accession: S28510; S22956
R:van Ranst, M.A.
submitted to the EMBL Data Library, April 1992
A/Reference number: S28509
A/Accession: S28510
A/Molecule type: DNA
A/Residues: 1-207 <VAN>
A/Cross-references: UNIPROT:P30735; UNIPARC:UPI00001383BA; EMBL:X65201; NID:g60575; PIDN
A/Note: the source is designated as Mastomys natalensis papillomavirus
R:van Ranst, M.; Tachezy, R.; Pruss, J.; Burk, R.D.
Nucleic Acids Res. 20, 2889, 1992
A/Title: Primary structure of the E6 protein of Microvirus minutus papillomavirus and Mast
A/Reference number: S22955; MUID:92310995; PMID:1319576
A/Accession: S22956
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 77-204 <VAN2>
A/Cross-references: UNIPARC:UPI0000178416; EMBL:X65201
A/Note: the source is designated as Mastomys natalensis papillomavirus
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; nucleus; zinc finger
F:95-171/Region: zinc finger C3HC4 motif

Query Match      15.6%; Score 129.5; DB 2; Length 207;
Best Local Similarity 22.1%; Pred. No. 4.2e-05;
Matches 32; Conservative 26; Mismatches 54; Indels 33; Gaps 3;

Qy      17 TELQTTIH-----DIIECVYCKQQLRREVYDFAFRDLCIVYRDGNPYAVXDK 65
Db      71 SRMRVYHSFVERLGIPELDLLPCTFCRSFLTOELTAFPFSAPFLVWGRGCAHICTA 130
Qy      66 CLKFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLL-----IRICINXQKPLCPBE 114
Db      131 CARCAASLDLFLH-----QNSRPLADYARDENLTLHGAKACRYCMKLTSTTE 179
Qy      115 KQRLDKKQRFHNI RGRWTRGCMSC 139
Db      180 KLECAERGESFAKVGQWRARCRIC 204

RESULT 42
S36473
E6 protein - human papillomavirus type 15
C/Species: human papillomavirus type 15
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36473
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A/Description: primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36473
A/Molecule type: DNA
A/Residues: 1-141 <DEL>
A/Cross-references: UNIPROT:P36804; UNIPARC:UPI00001383BB; EMBL:X74468; NID:g396924; PID

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C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match      15.5%; Score 128.5; DB 2; Length 141;
Best Local Similarity 27.1%; Pred. No. 3.6e-05;
Matches 36; Conservative 25; Mismatches 71; Indels 1; Gaps 1;

Qy      8 PRKLPLCTELQTTIHDIIECVYCKQQLRREVYDFAFRDLCIVYRDGNPYAVXDKC 66
Db      5 KPFVQQLADTLCLPVDIILPCRCQRFPLYIELVSLNKGQDLITWTEBDFVACSSC 64
Qy      67 LKFSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKORHLDKQRFH 126
Db      65 AFATAQEFNSFNFQSVSWIEIVEQKPVGDIIIRCKFCIKLIDLEKIDICYBERQFH 124
Qy      127 NIRGRWTRGCMSC 139
Db      125 KVRNWKGLCRHC 137

RESULT 43
I56705
E6 protein - human papillomavirus type 18
C/Species: human papillomavirus type 18
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I56705
R:Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.; Sugimura,
J. Virol. 62, 1640-1646, 1988
A/Title: Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in He
A/Reference number: I56705; MUID:88188247; PMID:2833614
A/Accession: I56705
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-57 <RES>
A/Cross-references: UNIPROT:Q90133; UNIPARC:UPI00000EDDSF; GB:M20324; NID:g183933; PIDN:
C/Superfamily: papillomavirus E6 protein

Query Match      15.3%; Score 127; DB 2; Length 57;
Best Local Similarity 58.5%; Pred. No. 2.1e-05;
Matches 24; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy      2 FQDPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREV 42
Db      4 FEDPTRRPRYKLPDLCTELMTSLQDIETCYVCKTVLTLTEV 44

RESULT 44
W6WLRB
E6 protein - cottontail rabbit papillomavirus
C/Species: cottontail rabbit papillomavirus
C/Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 16-Feb-1997
C/Accession: A03686
R:Girtl, I.; Danos, O.; Yaniv, M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985
A/Title: Genomic structure of the cottontail rabbit (Shope) papillomavirus.
A/Reference number: A94027; MUID:8516175; PMID:2984661
A/Accession: A03686
A/Molecule type: DNA
A/Residues: 1-273 <GIR>
A/Cross-references: UNIPARC:UPI0000000953
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger

Query Match      15.3%; Score 127; DB 1; Length 273;
Best Local Similarity 26.4%; Pred. No. 9.5e-05;
Matches 37; Conservative 21; Mismatches 68; Indels 14; Gaps 4;

Qy      9 PRKLPLCTELQTTIHDIIECVYCKQQLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK 68
Db      6 PRSLEKIQOIIQISLEDPFCGICRGLTGAERQLFKCTGLCTVHWKGMVGTGRDCTV 65
Qy      69 FYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRICINXQKPLCPBE---KQRH-----L 119

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Db 66 LSCALDYCHLALAPALBAALVGEISSWFRCTVCGRRLLTPEKIELBARNCITLCT 125

Qy 120 DKXQRFHNRGRWTCMSC 139

Db 126 DKQGYF-----QWRGHCSSC 140

RESULT 45

S36538 E6 protein - human papillomavirus type 12

C/Species: human papillomavirus type 12

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: S36538

R/Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36538

A/Molecule type: DNA

A/Residues: 1-157

A/Cross-references: UNIPROT:P36803; UNIPARC:UPI00001383B8; EMBL:X74466; NID:G396910; PII

C/Superfamily: papillomavirus B6 protein

C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 14.8%; Score 123; DB 2; Length 157;
Best Local Similarity 27.1%; Pred. No. 0.00014;
Matches 36; Conservative 18; Mismatches 79; Indels 0; Gaps 0;

7 ERPRKLPTCLTQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTVYRDGNFYAVXDKC 66

16 ELPTTIELADLDIPLVDLCVPCNFCGKPLDFEVCDFDKKQTLTWKGFVTRACRSC 75

Qy 67 LKEYSKISEYRHYCVSYGTTLEQOYNKPLCDLLIRICINXOKPLCPEBKQRHLDDKKQRF 126

Db 76 CAATAIYEFNEFVYQOTVLGRDIEIATGKISIFDLKIRQCOTCLSFDTTEKLDSCGRGPFH 135

Qy 127 NNRGRWTCMSC 139

Db 136 KVRDRWKGICRQC 148

RESULT 46

S36485 E6 protein - human papillomavirus type 19

C/Species: human papillomavirus type 19

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: S36485

R/Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36485

A/Molecule type: DNA

A/Residues: 1-166

A/Cross-references: UNIPROT:P36806; UNIPARC:UPI00001383BD; EMBL:X74470

C/Superfamily: papillomavirus B6 protein

C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 14.8%; Score 123; DB 2; Length 166;
Best Local Similarity 24.4%; Pred. No. 0.00014;
Matches 33; Conservative 24; Mismatches 75; Indels 0; Gaps 0;

9 PRKLPTCLTQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTVYRDGNFYAVXDKC 68

Db 29 PATIAGLAALIEIPLDCLVPCNFCGKFLSHLEACEFDDKRLSLTWKGLVYACRCWCCT 88

Qy 69 FYKISISEYRHYCVSYGTTLEQOYNKPLCDLLIRICINXOKPLCPEBKQRHLDDKKQRFHNI 128

Db 89 ATATFEENEFEHTVGTGEIEFVTGKSVFDIDVRCQNCMRYLDSIEKLDICGRRLPFHKV 148

Qy 129 RGRWTCMSC 139

Db 149 RDSWKGICRQC 159

RESULT 47

S36590

E6 protein - human papillomavirus type 9

C/Species: human papillomavirus type 9

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: S36590

R/Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36590

A/Molecule type: DNA

A/Residues: 1-148

A/Cross-references: UNIPROT:P36801; UNIPARC:UPI00001383B5; EMBL:X74464; NID:G397068; PII

C/Superfamily: papillomavirus B6 protein

C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 14.6%; Score 121.5; DB 2; Length 148;
Best Local Similarity 24.6%; Pred. No. 0.00018;
Matches 33; Conservative 31; Mismatches 67; Indels 3; Gaps 3;

8 RPRKLPTCLTQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTVYRDGNFYAVXDKC 66

Db 12 KPRVIELADTLVPLDILIPCKFCRFLSYFELNFDHKQLDTTEEDLVYGLCSSC 71

Qy 67 LKEYSKISEYRHYCVSYGTTLEQOYNKPLCDLLIRICINXOKPLCPEBKQRHLDDKKQRF 125

Db 72 -AVASQLEFTHFQFAVVGKDIEVGTAGTAINICIRCYCFKLLDVEKLTATCYKFEQF 130

Qy 126 NNRGRWTCMSC 139

Db 131 YKVNWSWKGICRHC 144

RESULT 48

W6MLEB

E6 protein - bovine papillomavirus type 1

C/Species: bovine papillomavirus type 1

C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004

C/Accession: C18151

R/Chen, E.Y.; Howley, P.M.; Levinson, A.D.; Seeburg, P.H.

Nature 299, 529-534, 1982

A/Title: The primary structure and genetic organization of the bovine papillomavirus typ

A/Reference number: A93289; PMID:83012974; PMID:6289124

A/Accession: C18151

A/Molecule type: DNA

A/Residues: 1-137 <CHE>

A/Cross-references: UNIPROT:P06931; UNIPARC:UPI0000033CF0; GB:X02346; GB:J02044; GB:M246

R/Danos, O.; Engel, L.W.; Chen, E.Y.; Yaniv, M.; Howley, P.M.

J. Virol. 46, 557-566, 1983

A/Title: Comparative analysis of the human type 1a and bovine type 1 papillomavirus geno

A/Reference number: A92993; PMID:83189357; PMID:6302319

A/Contents: annotation

R/Androphy, E.J.; Schiller, J.T.; Lowy, D.R.

Science 230, 442-445, 1985

A/Title: Identification of the protein encoded by the B6 transforming gene of bovine pap.

A/Reference number: A94282; PMID:86018841; PMID:2996134

A/Contents: annotation; identification of the protein

C/Comment: This protein is present in the cell nucleus and the cellular membrane.

C/Superfamily: papillomavirus B6 protein

C/Keywords: DNA binding; early protein; transforming protein; zinc finger

Query Match 14.3%; Score 119; DB 1; Length 137;
Best Local Similarity 28.9%; Pred. No. 0.00029;
Matches 35; Conservative 16; Mismatches 68; Indels 2; Gaps 2;

Qy 28 LECYCKQQLRREYVDFAFRDLCTVYRDGNFYAVXDKCLKFYSKISEYRHYCVSYGTT 87

Db 15 LDCIMCREPLTEVDFACWYKDFHVVIRGCRGACTICLNCIATERRLMOGVPTVGE 74

Qy 88 LEOQYNKPLDILLIRICINXOKPLCPEBKQRHLDDKKQRFHNRGR-WTGRGMSCCR-SSRT 145

Db 75 AELHAGKLDLRCRCVCGSKLTNMEGRHVLFNPEPCRTANIRRCVDCCHGRS 134
Oy 146 R 146
Db 135 K 135

RESULT 49

W6WL47
E6 protein - human papillomavirus type 47
C/Species: human papillomavirus type 47
A/Note: host Homo sapiens (man)
C/Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C/Accession: A35324
R/Kiyono, T.; Adachi, A.; Iehibashi, M.
Virology 177, 401-405, 1990
A/Title: Genome organization and taxonomic position of human papillomavirus type 47 infe
A/Reference number: A35324; MUID:90281611; PMID:2162112
A/Accession: A35324
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-156 <K1Y>
A/Cross-references: UNIPROT:P22422; UNIPARC:UPI00001383D9; GB:M32305; NID:G333062; PIDN:
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; transforming protein; zinc finger
F:40-76/Region: zinc finger CCCC motif
F:113-149/Region: zinc finger CCCC motif

Query Match 14.3%; Score 119; DB 1; Length 156;
Best Local Similarity 24.8%; Pred. No. 0.00032;

Matches 34; Conservative 23; Mismatches 80; Indels 0; Gaps 0;

Oy 3 QDPERPRKLPOLCTELQTTIHDIIEGVCKQQLREVVDFAFRDLCTVYRGNPYAV 62
Db 13 EEKLELPTTIGLQQLDIPVDCILPCNFCGRFDYLVCEFPDYKLTLLWKDYSVAC 72
Oy 63 XDCKLKFYSKISEVRYHCYSVYGTLEQYNNKPLCDLLIRCIINXQKPLCPREKORHLDK 122
Db 73 CRLCSATATYEFNVFYQYVGLGRDIELATGSLFEIDIRCHTCLSPFIDIEKLDSCGRG 132
Oy 123 QRFNIRGRWTRCMSG 139
Db 133 LPFHKVRNWKGVCRQC 149

RESULT 50

W6WL8
E6 protein - human papillomavirus type 8
C/Species: human papillomavirus type 8
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C/Accession: A03685
R/Fuchs, P.G.; Ittner, T.; Weninger, J.; Pfister, H.
J. Virol. 58, 626-634, 1986
A/Title: Epidermodyplasia verruciformis-associated human papillomavirus 8: genomic sequ
A/Reference number: A93019; MUID:86200410; PMID:3009874
A/Accession: A03685
A/Molecule type: DNA
A/Residues: 1-155 <FUC>
A/Cross-references: UNIPROT:P06428; UNIPARC:UPI00001383B4; GB:M12737; NID:G333074
A/Note: this ORF is not annotated in GenBank entry PPH8CG
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger
F:39-75/Region: zinc finger CCCC motif
F:112-148/Region: zinc finger CCCC motif

Query Match 14.2%; Score 118; DB 1; Length 155;
Best Local Similarity 25.0%; Pred. No. 0.0004;

Matches 34; Conservative 27; Mismatches 69; Indels 6; Gaps 3;

Oy 7 ERPRKLPOLCTELQTTIHDIIEGVCKQQLREVVDFAFRDLCTVYRGNPYAVXD-- 64
Db 16 ELPSITKELAAALGIPLDSCVPCNFCNFDPELCEFDKRLCLIKWN--YVVTACC 72

Oy 65 KCLKFYSKISEY-RHYCYSVYGTLEQYNNKPLCDLLIRCIINXQKPLCPREKORHLDKQ 123
Db 73 RCCCVATATFEFNVFYQYVGLGRDIELATGSLFEIDVRKCNCLSPFIDIEKLDCCGR 132
Oy 124 RFNIRGRWTRCMSG 139
Db 133 PFHKVRNWKGVCRQC 148

RESULT 51

W6WL5
E6 protein - human papillomavirus type 5b
C/Species: human papillomavirus type 5b
A/Note: host Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: E40480
R/Yabe, Y.; Sakai, A.; Hishimoto, T.; Kato, H.; Ogura, H.
Virology 183, 793-798, 1991
A/Title: A subtype of human papillomavirus 5 (HPV-5b) and its subgenomic segment amplifi
A/Reference number: A40480; MUID:91306467; PMID:1649510
A/Accession: E40480
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-157 <YAB>
A/Cross-references: UNIPROT:P26556; UNIPARC:UPI00000060C6; GB:D90252; NID:G222395; PIDN:
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger
F:41-77/Region: zinc finger CCCC motif
F:114-150/Region: zinc finger CCCC motif

Query Match 14.0%; Score 116; DB 1; Length 157;
Best Local Similarity 24.8%; Pred. No. 0.00063;

Matches 34; Conservative 22; Mismatches 81; Indels 0; Gaps 0;

Oy 3 QDPERPRKLPOLCTELQTTIHDIIEGVCKQQLREVVDFAFRDLCTVYRGNPYAV 62
Db 14 KDKALEPSTIRDLAETIGIPLDICIPNFCGRFLNVLNCEFPDYKLSLWKDYCVFAC 73
Oy 63 XDCKLKFYSKISEVRYHCYSVYGTLEQYNNKPLCDLLIRCIINXQKPLCPREKORHLDK 122
Db 74 CRVCCGATATYEFNVFYQYVGLGRDIELAGSLFIDIRCHTCLAFDLIEKLDCCGRG 133
Oy 123 QRFNIRGRWTRCMSG 139
Db 134 LPFHKVRNWKGVCRQC 150

RESULT 52

W6WL5
E6 protein - human papillomavirus type 5
C/Species: human papillomavirus type 5
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Feb-1997
C/Accession: F26277
R/Zachow, K.R.; Ostrow, R.S.; Paras, A.J.
Virology 158, 251-254, 1987
A/Title: Nucleotide sequence and genome organization of human papillomavirus type 5.
A/Reference number: A94360; MUID:87207670; PMID:3033892
A/Accession: F26277
A/Molecule type: DNA
A/Residues: 1-157 <ZAC>
A/Cross-references: UNIPARC:UPI000017495B
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger
F:41-77/Region: zinc finger CCCC motif
F:114-150/Region: zinc finger CCCC motif

Query Match 13.6%; Score 113; DB 1; Length 157;
Best Local Similarity 24.1%; Pred. No. 0.0012;

Matches 33; Conservative 22; Mismatches 82; Indels 0; Gaps 0;

Oy 3 QDPERPRKLPOLCTELQTTIHDIIEGVCKQQLREVVDFAFRDLCTVYRGNPYAV 62
Db 16 ELPSITKELAAALGIPLDSCVPCNFCNFDPELCEFDKRLCLIKWN--YVVTACC 72

Db 14 KDKAEPLSLRDLAEAGIPVLDCLIPCNFGNPLNTLAECEPHYKRLSLIMKDYCVFAC 73
 QY 63 XDKCLKFYSKISEYRHYCYSVYGTTLLEQYNNKPLCDLLIRNCINXQKPLCPEEKQRHLDDK 122
 Db 74 CRVCCGATATAYEFQYEQVTLGRDIELASGLSIFDIDIRQCOTLAFLDIETKLDCCGRG 133
 QY 123 QRFNINRGWRGRCMSC 139
 Db 134 LPFHKVRNWKIGICRQC 150

RESULT 53

S28509
 E6 protein - Old World harvest mouse papillomavirus (fragment)

C/Species: Old World harvest mouse papillomavirus
 C/Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
 C/Accession: S28509; S22955
 R:van Ranst, M.A.
 Submitted to the EMBL Data Library, April 1992
 A/Reference number: S28509
 A/Accession: S28509
 A/Molecule type: DNA
 A/Residues: 1-154 <VAN>
 A/Cross-references: UNIPROT:P30734; UNIPARC:UPI0000170F1E; EMBL:X65200; NID:G60571; PIDN
 A/Note: the source is designated as Microgms minutus papillomavirus
 R:van Ranst, M.; Tachezy, R.; Fruse, J.; Burk, R.D.
 Nucleic Acids Res. 20, 2889, 1992
 A/Title: Primary structure of the E6 protein of Microgms minutus papillomavirus and Mast
 A/Reference number: S22955; MUID:92310995; PMID:1319576
 A/Accession: S22955
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 20-147 <VAN2>
 A/Cross-references: UNIPARC:UPI0000178417; EMBL:X65200
 A/Note: the source is designated as Microgms minutus papillomavirus
 C/Superfamily: papillomavirus E6 protein
 C/Keywords: DNA binding; early protein; zinc finger
 F:38-74/Region: zinc finger
 F:11-147/Region: zinc finger

Query Match 10.4%; Score 86; DB 2; Length 154;
 Best Local Similarity 23.2%; Pred. No. 0.45;
 Matches 35; Conservative 19; Mismatches 75; Indels 22; Gaps 6;
 QY 5 PQ-ERPKRLPOLCTE-----LQTTIDHILIECYCKQQLIRREYDFAFDLCTIV 54
 Db 3 PQPRPYPSPMELCREYTLBQLKFLANTLDTLMPCHFCSSPMDLNKASYLAQQLKVIY 62
 QY 55 RDGNPVAVXDKCLKFYKISFYRHYCVS---YGTTLLEQYNNKPLCDLLIRNCINXQKPLC 111
 Db 63 KD---CCFKGACIKRRRLAFAEROKYQVCGEADLVEAVGVSHVINTLVACSECLALLT 119
 QY 112 PEKQRHLDDK---QRFNINRGWRGRCMSC 139
 Db 120 ASEK---LDAKCEIQTFLIVHMRRTSCRAC 147

RESULT 54

W6WLDP

E6 protein - deer papillomavirus

C/Species: deer papillomavirus
 C/Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
 C/Accession: A03687
 R:Groff, D.B.; Lancaster, W.D.
 J. Virol. 56, 85-91, 1985
 A/Title: Molecular cloning and nucleotide sequence of deer papillomavirus.
 A/Reference number: A93013; MUID:85293253; PMID:2993669
 A/Accession: A03687
 A/Molecule type: DNA
 A/Residues: 1-135 <GRO>
 A/Cross-references: UNIPROT:P03128; UNIPARC:UPI0000183JB; GB:M11910; NID:G333021; PIDN:
 C/Superfamily: papillomavirus E6 protein
 C/Keywords: DNA binding; early protein; zinc finger

Query Match 10.1%; Score 83.5; DB 1; Length 135;
 Best Local Similarity 28.6%; Pred. No. 0.68;
 Matches 34; Conservative 17; Mismatches 57; Indels 11; Gaps 4;

QY 28 LECYCKQQLLR---REYDFAFDLCTIVYRDGNPVAVXDKCLKFYKISFYRHYCVSV 84
 Db 9 LYCVFCYVLGKFKEARCYDKIR--TVVRGLRCVACTACLEKGLYLERVLANAPQPV 65
 QY 85 GTTLEQ--QYNNKPLCDLLIRNCINXQKPLCPEEKQRHLDDKQRFNINRGWRGRCMSCR 141
 Db 66 QGSIEBDDPFIQKAC--IRCMVCGGILTRDEKDRHRYPBELYVIFRNOVLGRCYCTCR 121

RESULT 55

S19906
 E6-II protein - human papillomavirus type 33 (fragment)

C/Species: human papillomavirus type 33
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C/Accession: S19906
 R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me
 submitted to the EMBL Data Library, January 1992
 A/Description: HPV type 33 in a consillar carcinoma generates its putative E7 mRNA via t
 A/Reference number: S19906
 A/Accession: S19906
 A/Molecule type: mRNA
 A/Residues: 1-32 <SNT>
 A/Cross-references: UNIPROT:Q81885; UNIPARC:UPI00000F932A; EMBL:X64086; NID:G60282; PIDN
 C/Superfamily: papillomavirus E6 protein
 C/Keywords: early protein

Query Match 10.0%; Score 83; DB 2; Length 32;
 Best Local Similarity 59.3%; Pred. No. 0.19;
 Matches 16; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 15 LCTELQTTIDHILIECYCKQQLLRRE 41
 Db 3 LQALLETTHINIELQVCECKKPLORSE 29

RESULT 56

S19909
 E6-III protein - human papillomavirus type 33 (fragment)

C/Species: human papillomavirus type 33
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C/Accession: S19909
 R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me
 submitted to the EMBL Data Library, January 1992
 A/Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via t
 A/Reference number: S19906
 A/Accession: S19909
 A/Molecule type: mRNA
 A/Residues: 1-35 <SNT>
 A/Cross-references: UNIPROT:Q81887; UNIPARC:UPI00000EBD75; EMBL:X64087; NID:G60286; PIDN
 C/Superfamily: papillomavirus E6 protein
 C/Keywords: early protein

Query Match 10.0%; Score 83; DB 2; Length 35;
 Best Local Similarity 59.3%; Pred. No. 0.21;
 Matches 16; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 15 LCTELQTTIDHILIECYCKQQLLRRE 41
 Db 3 LQALLETTHINIELQVCECKKPLORSE 29

RESULT 57

S23825
 E6-I protein - human papillomavirus type 33 (fragment)

C/Species: human papillomavirus type 33
 C/Date: 20-Feb-1995 #sequence_revision 20-Jan-1998 #text_change 09-Jul-2004
 C/Accession: S23825; S23829
 R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me

Db 535 YKC 537

RESULT 61

S11515
formin - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C/Accession: S11515

R/Moychik, R.P.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.

Nature 346, 850-853, 1990

A:Title: 'Formin': proteins deduced from the alternative transcripts of the limb deform

A:Reference number: S11515; MUID:90363291; PMID:2352150

A/Accession: S11515

A/Molecule type: mRNA

A/Residues: 1-1468 <NOY>

A/Cross-references: UNIPROT:Q05860; UNIPARC:UPI0000027927; EMBL:X53599; NID:g52877; PIDN

Query Match 9.3%; Score 77.5; DB 2; Length 1468;

Best Local Similarity 27.4%; Pred. No. 25;

Matches 34; Conservative 14; Mismatches 47; Indels 29; Gaps 5;

QY CTEIQTTHDIIIECVCKQQLRREYVDFAFRDLCTIVRDGNPYAVXDKLKFYSKISE 75

Db 6 CT-LQ--LHNPIALCYISFYLPRKGVGRGFSYKGTVTLDRSNNAF----- 47

QY 76 YRHYSYVVG---TTLEQYNRPLCDLLIRCLNXQKPL-----CPBEKORHLDKORFH 126

Db 48 --NHCVQVRBPDTISLQGFENHPGDIFFKQPTKNTLTYLTKAEKERLDSLRS 105

QY 127 NING 130

Db 106 NILG 109

RESULT 62

T09483
Cys-rich protein RAMP - human

C:Species: Homo sapiens (man)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C/Accession: T09483

R/Smedley, D.P.; Hamoudi, R.; Clark, J.; Warren, W.; Abdul-Rauf, M.; Somers, G.; Venter,

submitted to the EMBL Data Library, November 1997

A:Description: RAMP, a novel gene encoding a Cys-rich protein.

A/Reference number: Z16688

A/Accession: T09483

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-699 <SME>

A/Cross-references: UNIPARC:UPI0000169706; EMBL:AF035374; NID:g2665702; PID:g2665703

C/Genetics:

A:Gene: RAMP

A/Map position: 13q11-12

Query Match 9.3%; Score 77; DB 2; Length 699;

Best Local Similarity 22.2%; Pred. No. 14;

Matches 37; Conservative 17; Mismatches 49; Indels 64; Gaps 10;

QY 25 DIIIECVCKQQLLR-----EYVDFAFRDLCTIVRDGNPYAVXDKLKFYSKISE 76

Db 362 DIQKYNCKNSPFCSEKPEILEWENKHQFCCK-----TCSDDYKXLAHI 405

QY 77 RHVC-YGVYGTLEQYR-----KPLCD-----LIRCT--NXQKPLCPBE 114

Db 406 VTVEYECOEKKTLEHTVNFSGVKRPFSEGCGLYKODFARLGLRCVTCYCSQLCKG 465

QY 115 KQRLDKK-----QRFNIRGRW---TGRCMSCRSSTRRE 148

Db 466 ATKELDGVVRDPCSEDCCKKFD---WYKPARC-DCKSKQTLKE 507

RESULT 63

S44810

F44B9.7 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997

C/Accession: S44810

R/Antonacci-Fulton, L.

submitted to the EMBL Data Library, September 1993

A:Description: Sequence of the C. elegans cosmid F44B9.

A/Reference number: S44807

A/Accession: S44810

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-400 <ANT>

A/Cross-references: UNIPARC:UPI000017B6C2; EMBL:L23648; NID:g388585; PID:g388589

C/Genetics:

A:Insertions: 49/2; 124/3; 188/3; 233/2; 274/2; 321/1; 358/2

Query Match 9.2%; Score 76; DB 2; Length 400;

Best Local Similarity 17.2%; Pred. No. 10;

Matches 27; Conservative 35; Mismatches 57; Indels 38; Gaps 4;

QY 4 DPERPRKLPQ-----LCTELQTHDIIIECVCK--QQLRREYVDFAFR 48

Db 196 EPOSHIESFOKETNLEKYSTGEICLYRELVNDLVNKTSTYLSLTKVMERKPLN--- 251

QY 49 DLCTVARDGNPYAVXDKLKFYSKISYRHYCVSVGTLEQYNRPLCDLLIRCLNXQK 108

Db 252 -----QGENPNDLADCKNALQRMDSIRQIIEKRREPTKRMGTGEDYIELMLDSELUK 305

QY 109 PLCEBKORHLDKORFNI-----RGW 132

Db 306 PMDERQKRAELEQRALVISTPPVESHGWQKW 342

RESULT 64

S71522
outer dense fiber protein 2 - human

C:Species: Homo sapiens (man)

C>Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004

C/Accession: S71522; I38074

R/Hoffeibert, S.; Burfield, P.; Hoyer-Fender, S.; Lange, R.; Haidl, G.; Engel, W.

Hum. Mol. Genet. 2, 2167-2170, 1993

A:Title: A homozygous deletion of 27 basepairs in the coding region of the human outer d

A/Reference number: I38074; MUID:94154698; PMID:8111388

A/Accession: S71522

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-250 <HOF>

A/Cross-references: UNIPROT:Q14990; UNIPARC:UPI0000130BD2; EMBL:X74614; NID:g474425; PID

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1993

C/Genetics:

A:Gene: ODF2

A/Map position: 8

A:Insertions: 107/2

C/Function:

A:Description: provides the sperm tail with stabilizing and zinc binding properties

A>Note: one of the main component of the sperm tail

Query Match 9.1%; Score 75.5; DB 2; Length 250;

Best Local Similarity 27.5%; Pred. No. 7.1;

Matches 33; Conservative 14; Mismatches 36; Indels 37; Gaps 7;

QY 40 REYVDFAFRDLCTIVRDGNPYAVXD-----KCLKFYSKISYRHYCVSVGTLEQYNR 94

Db 26 RCIDFSTRCLCDLYM--HPYCCDLHPYCL-----CYS-----KRRSC 65

QY 95 PLCDLLIRCLNXQKPLCEBKORHL-----DKRQFHNIRGRWTCRCM--SCRRS 143

Db 66 GLCDLYPCCLDYKLYCLRSLSLSERKARAIABEDERELAKR--RTTNILASSCCSSN 124

RESULT 65

T21125

hypothetical protein F19H8.2 - Caenorhabditis elegans

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C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: J21125
R/Steward, C.
Submitted to the EMBL Data Library, March 1997
A/Reference number: Z19379
A/Accession: J21125
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-303 <WIL>
A/Cross-references: UNIPROT:O45378, UNIPARC:UPI0000075882, EMBL:Z93378, PIDN:CA07582.1;
A/Experimental source: clone F19H8
C/Genetics:
A/Gene: CESP:Fl9H8.2
A/Map position: 2
A/Introns: 27/2; 96/3; 147/3; 201/3

Query Match          9.0%; Score 75; DB 2; Length 303;
Best Local Similarity 19.1%; Pred. No. 9.5;
Matches 36; Conservative 29; Mismatches 49; Indels 74; Gaps 10;

Oy      6 QERRKRLPOLCTEQ-----TTHTDILECVYCKQQLLREYVD---FA 46
Db      70 ESQGRLCPSWCGHLKSNETIVNIGAVGNSFTTDLQDVSFECDDLKKNCLAVKXNGHCYF 129
Oy      47 FRDLC-----IYVRDQ-----NRYAVXDKCLKFYKSKISE-----YRHCVSYVGT 86
Db      130 FERRCEYDAIAISKXGSKTSRNP-KTAGECCLKQKCKGKXKGYACTFRHRC----- 182
Oy      87 TLEQYNNKPLCDL-----LIRCIYNXQKPLCPPEKORHLDKKORFHNIRG 130
Db      183 ---RKYMLPEIEVNNSTLTNSHTVQVSPLEQCLNFQK-ICAAKYKGFACRQ----- 231
Oy      131 RWTGRCMS 138
Db      232 -YRRKCL 238

RESULT 66
S56100
outer dense fiber protein - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C/Accession: S56100
R/Kim, Y.; Adham, I.M.; Haack, T.; Krenling, H.; Engel, W.
Biol. Chem. Hoppe-Seyler 376, 431-435, 1995
A/Title: Molecular cloning and characterization of the bovine and porcine outer dense fi
A/Reference number: S56100; MUID:96066278; PMID:7576240
A/Accession: S56100
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-262 <KIM>
A/Cross-references: UNIPROT:Q29077; UNIPARC:UPI0000130BD3; GB:X65913; NID:G1165146; PIDN:

Query Match          9.0%; Score 74.5; DB 2; Length 262;
Best Local Similarity 27.5%; Pred. No. 9.2;
Matches 33; Conservative 14; Mismatches 36; Indels 37; Gaps 7;

Oy      40 REVVDFAFRDLCIYVRDGNFYAVD-----KCLKFTYSKISRYRHCVYGTTLLEQYNNK 94
Db      26 RCIDFSTRCLCDLYM--HPYCCCDLHPYPCL-----CYS-----KRSRSC 65
Oy      95 PLCDLLIRCIYNXQKPLCPPEKORHL-----DKORFHNIRGRWTRGCM--SCCRSS 143
Db      66 GLCDLIPCLCDVLYLCIRPSLRSLERKAIPIAIEBKELAKLR-KITNRIILASCCSSN 124

RESULT 67
PFGO
alpha-fetoprotein precursor - gorilla
C/Species: Gorilla gorilla (gorilla)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A37970

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R/Ryan, S.C.; Zielinski, R.; Dugaiczky, A.
Genomics 9, 60-72, 1991
A/Title: Structure of the gorilla alpha-fetoprotein gene and the divergence of primates.
A/Reference number: A37970; MUID:9116517; PMID:11706310
A/Accession: A37970
A/Molecule type: DNA
A/Residues: 1-609 <RYA>
A/Cross-references: UNIPROT:P28050; UNIPARC:UPI000012A6F8; GB:M38272; NID:G817963; PIDN:

A/Map position: 4q11-12
A/Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 551/
C/Superfamily: serum albumin; serum albumin repeat homology
C/Keywords: embryo; fetus; globulin; glycoprotein; metal binding; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-609/Product: alpha-fetoprotein #status predicted <MAT>
F:29-202/Domain: serum albumin repeat homology <SA1>
F:221-394/Domain: serum albumin repeat homology <SA2>
F:413-592/Domain: serum albumin repeat homology <SA3>
F:22/Binding site: copper (His) #status predicted
F:99-114,113-124,148-193,192-201,224-270,269-303,302-313,384-462,461-472,
F:249/Binding site: bilirubin (Lys) #status predicted
F:251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          9.0%; Score 74.5; DB 1; Length 609;
Best Local Similarity 23.4%; Pred. No. 21;
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;

Oy      6 QERRKRLPOLCTEQTTHTDILECVYCKQQLLREYVDFAFRDLCTV----- 54
Db      279 QDGKIMSYICQ--QDPLSNKITEC--CKLTLE-----KQCCTIHNENDEKPEGLS 327
Oy      55 -----BDGNEVAVXDKCLKFYKSKISE--RHYCVSYGTTLEQYNNKPLCDLLIRCI 103
Db      328 PNLNRFILGDDDFNFGSSGKNIFPLASGVHEYSRRHPLQAV---SVLRVAKGYELLEKCK 384
Oy      104 INXQKPL-C---PEEKORHLDKKQ 123
Db      385 FQTEPNLECODKGEELQKYIOESQ 409

RESULT 68
PFGU
alpha-fetoprotein precursor [validated] - human
A/Alternate names: AFP; alpha-1-fetoprotein; alpha-fetoglobulin
C/Species: Homo sapiens (man)
C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
C/Accession: A26624; S37655; A33961; A9197; A23699; A61460; A90624; A90757; A93042; A03;
R/Gibbs, P.E.M.; Zielinski, R.; Boyd, C.; Dugaiczky, A.
Biochemistry 26, 1332-1343, 1987
A/Title: Structure, polymorphism, and novel repeated DNA elements revealed by a complete
A/Reference number: A26624; MUID:87185438; PMID:2436661
A/Accession: A26624
A/Molecule type: DNA
A/Residues: 1-609 <GIB>
A/Cross-references: UNIPROT:P02771; UNIPARC:UPI0000012A9; GB:M4110; NID:G773678; PIDN:
R/McVey, J.H.; Michaelides, K.; Hansen, L.P.; Ferguson-Smith, M.; Tilghman, S.; Krumlauf
Hum. Mol. Genet. 2, 379-384, 1993
A/Title: A G->A substitution in an HNF I binding site in the human alpha-fetoprotein gen
A/Reference number: S37655; MUID:93278385; PMID:7684942
A/Accession: S37655
A/Molecule type: DNA
A/Residues: 1-28 <MCV>
A/Cross-references: UNIPARC:UPI000016A4D; EMBL:Z19532; NID:G28527; PIDN:CAA79592.1; PID
A/Note: the authors translated the codon TAT for residue 26 as Thr
R/Motomaga, T.; Sakai, M.; Wegmann, T.G.; Tamaki, T.
Proc. Natl. Acad. Sci. U.S.A. 80, 4604-4608, 1983
A/Title: Primary structures of human alpha-fetoprotein and its mRNA.
A/Reference number: A93961; MUID:83273664; PMID:6192439
A/Accession: A93961
A/Molecule type: mRNA
A/Residues: 1-609 <MOR>
A/Cross-references: UNIPARC:UPI00000012A9; GB:J00077; NID:G311348; PIDN:CAA24758.1; PID:
R/Beattie, W.G.; Dugaiczky, A.

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Gene 20, 415-422, 1982
 A>Title: Structure and evolution of human alpha-fetoprotein deduced from partial sequenc
 A/Reference number: A91497; MUID:85158778; PMID:6187626
 A/Accession: A91497
 A/Molecule type: mRNA
 A/Residues: 429-556 <BEA>
 A/Cross-references: UNIPARC:UPI0000174421; GB:J00076
 R/Pucci, P.; Siciliano, R.; Malorni, A.; Marino, G.; Tecce, M.F.; Ceccarini, C.; Terrana
 Biochemistry 30, 5061-5066, 1991
 A>Title: Human alpha-fetoprotein primary structure: a mass spectrometric study.
 A/Reference number: A23699; MUID:91242409; PMID:1709810
 A/Accession: A23699
 A/Molecule type: protein
 A/Residues: 19-45;60-97;102-107;122-184;187-249;255-489;507-609 <PUC>
 A/Cross-references: UNIPARC:UPI0000174422; UNIPARC:UPI0000174423; UNIPARC:UPI0000174424;
 R/Tecce, M.F.; Terrana, B.; Giuliani, M.M.; Ceccarini, C.
 J. Nucl. Med. Allied Sci. 34, 213-216, 1990
 A>Title: Characterization of in vitro expressed human alpha-fetoprotein as highly reprod
 A/Reference number: A61480; MUID:91225826; PMID:1709209
 A/Accession: A61480
 A/Molecule type: protein
 A/Residues: 19-45;63-97;102-107;122-184;187-249;255-489;507-609 <TEC>
 A/Cross-references: UNIPARC:UPI0000174422; UNIPARC:UPI0000174424; UNIPARC:UPI0000174425;
 R/Vachnin, S.; Hsu, R.; Helmricon, R.L.; Miller, J.B.
 Biochim. Biophys. Acta 493, 418-428, 1977
 A>Title: Studies on human alpha-fetoprotein. Isolation and characterization of monomeric
 A/Reference number: A90624; MUID:77242506; PMID:70228
 A/Accession: A90624
 A/Molecule type: protein
 A/Residues: 'S', 20-22, 'S', 24-35 <YAC>
 A/Cross-references: UNIPARC:UPI0000174424
 A/Note: dimeric and trimeric forms have been found in addition to the monomeric form
 R/Aoyagi, Y.; Ikenaka, T.; Ichida, F.
 Cancer Res. 37, 3663-3667, 1977
 A>Title: Comparative chemical structure of human alpha-fetoproteins from fetal serum and
 A/Reference number: A90757; MUID:78001760; PMID:71198
 A/Accession: A90757
 A/Molecule type: protein
 A/Residues: 'S', 20-30, 'A', 32-37, 'A', <NOY>
 A/Cross-references: UNIPARC:UPI000017442B
 R/Ruoslahti, E.; Pihko, H.; Vanherl, A.; Seppala, M.; Virolainen, M.; Kontinen, A.
 Johns Hopkins Med. J. Suppl. 3, 249-255, 1974
 A>Title: 20. Alpha fetoprotein: structure and expression in man and inbred mouse strains
 A/Reference number: A93042; MUID:75018719; PMID:4118095
 A/Accession: A93042
 A/Molecule type: protein
 A/Residues: 'S', 20-24, 'Q', 26-30, 'A', 32-35, 'E', 37-39 <RUD>
 A/Cross-references: UNIPARC:UPI000017442C
 R/Sakai, M.; Morinaga, T.; Urano, Y.; Watanabe, K.; Wegmann, T.G.; Tamaki, T.
 J. Biol. Chem. 260, 5055-5060, 1985
 A>Title: The human alpha-fetoprotein gene. Sequence organization and the 5' flanking reg
 A/Reference number: A92520; MUID:85182629; PMID:2580830
 A/Contents: annotation; gene, exons and introns
 R/Aoyagi, Y.; Ikenaka, T.; Ichida, F.
 Cancer Res. 38, 3483-3486, 1978
 A>Title: Copper(II)-binding ability of human alpha-fetoprotein.
 A/Reference number: A90758; MUID:79001617; PMID:80265
 A/Contents: annotation; metal binding
 R/Aoyagi, Y.; Ikenaka, T.; Ichida, F.
 Cancer Res. 39, 3571-3574, 1979
 A>Title: alpha-fetoprotein as a carrier protein in plasma and its bilirubin-binding abil
 A/Reference number: A90759; MUID:80001710; PMID:89900
 A/Contents: annotation; bilirubin binding
 C/Comment: AFP is synthesized by the fetal liver and yolk sac. It occurs in the plasma
 C trace amounts after birth. The serum level in adults is usually less than 40 ng/ml. Af
 C/Comment: Human AFP binds copper, nickel, and fatty acids as well as, and the bilirubi
 properties.
 C/Genetics:
 A/Gene: GDB:AFP
 A/Cross-references: GDB:119660; OMIM:104150
 A/Map position: 4q11-q13
 A/Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 551
 C:Superfamily: serum albumin, serum albumin repeat homology

C:Keywords: embryo; fetus; globulin; glycoprotein; metal binding; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-609/Product: alpha-fetoprotein #status experimental <MAT>
 F:129-202/Domain: serum albumin repeat homology <SA1>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA3>
 F:22/Binding site: copper (His) #status experimental
 F:99-114, 113-124, 148-193, 192-201, 260-270, 289-303, 302-313, 384-393, 416-462, 461-472
 F:249/Binding site: bilirubin (Lys) #status predicted
 F:251/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 9.0%; Score 74.5; DB 1; Length 609;
 Best Local Similarity 23.4%; Pred. No. 21;
 Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;
 Oy 6 QERRPKLPOLCTELQTTIHDIIECVYCKQQLRREYDFRDLCTIV----- 54
 Db 279 QDGRKMSYICSQ-QDTLSNKTTC--CKLTTL-----RQCITHAENDEKPEGLS 327
 Oy 55 -----RDGNVAVXDKCKLKFYSKISEY--RHYCVSYGTLLEQYVNFCDLLIRC 103
 Db 328 PNLNRLFGDRDFNQFSSGKKNIFLASFVHEYSRRHPQLAV---SVILRVAKGYELLEKC 384
 Oy 104 INXKPL-C---PEEKQRLDKKQ 123
 Db 385 FQTEPNLECDKQGEELQKYIQESQ 409
 RESULT 69
 JC4258
 alpha-fetoprotein precursor (chimpanzee
 C/Species: Pan troglodytes (chimpanzee)
 C/Date: 27-Nov-1995 #sequence revision 08-Feb-1996 #text change 09-Jul-2004
 C/Accession: JC4258
 R/Nishio, H.; Gibbs, P.E.M.; Minghetti, P.F.; Zielinski, R.; Dugalczyk, A.
 Gene 162, 213-220, 1995
 A>Title: The chimpanzee alpha-fetoprotein-encoding gene shows structural similarity to t
 A/Reference number: JC4258; MUID:96032345; PMID:7557431
 A/Accession: JC4258
 A/Molecule type: DNA
 A/Residues: 1-609 <NS>
 A/Cross-references: UNIPROT:Q28789; UNIPARC:UPI000012A6FA; GB:U21916; NID:G841311; PIDN
 C/Comment: This protein is a plasma protein produced in the fetal and neonatal liver and
 C similar properties and structure.
 C/Genetics:
 A/Gene: afp
 A/Map position: 3p
 A/Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3; 551
 C:Superfamily: serum albumin, serum albumin repeat homology
 C/Keywords: glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-609/Product: alpha-fetoprotein #status predicted <MAT>
 F:129-202/Domain: serum albumin repeat homology <SA1>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA3>
 F:42/251/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 9.0%; Score 74.5; DB 2; Length 609;
 Best Local Similarity 23.4%; Pred. No. 21;
 Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;
 Oy 6 QERRPKLPOLCTELQTTIHDIIECVYCKQQLRREYDFRDLCTIV----- 54
 Db 279 QDGRKMSYICSQ-QDTLSNKTTC--CKLTTL-----RQCITHAENDEKPEGLS 327
 Oy 55 -----RDGNVAVXDKCKLKFYSKISEY--RHYCVSYGTLLEQYVNFCDLLIRC 103
 Db 328 PNLNRLFGDRDFNQFSSGKKNIFLASFVHEYSRRHPQLAV---SVILRVAKGYELLEKC 384
 Oy 104 INXKPL-C---PEEKQRLDKKQ 123
 Db 385 FQTEPNLECDKQGEELQKYIQESQ 409

activator of cAMP-responsive element modulator, testis - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C/Accession: J07686
 R:Palermo, I.; Litalico, L.; Emanuele, G.; Guaffrida, V.; Sassone-Corsi, P.; De Cesare, R.; Biochem. Biophys. Res. Commun. 283, 406-411, 2001
 A>Title: Cloning and expression of activator of CREM in testis in human testicular tissue
 A/Reference number: J07686; MUID:2126154; PMID:11327716
 A/Content: testis
 A/Accession: J07686
 A/Molecule type: mRNA
 A/Residues: 1-284 <PAL>
 A/Cross-references: UNIPROT:Q9N0U2; UNIPARC:UPI000017CB67; GB:AF278541
 C/Comment: This protein activates cAMP-responsive element modulator in a phosphorylation of human spermatogenesis.
 C/Genetics:
 A:Gene: act
 A:Map position: 6q
 A:Introns: 53/3; 112/3; 168/3; 231/3
 C/Keywords: spermatogenesis; testis

Query Match 8.8%; Score 73; DB 2; Length 284;
 Best Local Similarity 21.1%; Pred. No. 14;
 Matches 32; Conservative 23; Mismatches 59; Indels 38; Gaps 7;

15 LCTELQTTIHDIIECYCKQQL---RREYVPAFRDLCTVYRD----- 56

Db 89 LCTECYS--NESSKCPKCKRTIMPGRKMEKGNVMEETFCVENCROPITKPLSKE 146

Qy 57 -GNVYAVXDKLTKFYKISEYRHC-----YSVYGTLEQYVKKPLCDLLIRCKNOKP 109

Db 147 SGN-----YCVPFERK-EPAHYCNFKKVTITSGTITFCQLMHNKCFGL---CSGRKD 195

Qy 110 LCPBEKQRLDKKORFNIRGRWTCSCCR 141

Db 196 LCEQFMFRDYPFCMDCYNHLVANKVCVACSK 227

RESULT 75

A55933

paxillin - human

N/Alternate names: peroxisomal membrane protein 3

C/Species: Homo sapiens (man)

C>Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C/Accession: A55933

R:Salgia, R.; Li, J.L.; Lo, S.H.; Brunkhorst, B.; Kansas, G.S.; Sobhany, E.S.; Sun, Y.; J. Biol. Chem. 270, 5039-5047, 1995

A>Title: Molecular cloning of human paxillin, a focal adhesion protein phosphorylated by

A/Reference number: A55933; MUID:95197488; PMID:7534286

A/Accession: A55933

A/Molecule type: mRNA

A/Residues: 1-557 <SAL>

A/Cross-references: UNIPROT:P49023; UNIPARC:UPI0000280A7; GB:U14588; NID:G704347; PIDN:

C/Genetics:

A:Gene: GDB:PXN

A/Cross-references: GDB:702105

A:Map position: 12q24-12q24

C/Keywords: cell adhesion; cytoskeleton; peroxisome; phosphoprotein; zinc finger

F/46-55/Region: proline-rich

F/324-374/Domain: LIM metal-binding repeat homology <LIM1>

F/383-433/Domain: LIM metal-binding repeat homology <LIM2>

F/442-492/Domain: LIM metal-binding repeat homology <LIM3>

F/501-551/Domain: LIM metal-binding repeat homology <LIM4>

F/31,118/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 8.8%; Score 73; DB 2; Length 557;
 Best Local Similarity 20.7%; Pred. No. 26;
 Matches 19; Conservative 18; Mismatches 29; Indels 26; Gaps 3;

Qy 14 QCTELQTTIHDIIECYCKQQLRREYVPAFRDLCTVYRDGNVAVXDKLTKFYSKI 73

Db 334 QVTVAMKTMPEHFVCTHCOEIGSRNPF-----RDGPYCEKD---YHNL 379

Qy 74 SEYHVCYSVGTLEQYVKKPLCDLLIRCKIN 105

Db 380 SPRCYC-----NGPILDKVVTALD 399

RESULT 76

B55933

paxillin - chicken

C/Species: Gallus gallus (chicken)

C>Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C/Accession: B55933

R:Salgia, R.; Li, J.L.; Lo, S.H.; Brunkhorst, B.; Kansas, G.S.; Sobhany, E.S.; Sun, Y.; J. Biol. Chem. 270, 5039-5047, 1995

A>Title: Molecular cloning of human paxillin, a focal adhesion protein phosphorylated by

A/Reference number: A55933; MUID:95197488; PMID:7534286

A/Accession: B55933

A/Molecule type: mRNA

A/Residues: 1-559 <SAL>

A/Cross-references: UNIPROT:P49024; UNIPARC:UPI0000131378; GB:U14589; NID:G704349; PIDN:

C/Keywords: cell adhesion; cytoskeleton; phosphoprotein; zinc finger

F/46-55/Region: proline-rich

F/326-376/Domain: LIM metal-binding repeat homology <LIM1>

F/385-435/Domain: LIM metal-binding repeat homology <LIM2>

F/444-494/Domain: LIM metal-binding repeat homology <LIM3>

F/503-553/Domain: LIM metal-binding repeat homology <LIM4>

F/31,118/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 8.8%; Score 73; DB 2; Length 559;
 Best Local Similarity 20.7%; Pred. No. 27;
 Matches 19; Conservative 18; Mismatches 29; Indels 26; Gaps 3;

Qy 14 QCTELQTTIHDIIECYCKQQLRREYVPAFRDLCTVYRDGNVAVXDKLTKFYSKI 73

Db 336 QVTVAMKTMPEHFVCTHCOEIGSRNPF-----RDGPYCEKD---YHNL 381

Qy 74 SEYHVCYSVGTLEQYVKKPLCDLLIRCKIN 105

Db 382 SPRCYC-----NGPILDKVVTALD 401

RESULT 77

T01171

G1/S transition control protein Rb1 - maize

N/Alternate names: retinoblastoma susceptibility protein Rb1; retinoblastoma-related prot

C/Species: Zea mays (maize)

C/Accession: T01171; S72272

C/Accession: T01171; S72272

R:Arch, R.A.; Durfee, T.; Miller, A.B.; Taranto, P.; Hanley-Bowdoin, L.; Zambryski, P.C.; Mol. Cell. Biol. 17, 5077-5086, 1997

A>Title: Rb1 and Rb2 encode maize retinoblastoma-related proteins that interact with a

A/Reference number: 209601; MUID:97415586; PMID:9271385

A/Accession: T01171

A/Molecule type: mRNA

A/Residues: 1-866 <ARCH>

A/Cross-references: UNIPROT:O23344; UNIPARC:UPI0000033DFE; EMBL:AF007793; NID:G2352794; F

R:Xie, Q.; Sanz-Burgos, A.P.; Hannon, G.J.; Gutierrez, C.

EMBO J. 15, 4900-4908, 1996

A>Title: Plant cells contain a novel member of the retinoblastoma family of growth regula

A/Reference number: S72272; MUID:97045098; PMID:8890163

A/Accession: S72272

A/Molecule type: mRNA

A/Residues: 184-866 <XIE>

A/Cross-references: UNIPARC:UPI000002EEEB; EMBL:X98923; NID:G1617473; PIDN:CAA67422.1; P

C/Genetics:

A:Gene: RRB1; Rb1

A/Description: cell cycle control, probably controls G1/S phase transition in plants

C/Superfamily: retinoblastoma-associated protein

C/Keywords: cell cycle control

Query Match 8.7%; Score 72.5; DB 2; Length 866;
 Best Local Similarity 23.3%; Pred. No. 45;

Matches 34; Conservative 22; Mismatches 49; Indels 41; Gaps 7;
 Qy 4 DPGRPRKLPOLCETLEQTHIDILLECVCYCKQ-----LLRREYV-----DAFRLDLCIV 54
 Db 526 DDNADPSPKSKCSBESRATVERNLQPPPKQSHWSTSLAKACHPLQSTPASPVC--- 582
 Qy 55 RDGNPVAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTTLLEQO- 91
 Db 563 ---NPVGNEKCAVDVTHIFFSKILKLAIRINLNCERVCVEQTERVYVNFKQLEQOT 639
 Qy 92 ---YKPLCDLLIRINCXKQKPLCPBE 114
 Db 640 TLFPRRHIDQLILCCLGVAKVCOLE 665

RESULT 78
 G82108
 conserved hypothetical protein VC2176 [imported] - Vibrio cholerae (strain N16961 serogroup C)
 C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: G82108
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406633; PMID:10952301
 A:Accession: G82108
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-270 <HE>
 A:Cross-references: UNIPROT:Q9KQ28; UNIPARC:UPI00001387DF; GB:AE004289; GB:AE003852; NID: A:Experimental source: serogroup O1, strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC2176
 A:Map position: 1
 Query Match 8.7%; Score 72; DB 2; Length 270;
 Best Local Similarity 27.5%; Pred. No. 16;
 Matches 22; Conservative 13; Mismatches 29; Indels 16; Gaps 3;
 Qy 34 KQQLLRREYVDPAPR--DLCTVARDGNPYAVXDKCLKFY-----KISYRHYCYSVYG 85
 Db 188 KSALLRERYTLARCTDLALTFVDDPYEIRDRGFYQQLQCHQIAISDYQF----- 241
 Qy 86 TTLEQYKPKLDCILLIRINCIN 105
 Db 242 --IEHCPMDPAELKTOVN 259

RESULT 79
 T21820
 hypothetical protein F35H8.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T21820
 R:Berks, M.
 submitted to the EMBL Data Library, August 1994
 A:Reference number: Z19475
 A:Accession: T21820
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-422 <ML>
 A:Cross-references: UNIPROT:Q20082; UNIPARC:UPI000007866E; EMBL:Z36752; PIDN:CAA85325.1;
 A:Experimental source: clone F35H8
 C:Genetics:
 A:Gene: CESP:F35H8.3
 A:Map position: 2
 A:Introns: 24/1; 52/2; 98/1; 191/3; 274/3; 368/2
 Query Match 8.7%; Score 72; DB 2; Length 422;
 Best Local Similarity 23.6%; Pred. No. 25;
 Matches 29; Conservative 13; Mismatches 43; Indels 38; Gaps 7;

Qy 27 ILECVCYKQQLLRREYVDFAFRLDLCIVRDGNPYAVXDKCLKFYKISYRHYCYSVYGT 86
 Db 170 LYRCTNCKTYTGNKVEYQ---RHIGVHGDAFRPCNCGRFPANKTSMTH----- 218
 Qy 87 TLEQYKPKL--CDLLIRINCXKQKPLCP-----EEKQRLDKQRFPHNIRGRTGCM 138
 Db 219 LKDHSLKPKMPSCD-----YCPRIFSKLESXTRH---HKMHFTF---STCOT 259
 Qy 139 CCR 141
 Db 260 CWR 262

RESULT 80
 H86477
 protein F1504.19 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: H86477
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, Chitt, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizart, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salberg, S.L.; Schwartz, J.R.; Shim, P.; Souhwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H86477
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-565 <STO>
 A:Cross-references: UNIPROT:Q9LQ66; UNIPARC:UPI00000A7592; GB:AE005172; NID:9878343; PII: A:Genetics:
 A:Gene: F1504.19
 A:Map position: 1
 Query Match 8.6%; Score 71.5; DB 2; Length 565;
 Best Local Similarity 33.9%; Pred. No. 37;
 Matches 20; Conservative 6; Mismatches 26; Indels 7; Gaps 3;

Qy 83 VYGTLEQYKPKLDCILLIRINCXKQKPLCPBEKQRLDKQRFPHNIRGRTGCMSCC 140
 Db 217 VYSGVLEBSSTSVYCAL---CID---DYCVGEKRIILPCGHKHYAVCDISLGRGRSFC 269
 RESULT 81
 T11850
 DNA primase (EC 2.7.7.-) - Synechococcus sp. (PCC 7942)
 C:Species: Synechococcus sp.
 A:Variety: PCC 7942
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T11850
 R:Bird, A.D.; Turner-Cavet, J.S.; Lakey, J.H.; Robinson, N.J.
 J. Biol. Chem. 273, 21246-21252, 1998
 A:Title: A carboxyl-terminal Cys2/His2-type zinc-finger motif in DNA primase influences D:
 A:Reference number: Z17359; MUID:98362004; PMID:9694883
 A:Accession: T11850
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-616

 A:Cross-references: UNIPROT:P74893; UNIPARC:UPI00001321F0; EMBL:X94247
 C:Genetics:
 A:Gene: dnaG
 C:Function:
 A:Description: interacts with DNA to synthesize the primer RNA that initiates DNA replic
 C:Superfamily: DNA primase
 C:Keywords: DNA replication, nucleotidyltransferase
 Query Match 8.6%; Score 71.5; DB 2; Length 616;

A:Residues: 1-2488 <STE>
A:Cross-references: UNIPROT:O61528; UNIPARC:UPI00000611F8; EMBL:AF048834; NID:G2944395;
A:Accession: T342740
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1634,'OV',1637,'E' <ST2>
A:Cross-references: UNIPARC:UPI000002A21C; EMBL:AF048835; NID:G2944397; PIDN:AACT12932.1;
R:Du, Z.; Le, T.
submitted to the EMBL Data Library, November 1996
A:Description: The sequence of C. elegans coemid F55C7.
A:Reference number: 221524
A:Accession: T34427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2488 <DU2>
A:Cross-references: UNIPARC:UPI00000611F8; EMBL:U80436; PIDN:AACT1108.1; GSPDB:GN00019;
A:Experimental source: strain Bristol N2; clone F55C7
A:Accession: T34430
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1634,'ON',1637,'E' <DU2>
A:Cross-references: UNIPARC:UPI000002A21C; EMBL:U80436; PIDN:AACT1109.1; GSPDB:GN00019;
A:Experimental source: strain Bristol N2; clone F55C7
A:Accession: T34426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 'MWIKCFT',1568,'LRK',1572-2488 <DU3>
A:Cross-references: UNIPARC:UPI000002A21D; EMBL:U80436; PIDN:AACT1110.1; GSPDB:GN00019;
A:Experimental source: strain Bristol N2; clone F55C7
C:Genetics:
A:Gene: unc-73; F55C7.7a; unc-73; F55C7.7b; CESP:F55C7.7c
A:Map position: 1
A:Insertions: 7/3; 64/2; 95/3; 230/3; 265/2; 335/3; 360/3; 488/3; 569/1; 695/1; 1028/2; 106
19/3; 2262/2; 2331/1; 2351/3; 2396/1; 2431/1

Query Match 8.6%; Score 71; DB 2; Length 2488;
Best Local Similarity 24.2%; Pred. No. 1.7e+02;
Matches 40; Conservative 25; Mismatches 52; Indels 48; Gaps 11;

34 KOQLLR-----REYVD---FAFRDLC---IVYDGNPY---AXXDCIKRY----- 70
Db 872 KOELRAFRADVONHKLKEPYDAFVIRFRELENNRANLDEVVYHNEALQAKYCRIMNLCE 931

Qy 71 --SKISEYRHVCYSVYGT-----LEQYNNKP-LCDLLIRCIKX-----QKPLCPBEKQ 116
Db 932 DRNKLKSAHGCYKTYERAVLPIINQLESEVHSPVTVMCAGCTSSIDADAAYVADLLS 991

Qy 117 RHLDKQRF-----HNIRG-----RWGRCMSCCRSSRTRETOL 151
Db 992 KHM DYKERFEGKGTVALRNGDFLRLRYIRR-STVNSERKRHETKI 1035

RESULT 86
C97723
aspartate-CRNA ligase (EC 6.1.1.12) - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 03-Jun-2002
C:Accession: C97723
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A>Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: C97723
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-615 <KUR>
A:Cross-references: UNIPARC:UPI0000164BE8; GB:AE006914; PIDN:AAL02725.1; PID:G15619236;
C:Genetics:
A:Gene: asps
C:Superfamily: lysine-CRNA ligase
C:Keywords: ligase

Query Match 8.5%; Score 70.5; DB 2; Length 615;

Best Local Similarity 27.3%; Pred. No. 50;
Matches 39; Conservative 13; Mismatches 50; Indels 41; Gaps 8;

Qy 16 CTEIQTTHIDILIECVCKQQLRREYVDFARFL-----CIVYDDGNPYAXXDCIK 68
Db 22 CNELO--ISDVEYVKLSGWVHRRRDGNLVFIDLDRHYGITQIVFDQNFQMEDASRL 79

Qy 69 FYSKISEYRHVCYSVYGTTL---EQYNNKP-----CDLLIRCIKXOK 108
Db 80 RYSEV-----IVRGTVVARS EDTINNTLPCHVEVLAVFSEVESAADLPVINTTEK 132

Qy 109 PLCPSE---KQRHLD-KKQRFHN 127
Db 133 D-APEESRLKRFIDLRREKLN 154

RESULT 87
C86496
hypothetical protein CPJ0041 [imported] - Chlamydia pneumoniae (strain J138)
C:Species: Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C86496
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ito
Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871162
A:Accession: C86496
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <STO>
A:Cross-references: UNIPROT:Q9JS25; UNIPARC:UPI00000D2F9A; GB:BA000008; NID:G8978416; PII
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPJ0041

Query Match 8.4%; Score 70; DB 2; Length 449;
Best Local Similarity 27.6%; Pred. No. 42;
Matches 27; Conservative 13; Mismatches 40; Indels 18; Gaps 6;

Qy 40 REYVDFAFRDLCTIYR-----DGNPYAVXDKCLKFYSKISEYRHVCYSVYGTLEQYNNK 94
Db 210 REYVDFRFRITTCNIRKIAMTFDRHVSVAKTA---FEKAGALETC--VY-ESMRSEYRE 263

Qy 95 PLCDLLIRCIKXOKPLCPBEKORHLDKORFHNIRGM 132
Db 264 AFCE-----YEKALIDGEEKSAVAE--QRQDIKRM 294

RESULT 88
D72127
hypothetical protein - Chlamydia pneumoniae (strain CWL029)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: D72127
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A>Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: D72127
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <ARN>
A:Cross-references: UNIPROT:Q9Z9E0; UNIPARC:UPI00000C11BC; GB:AE001589; GB:AE001363; NID
A:Experimental source: strain CWL029
C:Genetics:
A:Gene: Cpn0041

Query Match 8.4%; Score 70; DB 2; Length 449;
Best Local Similarity 27.6%; Pred. No. 42;
Matches 27; Conservative 13; Mismatches 40; Indels 18; Gaps 6;

Qy 40 REYVDFAFRDLCTIYR-----DGNPYAVXDKCLKFYSKISEYRHVCYSVYGTLEQYNNK 94

Db 210 REVVDPRMRTTCNRIKIAMTFDRHVSVAKTA---FEKAFGALFTC--VY-ESMRSESTRE 263

Qy 95 PLCDLIRICINXOKPLCEPEKORHLDDKORFNIRGM 132

Db 264 AFCE-----YEKALIGDEKSAHAE--QRFDIDIKNM 294

RESULT 89

hypotheical protein CP0733 (imported) - Chlamydia pneumoniae (strain AR39)

C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: AB1544

R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.

A/Reference number: AB1500; MUID:20150255; PMID:10684935

A/Accession: AB1544

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-449 <REA>

A/Cross-references: UNIPROT:Q9US25; UNIPARC:UPI00000D2P9A; GB:AE002232; GB:AE002161; NID

C/Genetics:

A/Gene: CP0733

Query Match 8.4%; Score 70; DB 2; Length 449;

Best Local Similarity 27.6%; Pred. No. 42;

Matches 27; Conservative 13; Mismatches 40; Indels 18; Gaps 6;

Qy 40 REVVDPRMRTTCNRIKIAMTFDRHVSVAKTA---FEKAFGALFTC--VY-ESMRSESTRE 263

Db 210 REVVDPRMRTTCNRIKIAMTFDRHVSVAKTA---FEKAFGALFTC--VY-ESMRSESTRE 263

Qy 95 PLCDLIRICINXOKPLCEPEKORHLDDKORFNIRGM 132

Db 264 AFCE-----YEKALIGDEKSAHAE--QRFDIDIKNM 294

RESULT 90

hypotheical protein K11E8.1c - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004

C/Accession: T23616

R/Wild, A.

submitted to the EMBL Data Library, March 1996

A/Reference number: Z19771

A/Accession: T23616

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-708 <WIL>

A/Cross-references: UNIPROT:O62305; UNIPARC:UPI000017A3A1; EMBL:Z70279; PIDN:CAA94244.1;

C/Genetics:

A/Gene: CESP:K11E8.1c

A/Map position: 4

A/Introns: 8/2; 78/2; 100/2; 124/3; 186/1; 217/3; 258/3; 286/3; 401/2; 501/1; 536/1; 574

RESULT 91

conserved hypotheical protein TC0424 (imported) - Chlamydia muridarum (strain Nigg)

C/Species: Chlamydia muridarum, Chlamydia trachomatis Mopn

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: B81704

R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.

A/Reference number: AB1500; MUID:20150255; PMID:10684935

A/Accession: B81704

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1436 <TET>

A/Cross-references: UNIPROT:Q9PKP1; UNIPARC:UPI0000057904; GB:AE002309; GB:AE002160; NID

A/Experimental source: strain Nigg (Mopn)

C/Genetics:

A/Gene: TC0424

Query Match 8.4%; Score 70; DB 2; Length 1436;

Best Local Similarity 21.9%; Pred. No. 1.3e+02;

Matches 40; Conservative 21; Mismatches 50; Indels 72; Gaps 9;

Qy 6 QERPKLPOLCTELQTHIHILCEVCCKOQLRREYVDFAFRDLCTVYRDG-NPY----- 60

Db 358 KDRIRSLAQ-----QKTLTALRLKLYC-----ETED-AMHIC1-EDGISPIYODQ 402

Qy 61 -AVXDKCLK-----KPLCDLIRICINXOKPLCEPEKOR-HDKKORFNTI 128

Db 403 VRIYQKCLREBELDLKGTDEBLKPCDSKIQRSVCLPATSVVSLLEGKGVSEKSIK 462

Qy 75 EYRHVCYSVGTTLBOQYN-----KPLCDLIRICINXOKPLCEPEKOR-HDKKORFNTI 128

Db 463 EIBETVRELGSTILQGLSGGITPLIDNVHKAIRGALSNELRSISIQHPERRFRRL 522

Qy 129 RGR 131

Db 523 QAK 525

RESULT 92

hypotheical protein C15H9.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T15519

R/Bentley, D.

submitted to the EMBL Data Library, April 1996

A/Description: The sequence of C. elegans cosmid C15H9.

A/Reference number: Z18364

A/Accession: T15519

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-314 <BEN>

A/Cross-references: UNIPROT:Q18029; UNIPARC:UPI000007A22F; EMBL:U56965; NID:g1945492; PII

A/Experimental source: strain Bristol N2; clone C15H9

C/Genetics:

A/Gene: CESP:C15H9.3

A/Map position: X

A/Introns: 76/1; 177/3; 210/3; 266/2

RESULT 93

conserved hypotheical protein TC0424 (imported) - Chlamydia muridarum (strain Nigg)

C/Species: Chlamydia muridarum, Chlamydia trachomatis Mopn

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: B81704

R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.

A/Reference number: AB1500; MUID:20150255; PMID:10684935

A/Accession: B81704

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1436 <TET>

A/Cross-references: UNIPROT:Q9PKP1; UNIPARC:UPI0000057904; GB:AE002309; GB:AE002160; NID

A/Experimental source: strain Nigg (Mopn)

C/Genetics:

A/Gene: TC0424

Query Match 8.4%; Score 70; DB 2; Length 1436;

Best Local Similarity 21.9%; Pred. No. 1.3e+02;

Matches 40; Conservative 21; Mismatches 50; Indels 72; Gaps 9;

Qy 6 QERPKLPOLCTELQTHIHILCEVCCKOQLRREYVDFAFRDLCTVYRDG-NPY----- 60

Db 358 KDRIRSLAQ-----QKTLTALRLKLYC-----ETED-AMHIC1-EDGISPIYODQ 402

Qy 61 -AVXDKCLK-----KPLCDLIRICINXOKPLCEPEKOR-HDKKORFNTI 128

Db 403 VRIYQKCLREBELDLKGTDEBLKPCDSKIQRSVCLPATSVVSLLEGKGVSEKSIK 462

Qy 75 EYRHVCYSVGTTLBOQYN-----KPLCDLIRICINXOKPLCEPEKOR-HDKKORFNTI 128

Db 463 EIBETVRELGSTILQGLSGGITPLIDNVHKAIRGALSNELRSISIQHPERRFRRL 522

Qy 129 RGR 131

Db 523 QAK 525

RESULT 94

hypotheical protein C15H9.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T15519

R/Bentley, D.

submitted to the EMBL Data Library, April 1996

A/Description: The sequence of C. elegans cosmid C15H9.

A/Reference number: Z18364

A/Accession: T15519

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-314 <BEN>

A/Cross-references: UNIPROT:Q18029; UNIPARC:UPI000007A22F; EMBL:U56965; NID:g1945492; PII

A/Experimental source: strain Bristol N2; clone C15H9

C/Genetics:

A/Gene: CESP:C15H9.3

A/Map position: X

A/Introns: 76/1; 177/3; 210/3; 266/2

RESULT 93
B84474
hypothetical protein At2g06010 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84474
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffatt, K.S.; Clifton, L.A.; Shen, M.; Vanden, S.E.; Umayan, L.; Tallon, L.;
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617157
A:Accession: B84474
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <STD>
A:Cross-references: UNIPROT:Q8VY85; UNIPARC:UPI000017A73D; GB:AE002093; NID:g4388730; PI
C:Genetics:
A:Gene: At2g06010
A:Map position: 2

Query Match 8.3%; Score 69; DB 2; Length 298;
Best Local Similarity 30.9%; Pred. No. 35;
Matches 29; Conservative 7; Mismatches 28; Indels 30; Gaps 6;

Qy 86 TTLEQYVKKPLCDLLIRCIINXKQKPCPEEK-----QRHDKK---QRF----- 125
Db 109 STNNQVNEPTNDHAKLV--LKPLCPERKWKFIYEPHGEVRLSKKIPTVRFILNIQVG 166
Qy 126 --HNIRGR--WTRGCMSCRS---SRTRETOQL 151
Db 167 VGHNFQWNAIGMKWKLTSCLGSDGVSRIRNKTTL 200

RESULT 94
T33884
hypothetical protein H14E04.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C:Accession: T33884
R:Becker, M.; Wamaley, P.; Twyman, B.; Beck, C.; Bradshaw, H.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid H14E04.
A:Reference number: Z21431
A:Accession: T33884
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-327 <BEC>
A:Cross-references: UNIPROT:Q9TYP2; UNIPARC:UPI000007A0C9; EMBL:AF125448; PIDN:AD12812.
A:Experimental source: strain Bristol N2; clone H14E04
C:Genetics:
A:Gene: CESP:H14E04.5
A:Map position: 4
A:Initrions: 11/2; 47/1; 84/2; 125/1; 167/2; 181/1; 215/1; 275/3
C:Superfamily: cyclin, C/H/G types

Query Match 8.3%; Score 69; DB 2; Length 327;
Best Local Similarity 23.7%; Pred. No. 38;
Matches 28; Conservative 15; Mismatches 35; Indels 40; Gaps 6;

Qy 31 VYCKQQLRRVYDFAPFDLCIVYRDGNPYAVXDCKLFYSKISEYRYCVSV----- 83
Db 76 IYFKRFYIRQ-----SFRDMC-----PFLVASTALFLACKVER--HTTISVSSFLKNT 121

Qy 84 -----YGTLEQYVKKPLCDLLIRCI--NXQKPLCPERKQRLDKK 122
Db 122 AIVLPKRGVTFETSTKGVVYDSEFIVELIDCLVHHASRWCPPPPRRIFDK 179
RESULT 95
A71928

cag island protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: A71928
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Medberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: A71928
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1819 <ARN>
A:Cross-references: UNIPROT:Q9ZLV0; UNIPARC:UPI00000D3637; GB:AE001481; GB:AE001439; NID
A:Experimental source: strain J99
C:Genetics:
A:Gene: orf13/14

Query Match 8.3%; Score 69; DB 2; Length 1819;
Best Local Similarity 23.2%; Pred. No. 28+02;
Matches 33; Conservative 13; Mismatches 48; Indels 48; Gaps 5;

Qy 8 RPRRLPOLCTELQTTIHDIIECVYCKQQLRRVYDFAPFDLCIVYRDGNPYAVXDCKL 67
Db 1252 RNEKEKQCEKXLTLPARKFLE---KQ---RQKDKAIKD-CLKVADPDRAAIMKCL 1302
Qy 68 KFYs-----KISEYRYCVSVYGTLEQYVKKPLCDLLIRCI 104
Db 1303 DGLSDEKLYLOAEKRAVALDCLTKARTDBEKKCONLISDLIQEYONKK----- 1353

Qy 105 NXQKPLCPERKQRLDKKORFH 126
Db 1354 -----AQNKQNLSTERLH 1368

RESULT 96
S56101
outer dense fiber protein - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S56101
R:Kim, Y.; Adham, I.M.; Haack, T.; Kremling, H.; Engel, W.
Biol. Chem. Hoppe-Seyler 376, 431-435, 1995
A:Title: Molecular cloning and characterization of the bovine and porcine outer dense fil
A:Reference number: S56100; MUID:96062278; PMID:7576240
A:Accession: S56101
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-262 <KIM>
A:Cross-references: UNIPROT:Q29438; UNIPARC:UPI0000130BD1; GB:X69514; NID:g1165005; PIDN

Query Match 8.3%; Score 68.5; DB 2; Length 262;
Best Local Similarity 26.7%; Pred. No. 34;
Matches 32; Conservative 14; Mismatches 37; Indels 37; Gaps 7;

Qy 40 REVYDFAPFDLCIVYRDGNPYAVXD-----KCLFYSKISEYRYCVSVYGTLEQYVKK 94
Db 26 RCIDELSLARCLCDLYM--HPYCCCDLHPYICL-----CYS-----KGRSQC 65
Qy 95 PLCDLLIRCIINXKQKPLCPERKQRL-----DKQRFHNTIGRWYTCRM--SCCRSS 143
Db 66 GLCDLYPCCLCDVLYCLRLSLRLERKAIKRAIEDERELAKLR-RTTNRIILASSCCSSN 124

RESULT 97
GQHTU1
tumor necrosis factor receptor 1 precursor (validated) - human
N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
M:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A38208; A34899; A34900; A36555; A36555; A38281; S12057; J10758; A60231; A38

R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
 Genomics 13, 219-224, 1992
 A;Title: Structure of the human TNF receptor 1 (p60) gene (TNFRP1) and localization to ch
 A;Reference number: A38208; MUID:92250049; PMID:1315717
 A;Accession: A38208
 A;Molecule type: DNA
 A;Residues: 1-455 <FUC>
 A;Cross-references: UNIPROT:P19438; UNIPARC:UPI000002CE11; GB:M75864; GB:M75865; GB:M7586
 R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lessl
 Cell 61, 351-359, 1990
 A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep
 A;Reference number: A34899; MUID:90235284; PMID:2158862
 A;Accession: A34899
 A;Molecule type: mRNA
 A;Residues: 1-455 <LOB>
 A;Cross-references: UNIPARC:UPI000002CE11; GB:M58286; GB:M33480; NID:9339753; PIDN:AAA36
 A;Experimental source: placenta
 A;Note: part of this sequence, including the amino end of the mature protein, confirmed
 R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.
 Cell 61, 361-370, 1990
 A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor
 A;Reference number: A34900; MUID:90235285; PMID:2158863
 A;Accession: A34900
 A;Molecule type: mRNA
 A;Residues: 1-455 <SCG>
 A;Cross-references: UNIPARC:UPI000002CE11; GB:M33294; NID:9339744; PIDN:AAA03210.1; PID
 R;Himmeler, A.; Maurer-Fogy, I.; Krenke, M.; Scheutich, P.; Flitzemaler, K.; Lantze, M.;
 DNA Cell Biol. 9, 705-715, 1990
 A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recept
 A;Reference number: A36555; MUID:91090841; PMID:1702293
 A;Accession: A36555
 A;Molecule type: mRNA
 A;Residues: 1-455 <HIM>
 A;Cross-references: UNIPARC:UPI000002CE11; GB:M63121; NID:9339755; PIDN:AAA36754.1; PID
 A;Accession: C36555
 A;Molecule type: protein
 A;Residues: 30-38;41-53, 'X',55-79, 'XX',82-94, 'NK', 'XX',100-104;107-128;162-167, 'X',169-2
 A;Cross-references: UNIPARC:UPI000002399; UNIPARC:UPI000002836; UNIPARC:UPI00001736DE;
 A;Note: the purified cloning, called tumor necrosis factor binding protein, is a soluble
 R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
 A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re
 A;Reference number: A38281; MUID:91017509; PMID:2170974
 A;Accession: A38281
 A;Molecule type: mRNA
 A;Residues: 1-455 <GPA>
 A;Cross-references: UNIPARC:UPI000002CE11; GB:M37764
 A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
 R;Nophar, Y.; Kemper, O.; Brakubusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
 EMBO J. 9, 3269-3278, 1990
 A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the TNF
 le form of the receptor.
 A;Reference number: S12057; MUID:91006021; PMID:1638610
 A;Accession: S12057
 A;Molecule type: mRNA
 A;Residues: 1-455 <NOP>
 A;Cross-references: UNIPARC:UPI000002CE11; EMBL:X55313; NID:937223; PIDN:CAA39021.1; PID
 A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
 R;Kemper, O.; Wallach, D.
 Gene 134, 209-216, 1993
 A;Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
 A;Reference number: J70758; MUID:94085779; PMID:8262379
 A;Accession: J70758
 A;Molecule type: DNA
 A;Residues: 1-13 <KEM>
 A;Cross-references: UNIPARC:UPI0000155CFB
 R;Secklinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
 Eur. J. Immunol. 20, 1167-1174, 1990
 A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
 A;Reference number: A60231; MUID:90292116; PMID:2113477
 A;Accession: A60231
 A;Molecule type: protein
 A;Residues: 41-43, 'X',45-53, 'X',55-57 <SEC>

A;Cross-references: UNIPARC:UPI0000072FDB
 R;Gatanaga, T.; Huang, C.; Kohr, W.; Capuccini, F.; Lucchi III, J.A.; Jeffes, E.W.B.; Ler
 Proc. Natl. Acad. Sci. U.S.A. 87, 8761-8784, 1990
 A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
 clients.
 A;Reference number: A38258; MUID:91062364; PMID:2174164
 A;Accession: A38258
 A;Molecule type: protein
 A;Residues: 41-60 <GAT>
 A;Cross-references: UNIPARC:UPI00001736E1
 A;Experimental source: cancer patient serum
 R;Olsson, I.; Lantze, M.; Nilsson, E.; Peetre, C.; Thyrell, H.; Grubb, A.; Adolf, G.
 Eur. J. Haematol. 42, 270-275, 1989
 A;Title: Isolation and characterization of a tumor necrosis factor binding protein from
 A;Reference number: A60594; MUID:89171156; PMID:2924890
 A;Accession: A60594
 A;Molecule type: protein
 A;Residues: 41-43, 'X',45-53, 'V',55-57, 'XK',60 <OLS>
 A;Cross-references: UNIPARC:UPI00001736E2
 A;Experimental source: renal failure patient urine
 R;Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 1531-1536, 1990
 A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence f
 A;Reference number: A35010; MUID:90110215; PMID:2153136
 A;Accession: A35010
 A;Molecule type: protein
 A;Residues: 41-45 <ENG>
 A;Cross-references: UNIPARC:UPI00001736E3
 A;Experimental source: normal urine
 R;Kajihara, J.; Asada, A.; Kishihara, S.; Kato, K.
 Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
 A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
 A;Reference number: J02404; MUID:95128033; PMID:7765720
 A;Accession: J02404
 A;Molecule type: protein
 A;Residues: 41-53, 'X',55-144, 'X',146-150, 'X',152-186, 'X',188-201 <KAJ>
 A;Cross-references: UNIPARC:UPI00001736E4
 A;Experimental source: urine
 C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
 C;Genetics:
 A;Gene: GDB:TNFR1
 A;Cross-references: GDB:125913; OMIM:191190
 A;Map position: 12p13.2-12p13.2
 A;Intons: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
 C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo
 C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-45/Domain: signal sequence #status predicted <SIG>
 F;30-211/Domain: extracellular #status predicted <EXT>
 F;41-201/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
 F;44-82/Domain: NGF receptor repeat homology <NG1>
 F;84-126/Domain: NGF receptor repeat homology <NG2>
 F;127-167/Domain: NGF receptor repeat homology <NG3>
 F;168-196/Domain: NGF receptor repeat homology <NG4>
 F;212-234/Domain: transmembrane #status predicted <MEM>
 F;235-455/Domain: intracellular #status predicted <INT>
 F;54;145;151/binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 8.3%; Score 68.5; DB 1; Length 455;
 Best Local Similarity 25.0%; Pred. No. 58;
 Matches 31; Conservative 18; Mismatches 46; Indels 29; Gaps 7;

Qy	28	LECYCKQQLRREVDPAFRDCTIVRDGNPVAVXKCLKFKYSIEYHYHCYVGT	87
Db	100	LSGSKCKRKEGQVEI-----SSCTVDRD-----TVGCKR-----NQYHY-----WSEN	139
Qy	88	LEQGVNPLDLDLRINCXQKPLCPKPKORHLDDKKQFFHNIIRGRWTRCSCGSRSTR	147
Db	140	LPGCFN---CSL---CLNGTVHLSCKQKQNTVCTCHAGFLR---ENECVSCSKCKSL	190
Qy	148	ETQI 151	
Db	191	CTKL 194	

RESULT 98

T28260
hypothetical protein 99 - Melanoplus sanguinipes entomopoxvirus
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T28260
R:Atenoe, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J:Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359
A:Accession: T28260
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-519 <AF0>
A:Cross-references: UNIPROT:Q9YVZ3; UNIPARC:UPI00000F8BA9; EMBL:AF063866; NID:G4049647;
C:Genetic8:
A:Note: MSV099
C:Superfamily: Melanoplus sanguinipes entomopoxvirus hypothetical protein 99

Query Match 8.3%; Score 68.5; DB 2; Length 519;
Best Local Similarity 22.6%; Pred. No. 66;
Matches 31; Conservative 19; Mismatches 54; Indels 33; Gaps 7;

Oy 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRLDCIVRDGPNPY 60
Db 289 LYDISSENFNRIFQLCNEMSSISIMELVALCAVSPQCISVLINDPNT-NVNIV---GKKY 344
Oy 61 AVXDKCL-----KEYSKISEYR-----HYCVSYVGTLEQ-----QYNK 94
Db 345 LI-NKCSSAKINKFLPSAEYGCSLFPKVEILVQSGKISNCY--YNTKEQLFSSSTKYTS 401
Oy 95 PLCDLLRCINXQKPLC 111
Db 402 NCNDITFVCLDDPDSL C 418

RESULT 99

A30817
serendipity (ery h-1) locus protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: A30817
R:Vincent, A.; Keizlarova-Lepesant, J.; Segalat, L.; Yanicostas, C.; Lepesant, J.A.
Mol. Cell. Biol. 8, 4459-4468, 1988
A:Title: Ery h-1, a new Drosophila melanogaster multifingered protein gene showing mater
A:Reference number: A30817; MUID:89039875; PMID:3141791
A:Accession: A30817
A:Molecule type: DNA
A:Residues: 1-868 <VIN>
A:Cross-references: UNIPROT:P15619; UNIPARC:UPI0000135F6B; GB:M23391; NID:G340903; PID:G
C:Genetic8:
A:Gene: FlyBase:wdb
A:Cross-references: FlyBase:FBgn0005642
A:Introns: 338/2; 740/1
C:Keywords: DNA binding; transcription regulation; zinc finger

Query Match 8.3%; Score 68.5; DB 2; Length 868;
Best Local Similarity 27.4%; Pred. No. 11e+02;
Matches 26; Conservative 16; Mismatches 36; Indels 17; Gaps 6;

Oy 65 KCLK-----FYSKI-SEYRHYCVSVYGTLEQYVYKPLCDLLIRGINXQKPL-CPE---- 113
Db 337 KCLKLGSMMWRKRIHSDMKYQCDICGQKPVOKIN--LTHHRIHSSEKPECECQKR 393
Oy 114 -EKQRHLDPKQRFNIRIGRWTCRCMSCRSSRTRR 147
Db 394 FOERSHLORHQYVHAQTRSY--RCEKCGMVKTER 426

RESULT 100

G02741

skeletal muscle LIM-protein SLIM1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: J04893; G02741
R:Moqan, M.J.; Madgwick, A.J.A.
Biochem. Biophys. Res. Commun. 225, 632-638, 1996
A:Title: Slim defines a novel family of LIM-proteins expressed in skeletal muscle.
A:Reference number: J04893; MUID:96354835; PMID:8753811
A:Accession: J04893
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-280 <MO2>
A:Cross-references: UNIPROT:Q9Y630; UNIPARC:UPI000017C350; EMBL:U60115; NID:G1381807; PII
F:162-212/Domain: LIM metal-binding repeat homology <LIM>

Query Match 8.2%; Score 68; DB 2; Length 280;
Best Local Similarity 20.4%; Pred. No. 41;
Matches 23; Conservative 15; Mismatches 27; Indels 48; Gaps 6;

Oy 29 ECVYCKQQLRREYDPAFRLDCIVRDGPNPYAVXDCLKFYSKISEYRHYCVSVYGTTL 88
Db 6 DCHYCRPLOGKK-----YVQKDG-----HCLKCFDK-----FCANT----- 39
Oy 89 EQQYVYKPLCDLLRCINXQKPLCEEKQRIHSDMKYQCDICGQKPVOKIN--LTHHRIHSSEKPECECQKR 141
Db 40 -----CVCRRKPIGADSKVHY--KNRF-----WHDTCFRCAK 70

Search completed: May 27, 2006, 05:17:16
Job time : 33.1084 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:00:16 ; Search time 232.867 Seconds
(without alignments)
599.815 Million cell updates/sec

Title: US-10-530-253-13ED
Perfect score: 830
Sequence: 1 MFQDPQERPKLPQLCTELQ.....WTGRCMSCCRSSRTRETLQ 151

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	826	99.5	151	2	077Jc7_HPV16
2	826	99.5	151	2	089852_9PAP1
3	826	99.5	151	2	09WH13_HPV16
4	824	99.3	151	2	09WMP5_HPV16
5	823	99.2	151	2	077816_HPV16
6	823	99.2	151	2	089755_9PAP1
7	823	99.2	151	2	08B820_HPV16
8	823	99.2	151	1	VE6_HPV16
9	823	99.2	158	2	054702_HPV16
10	823	99.2	161	2	0919C6_HPV16
11	821	98.9	151	2	08B819_HPV16
12	821	98.9	158	2	04VRN5_HPV16
13	820	98.8	158	2	08ORP7_HPV16
14	820	98.8	158	2	08QRD8_HPV16
15	819	98.7	151	2	077205_HPV16
16	819	98.7	151	2	089640_9PAP1
17	819	98.7	151	2	089648_HPV16
18	819	98.7	151	2	09W931_HPV16
19	819	98.7	158	2	02PRU9_HPV16
20	819	98.7	158	2	08QHT0_HPV16
21	818	98.6	151	2	080963_9PAP1
22	818	98.6	158	2	08QHP5_HPV16
23	817	98.4	151	2	08B564_HPV16
24	817	98.4	151	2	09W8C3_HPV16
25	817	98.4	151	2	0919P4_HPV16
26	816	98.3	158	2	08QRP9_HPV16
27	816	98.3	158	2	08QRE0_HPV16
28	816	98.3	158	2	09QDH9_HPV16
29	815	98.2	151	2	089887_9PAP1
30	815	98.2	158	2	08QRD5_HPV16
31	814	98.1	158	2	08QRD6_HPV16

32	814	98.1	158	2	09QDH3_HPV16	09qdh3 human papil
33	814	98.1	161	2	0919B1_HPV16	0919b1 human papil
34	813	98.0	158	2	08QRE1_HPV16	08qre1 human papil
35	812	97.8	151	2	012335_HPV16	012335 human papil
36	811	97.7	151	2	09WMP4_HPV16	09wmp4 human papil
37	810	97.6	151	2	012336_HPV16	012336 human papil
38	809	97.5	158	2	09QDH7_HPV16	09qdh7 human papil
39	808	97.3	151	2	08B821_HPV16	08b821 human papil
40	808	97.3	151	2	09WMP2_HPV16	09wmp2 human papil
41	808	97.3	161	2	0919A9_HPV16	0919a9 human papil
42	806	97.1	151	2	076TS0_9PAP1	076ts0 human papil
43	806	97.1	151	2	080966_HPV16	080966 human papil
44	806	97.1	158	2	08JMW8_HPV16	08jmw8 human papil
45	804	96.9	151	2	077816_HPV16	077816 human papil
46	804	96.9	151	2	089708_9PAP1	089708 human papil
47	804	96.9	151	2	09WMP3_HPV16	09wmp3 human papil
48	803	96.9	158	2	08QHN0_HPV16	08qhn0 human papil
49	803	96.7	158	2	09QDH5_HPV16	09qdh5 human papil
50	781	94.1	143	2	0919C4_HPV16	0919c4 human papil
51	774	93.3	143	2	0919B6_HPV16	0919b6 human papil
52	754	90.8	138	2	0919D2_HPV16	0919d2 human papil
53	712	85.8	130	2	0919C0_HPV16	0919c0 human papil
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55	707	85.2	130	2	0919B8_HPV16	0919b8 human papil
56	707	85.2	130	2	0919C8_HPV16	0919c8 human papil
57	704	84.8	130	2	0919B4_HPV16	0919b4 human papil
58	702	84.6	130	2	0919D0_HPV16	0919d0 human papil
59	580	69.9	149	2	04TU09_HPV16	04tuo9 human papil
60	580	69.9	149	2	084298_9PAP1	084298 human papil
61	578	69.6	149	1	VE6_HPV35	VE6_HPV35
62	578	69.6	149	2	04TUF4_HPV16	04tuf4 human papil
63	560	67.5	103	2	04TUF4_HPV16	04tuf4 human papil
64	532	64.1	99	2	0919B2_HPV16	0919b2 human papil
65	525	63.3	149	1	04TUG1_HPV31	04tug1 human papil
66	523	63.0	149	1	VE6_HPV31	VE6_HPV31
67	523	63.0	149	2	04TUG5_HPV31	04tug5 human papil
68	520	62.7	149	1	VE6_HPV33	VE6_HPV33
69	503	60.6	149	2	08QSE7_HPV16	08qse7 human papil
70	502	60.5	149	2	091ZG6_HPV16	091zg6 human papil
71	498	60.0	149	2	090723_HPV16	090723 human papil
72	497	59.9	149	2	04TUG8_HPV16	04tug8 human papil
73	497	59.9	149	2	091ZG5_HPV16	091zg5 human papil
74	496	59.8	149	1	VE6_HPV58	VE6_HPV58
75	496	59.8	149	2	0547M1_HPV16	0547m1 human papil
76	496	59.8	149	2	08QHO3_HPV16	08qho3 human papil
77	495	59.6	91	2	080887_9PAP1	080887 human papil
78	492	59.3	148	2	04TUG6_HPV16	04tug6 human papil
79	487	58.7	148	1	VE6_HPV52	VE6_HPV52
80	487	58.7	148	2	04TTH4_HPV16	04tth4 human papil
81	487	58.7	148	2	04TTH7_HPV16	04tth7 human papil
82	484	58.3	148	1	VE6_HPV34	VE6_HPV34
83	483	58.2	148	2	082005_HPV16	082005 human papil
84	481	58.0	90	2	080883_9PAP1	080883 human papil
85	481	58.0	90	2	080885_9PAP1	080885 human papil
86	476	57.3	90	2	080884_9PAP1	080884 human papil
87	468.5	56.4	158	1	VE6_HPV58	VE6_HPV58
88	468.5	56.4	158	1	VE6_HPV70	VE6_HPV70
89	468.5	56.4	158	2	02VJD5_HPV16	02vj5 human papil
90	460	55.4	151	1	VE6_HPV51	VE6_HPV51
91	459.5	55.4	158	1	VE6_HPV45	VE6_HPV45
92	457	55.1	84	2	080862_9PAP1	080862 human papil
93	455.5	54.9	158	1	VE6_HPV18	VE6_HPV18
94	455.5	54.9	158	2	076Z77_HPV16	076z77 human papil
95	451.5	54.4	158	1	VE6_HPV56	VE6_HPV56
96	451.5	54.4	158	2	07KTX8_HPV16	07ktx8 human papil
97	451.5	54.4	162	2	09U1Z9_9PAP1	09u1z9 human papil
98	449.5	54.2	158	1	VE6_HPV39	VE6_HPV39
99	449.5	54.2	158	1	09QNP8_HPV16	09qnp8 human papil
100	449.5	54.1	151	2	0994A0_HPV16	0994a0 human papil

ALIGNMENTS

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RESULT 1
073C7 HPV16
ID 073C7 HPV16 PRELIMINARY; PRT; 151 AA.
AC 073C7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Early transforming protein E6 variant (Transforming protein E6).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=333760;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Xinjiang.
RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
RT Biopsies in Xinjiang."
RL Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
[2]
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis."
RL J. Gen. Virol. 81:317-325(2000).
[3]
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2224222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA DeFillipis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
RT but not E7 oncogenes."
RL J. Mol. Evol. 55:491-499(2002).
[4]
RN
RP NUCLEOTIDE SEQUENCE.
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
[5]
RN
RP NUCLEOTIDE SEQUENCE.
RA Cruz M.R., Martins C.R.F.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AF327851; AAG45940.1; -; Genomic DNA.
CC EMBL; AJ388057; CAB45106.1; -; Genomic DNA.
CC EMBL; AJ388059; CAB45130.1; -; Genomic DNA.
CC EMBL; AY089951; AAM11875.1; -; Genomic DNA.
CC EMBL; AY089954; AAM11881.1; -; Genomic DNA.
CC EMBL; AY112663; AAM51854.1; -; Genomic DNA.
CC DR GO; GO:0042025; C:host cell nucleus; IEA.
CC DR GO; GO:0003677; F:DNA binding; IEA.
CC DR InterPro; IPR001334; E6.
CC DR Pfam; PF00518; E6; 1.
CC SQ SEQUENCE 151 AA; 18320 MM; 617D2A2FDB4F8C17 CRC64;

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Best Local Similarity 98.7%; Pred. No. 2,4e-73;
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DB 1 MFQDPQRRPKLPLQLCTELQTTIHDIILCEVCYKQQLRRVYDFARFDCIYVRDGNPY 60
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DB 61 AYVDKCLAFYSKISEYHYCYSVYGTLEQYNNKPLCDLIRICINXOKPLCPBEKQRIHD 120
QY 121 KQRFHNIRGRWTRGCMSCCRSSRTTRRETQL 151
DB 121 KQRFHNIRGRWTRGCMSCCRSSRTTRRETQL 151
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Q89852_9PAPI
ID Q89852_9PAPI PRELIMINARY; PRT; 151 AA.
AC Q89852;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
NCBI_TaxID=10566;
RN
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments."
RL J. Virol. 69:7743-7753(1995).
[2]
RN
RP NUCLEOTIDE SEQUENCE.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; U34134; AAA91681.1; -; Genomic DNA.
CC EMBL; U34127; AAA91674.1; -; Genomic DNA.
CC EMBL; U34133; AAA91680.1; -; Genomic DNA.
CC DR GO; GO:0042025; C:host cell nucleus; IEA.
CC DR GO; GO:0003677; F:DNA binding; IEA.
CC DR InterPro; IPR001334; E6.
CC DR Pfam; PF00518; E6; 1.
CC SQ SEQUENCE 151 AA; 18320 MM; 617D2A2FDB4F8C17 CRC64;

Query Match 99.5%; Score 826; DB 2; Length 151;
Best Local Similarity 98.7%; Pred. No. 2,4e-73;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRRPKLPLQLCTELQTTIHDIILCEVCYKQQLRRVYDFARFDCIYVRDGNPY 60
DB 1 MFQDPQRRPKLPLQLCTELQTTIHDIILCEVCYKQQLRRVYDFARFDCIYVRDGNPY 60
QY 61 AYVDKCLAFYSKISEYHYCYSVYGTLEQYNNKPLCDLIRICINXOKPLCPBEKQRIHD 120
DB 61 AYVDKCLAFYSKISEYHYCYSVYGTLEQYNNKPLCDLIRICINXOKPLCPBEKQRIHD 120
QY 121 KQRFHNIRGRWTRGCMSCCRSSRTTRRETQL 151
DB 121 KQRFHNIRGRWTRGCMSCCRSSRTTRRETQL 151

RESULT 3
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ID Q9WH13 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q9WH13;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=333760;
RN
RN NUCLEOTIDE SEQUENCE.
[1]
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RX MEDLINE=99434235; PubMed=10502513; DOI=10.1006/viro.1999.9868;
 RA Flores E.R., Allen-Hoffmann B.L., Lee D., Sattler C.A., Lambert P.F.;
 RT "establishment of the human papillomavirus type 16 (HPV-16) life cycle
 in an immortalized human foreskin keratinocyte cell line.";
 RL Virology 263:344-354(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=E-C109G;
 RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "human papillomavirus type 16 intracyclic infection and risk
 for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=QY16936E;
 RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
 RA Chen Z., Teraï M., Fu L., Herrero R., Desalle R., Burk R.D.;
 RT "diversifying selection in human papillomavirus type 16 lineages based
 on complete genome analyses.";
 RL J. Virol. 79:7014-7023(2005).
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 CC
 CC EMBL; AF125673; AAD33252.1; -; Genomic DNA.
 DR EMBL; AF486322; AAL96627.1; -; Genomic DNA.
 DR EMBL; AY68580; AAV91652.1; -; Genomic DNA.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 DR SEQUENCE 158 AA; 19173 MW; 9F0CF5ADDA2ED7EE CRC64;
 SQ
 Query Match 99.5%; Score 826; DB 2; Length 158;
 Best Local Similarity 98.7%; Pred. No. 2.5e-73;
 Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFODPOBRPKLPOLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYVRDGNPY 60
 DB 8 MFODPOBRPKLPOLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYVRDGNPY 67
 QY 61 AVXDCKLKFYSKISEYRHVCYVGTLEQYNNKPLCDLLIRCNXKPLCPBEKQRLD 120
 DB 68 AVCDCKLKFYSKISEYRHVCYVGTLEQYNNKPLCDLLIRCNXKPLCPBEKQRLD 127
 QY 121 KKORFNIRGRWTCSCCRSSRTRETOL 151
 DB 128 KKORFNIRGRWTCSCCRSSRTRETOL 158
 RESULT 4
 Q9WMP5 HPV16 PRELIMINARY; PRT; 151 AA.
 AC Q9WMP5;
 DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1999, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 NC NCB1_Taxid=333760;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RA Duin M.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL; AJ242681; CAB45381.1; -; Genomic DNA.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 DR SEQUENCE 151 AA; 18320 MW; 617D25FD93F8917 CRC64;
 SQ
 Query Match 99.3%; Score 824; DB 2; Length 151;
 Best Local Similarity 98.0%; Pred. No. 3.8e-73;
 Matches 149; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFODPOBRPKLPOLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYVRDGNPY 60
 DB 1 MFODPOBRPKLPOLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYVRDGNPY 60
 QY 61 AVXDCKLKFYSKISEYRHVCYVGTLEQYNNKPLCDLLIRCNXKPLCPBEKQRLD 120
 DB 61 AVCDCKLKFYSKISEYRHVCYVGTLEQYNNKPLCDLLIRCNXKPLCPBEKQRLD 120
 QY 121 KKORFNIRGRWTCSCCRSSRTRETOL 151
 DB 121 KKORFNIRGRWTCSCCRSSRTRETOL 151
 RESULT 5
 Q77816 HPV16 PRELIMINARY; PRT; 151 AA.
 AC Q77816;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 NC NCB1_Taxid=333760;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 RN [2]
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 CC
 CC EMBL; AJ388056; CAB45104.1; -; Genomic DNA.
 DR EMBL; AJ388061; CAB45114.1; -; Genomic DNA.
 DR EMBL; AJ388066; CAB45124.1; -; Genomic DNA.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 DR SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;
 SQ
 Query Match 99.2%; Score 823; DB 2; Length 151;
 Best Local Similarity 98.0%; Pred. No. 4.7e-73;
 Matches 149; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFODPOBRPKLPOLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYVRDGNPY 60
 DB 1 MFODPOBRPKLPOLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYVRDGNPY 60
 QY 61 AVXDCKLKFYSKISEYRHVCYVGTLEQYNNKPLCDLLIRCNXKPLCPBEKQRLD 120

Db 61 AVCDKCLKFKYSKISEYRHYCYSVYGTTLLEQYKNRPLCDLLIRICINCQKPLCPBEKQRHLD 120

Qy 121 KKQRFHNIRGRWTCRMCSCCRSSRTRETOL 151
Db 121 KKQRFHNIRGRWTCRMCSCCRSSRTRETOL 151

RESULT 6

Q89755_9PAPI PRELIMINARY; PRT; 151 AA.
ID Q89755;
AC Q89755;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxId=10566;

NP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Farmer A.D.;

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

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CC -----
DR EMBL: U34126; AAA91673.1; -; Genomic DNA.
DR EMBL: U34121; AAA91658.1; -; Genomic DNA.
DR EMBL: U34123; AAA91670.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; F8F82A2FCEBA6C02 CRC64;

Query Match 99.2%; Score 823; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 4.7e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVYRDGMPY 60
Db 1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVYRDGMPY 60
Qy 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLLEQYKNRPLCDLLIRICINCQKPLCPBEKQRHLD 120
Db 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLLEQYKNRPLCDLLIRICINCQKPLCPBEKQRHLD 120
Qy 121 KKQRFHNIRGRWTCRMCSCCRSSRTRETOL 151
Db 121 KKQRFHNIRGRWTCRMCSCCRSSRTRETOL 151
Qy 121 KKQRFHNIRGRWTCRMCSCCRSSRTRETOL 151
Db 121 KKQRFHNIRGRWTCRMCSCCRSSRTRETOL 151

RESULT 7

Q8BB20_HPV16 PRELIMINARY; PRT; 151 AA.
ID Q8BB20_HPV16
AC Q8BB20;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Early transforming protein E6.
OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2224222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA DeFillipis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
RT but not E7 oncogenes.";
RL J. Mol. Evol. 55:491-499(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-V cells,
RT a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [4]

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CC -----
DR EMBL: AY089953; AAM1879.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18319 MW; 7CBDD23EFCFAF8C17 CRC64;

Query Match 99.2%; Score 823; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 4.7e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVYRDGMPY 60
Db 1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLRREYVDFARFDLCIVYRDGMPY 60
Qy 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLLEQYKNRPLCDLLIRICINCQKPLCPBEKQRHLD 120
Db 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLLEQYKNRPLCDLLIRICINCQKPLCPBEKQRHLD 120
Qy 121 KKQRFHNIRGRWTCRMCSCCRSSRTRETOL 151
Db 121 KKQRFHNIRGRWTCRMCSCCRSSRTRETOL 151

RESULT 8

VB6_HPV16 STANDARD; PRT; 158 AA.
ID VB6_HPV16
AC P03126; Q71B17;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 45.
DE Protein E6.
GN Name=E6;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;

RN [1]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Krammer G., Durst M., Suhai S., Roweikamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virol. 145:181-185(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RC STRAIN=Isolate European German 131;
RA Terafi M., Fu L., Ma Z., Burk R.D.;
RT "Cloning and sequencing of non-European human papillomavirus (HPV)
RT variant complete genomes from cervicovaginal cells by an overlapping
RT PCR method.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

RN [3]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA) OF 31-50.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-V cells,
RT a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [4]

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CC -----
DR EMBL: U34126; AAA91673.1; -; Genomic DNA.
DR EMBL: U34121; AAA91658.1; -; Genomic DNA.
DR EMBL: U34123; AAA91670.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18319 MW; 7CBDD23EFCFAF8C17 CRC64;

RP INTERACTION WITH HUMAN FBLN1, AND INHIBITION OF E6-MEDIATED
RP TRANSFORMATION.
RX MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.J.;
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1";
RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded
CC DNA. Has transforming activity. Inactivates, with E6-AP ubiquitin-
CC protein ligase, the human TP53/p53 tumor suppressor protein by
CC targeting it to degradation. Binds and targets human MDM2/MDM4
CC protein to degradation. Those two functions presumably contribute
CC to transforming activity (By similarity). Interaction with human
CC FBLN1 protein also seems to be linked to cell transformation.
CC -1- SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which
CC interacts with human p53. Binds to human FBLN1 and MDM2 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -1- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more
CC often associated with malignant genital cancers in humans.
CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
CC -----
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CC -----
DR EMBL: K02718; AAA4693.1; -; Genomic DNA.
DR EMBL: AF536179; AA010712.1; -; Genomic DNA.
DR EMBL: D00735; BAA00632.1; -; Genomic DNA.
DR PIR: A03682; W6MLHS.
DR PDB: 2FK4; NMR: A=87-158.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
KM 3D-structure: Activator; DNA-binding; Early protein; Metal-binding;
KM Nuclear protein; Oncogene; Transcription; Transcription regulation;
KM Zinc; Zinc-finger.
FT CHAIN 1 158 Protein E6.
FT FTID=PRO_000013336.
FT ZN_FING 37 73 Potential.
FT ZN_FING 110 146 Potential.
FT MOTIF 155 158 PDZ-binding (By similarity).
FT CONFLICT 17 17 R -> G (in Ref. 2).
FT CONFLICT 90 90 L -> V (in Ref. 2).
SQ SEQUENCE 158 AA; 19187 MW; 01FEF5ADCDFD37EB CRC64;
Query Match 99.2%; Score 823; DB 1; Length 158;
Best Local Similarity 98.0%; Pred. No. 4.9e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREVDYFAFADLCIVYRDGPNY 60
DB 8 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREVDYFAFADLCIVYRDGPNY 67
QY 61 AVXDCKLFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHLD 120
DB 68 AVCDKCLKFSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHLD 127
QY 121 KKQRFNIRGRWTCRCMSCCSSSRTRETOL 151
DB 128 KKQRFNIRGRWTCRCMSCCSSSRTRETOL 158
RESULT 9
ID Q54702_HPV16 PRELIMINARY; PRT; 158 AA.
AC Q54702;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Transforming protein E6.
GN Name=E6;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=333760;
QX

RN [1].
RE NUCLEOTIDE SEQUENCE.
RC STRAIN=E-P, E-G241T, E-G187T, and E-G538T;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Chang J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China";
RL J. Infect. Dis. 186:696-700(2002).
RN [2].
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=QV17722E, and QV15521E;
RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
RA Chen Z., Terai M., Fu L., Herrero R., Desalle R., Burk R.D.;
RT "Diversifying selection in human papillomavirus type 16 lineages based
RT on complete genome analyses";
RL J. Virol. 79:7014-7023(2005).
RN [3].
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Beb-102;
RA Cruz M.R., Cergueta D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;
RT "Human papillomavirus type 16 variants in Central Brazil";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AF486311; AAL96616.1; -; Genomic DNA.
DR EMBL: AY686584; AAV91684.1; -; Genomic DNA.
DR EMBL: AF486310; AAL96615.1; -; Genomic DNA.
DR EMBL: AF486312; AAL96617.1; -; Genomic DNA.
DR EMBL: AF486313; AAL96618.1; -; Genomic DNA.
DR EMBL: AF486320; AAL96622.1; -; Genomic DNA.
DR EMBL: AF486320; AAL96625.1; -; Genomic DNA.
DR EMBL: AF486321; AAL96626.1; -; Genomic DNA.
DR EMBL: AF486321; AAL96626.1; -; Genomic DNA.
DR EMBL: AY098919; AAM29167.1; -; Genomic DNA.
DR EMBL: AY686581; AAV91660.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 158 AA; 19187 MW; 01FEF5ADCDFD37EB CRC64;
Query Match 99.2%; Score 823; DB 2; Length 158;
Best Local Similarity 98.0%; Pred. No. 4.9e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREVDYFAFADLCIVYRDGPNY 60
DB 8 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREVDYFAFADLCIVYRDGPNY 67
QY 61 AVXDCKLFYSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHLD 120
DB 68 AVCDKCLKFSKISEYHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPBEKORHLD 127
QY 121 KKQRFNIRGRWTCRCMSCCSSSRTRETOL 151
DB 128 KKQRFNIRGRWTCRCMSCCSSSRTRETOL 158
RESULT 10
ID Q919C6_HPV16 PRELIMINARY; PRT; 161 AA.
AC Q919C6;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=333760;
RN [1].
RN NUCLEOTIDE SEQUENCE.

```

RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
CC -----
CC Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL: AF404697; AAL01351.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
DR NON TER
FT SEQUENCE 161 AA; 19628 MW; 15D32F0F12E00460 CRC64;

Query Match 99.2%; Score 823; DB 2; Length 161;
Best Local Similarity 98.0%; Pred. No. 5e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQPERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60
DB 11 MFQDPQPERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFAFRDLCTIVYRDGNPY 70
QY 61 AVCDKCLKFKYSKISEYRHVYCSVYGTTLBOQYNKPLCDLLIRCIHQKPLCPBEKQKRLD 120
DB 71 AVCDKCLKFKYSKISEYRHVYCSVYGTTLBOQYNKPLCDLLIRCIHQKPLCPBEKQKRLD 130
QY 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151
DB 131 KKQRFHNIRGRWTRCSCSSSRTRETOL 161

RESULT 11
Q8BB19 HPV16 PRELIMINARY; PRT; 151 AA.
AC Q8BB19;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Early transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA Deillipis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
RL but not E7 oncogenes.";
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CC J. Mol. Evol. 55:491-499(2002).
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CC -----
DR EMBL: AY089955; AAM11883.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
DR SEQUENCE 151 AA; 18319 MW; 6F9D2A2FD5AF08F7 CRC64;

Query Match 98.9%; Score 821; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 7.4e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQPERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60
DB 1 MFQDPQPERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60
QY 61 AVCDKCLKFKYSKISEYRHVYCSVYGTTLBOQYNKPLCDLLIRCIHQKPLCPBEKQKRLD 120
DB 61 AVCDKCLKFKYSKISEYRHVYCSVYGTTLBOQYNKPLCDLLIRCIHQKPLCPBEKQKRLD 120
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DB 61 AVCDKCLKFKYSKISEYRHVYCSVYGTTLBOQYNKPLCDLLIRCIHQKPLCPBEKQKRLD 120
QY 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151
DB 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151

RESULT 12
Q4VRN5 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q4VRN5;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=QV18158;
RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
RA Chen Z., Terai M., Fu L., Herrero R., Desalle R., Burk R.D.;
RT "Diversifying selection in human papillomavirus type 16 lineages based
RL on complete genome analyses.";
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CC J. Virol. 79:7014-7023(2005).
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CC -----
DR EMBL: AY686583; AAV91676.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR SEQUENCE 158 AA; 19172 MW; 91ECF5ADD4CED31E CRC64;

Query Match 98.9%; Score 821; DB 2; Length 158;
Best Local Similarity 98.0%; Pred. No. 7.8e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQPERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60
DB 8 MFQDPQPERPRKLPOLCTELQTTIHDIILECYCKQQLRREYVDFAFRDLCTIVYRDGNPY 67
QY 61 AVCDKCLKFKYSKISEYRHVYCSVYGTTLBOQYNKPLCDLLIRCIHQKPLCPBEKQKRLD 120
DB 68 AVCDKCLKFKYSKISEYRHVYCSVYGTTLBOQYNKPLCDLLIRCIHQKPLCPBEKQKRLD 127
QY 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151
DB 128 KKQRFHNIRGRWTRCSCSSSRTRETOL 158

RESULT 13
Q8ORD7 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q8ORD7;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E-C442T;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RT "Human papillomavirus type 16 intracyclic variant infection and risk
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RT for cervical neoplasia in southern China."
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DR EMBL: AF486318; AAL96623.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19173 MW; 14BFB5ADCDB3640 CRC64;

Query Match 98.8%; Score 820; DB 2; Length 158;
Best Local Similarity 97.4%; Pred. No. 9.8e-73;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 60
DB 8 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 67
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLBOQYNKPLCDLLIRCIKXQKPLCPBEKORHLD 120
DB 68 AVCDKCLKFYSKISEYRHYCYSLVGTTLBOQYNKPLCDLLIRCIKXQKPLCPBEKORHLD 127
QY 121 KKQRFNHRGWRGRCMSCCRSSRTRETOL 151
DB 128 KKQRFNHRGWRGRCMSCCRSSRTRETOL 158

RESULT 14
OBORD8_HPV16 PRELIMINARY; PRT; 158 AA.
ID OBORD8_HPV16
AC OBORD8;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E-G449T;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DR EMBL: AF486316; AAL96621.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19188 MW; 01PEFSBD21AF7B8 CRC64;

Query Match 98.8%; Score 820; DB 2; Length 158;
Best Local Similarity 97.4%; Pred. No. 9.8e-73;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 60
DB 8 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 67
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLBOQYNKPLCDLLIRCIKXQKPLCPBEKORHLD 120
DB 68 AVCDKCLKFYSKISEYRHYCYSLVGTTLBOQYNKPLCDLLIRCIKXQKPLCPBEKORHLD 127

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QY 121 KKQRFNHRGWRGRCMSCCRSSRTRETOL 151
DB 128 KKQRFNHRGWRGRCMSCCRSSRTRETOL 158

RESULT 15
077ZJ5_HPV16 PRELIMINARY; PRT; 151 AA.
ID 077ZJ5_HPV16
AC 077ZJ5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Bech-Girardo E., Girardo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
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CC -----
DR EMBL: AF003019; AAB70736.1; -; Genomic DNA.
DR EMBL: AF003018; AAB70735.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48C7 CRC64;

Query Match 98.7%; Score 819; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 1.2e-72;
Matches 148; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 60
DB 1 MFODPOBPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 60
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLBOQYNKPLCDLLIRCIKXQKPLCPBEKORHLD 120
DB 61 AVCDKCLKFYSKISEYRHYCYSVYGTTLBOQYNKPLCDLLIRCIKXQKPLCPBEKORHLD 120
QY 121 KKQRFNHRGWRGRCMSCCRSSRTRETOL 151
DB 121 KKQRFNHRGWRGRCMSCCRSSRTRETOL 151

RESULT 16
Q89640_9PAPI PRELIMINARY; PRT; 151 AA.
ID Q89640_9PAPI
AC Q89640;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OC NCBI_TaxId=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States

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RT populations characterized by nucleotide sequence analysis of the E6,
 RT 12, and 14 coding segments.";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RA NUCLEOTIDE SEQUENCE.
 RP Farmer A.D.;
 RL Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA ponglikitmongkol M.; Vaeteewootacharn K.;
 RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
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 CC -----
 DR EMBL; U34129; AAA91676.1; -; Genomic DNA.
 DR EMBL; AF469198; AA015693.1; -; Genomic DNA.
 DR EMBL; U34115; AAA91662.1; -; Genomic DNA.
 DR EMBL; U34120; AAA91667.1; -; Genomic DNA.
 DR EMBL; U34124; AAA91671.1; -; Genomic DNA.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18348 MW; FE3F2A2FCF0A6CB2 CRC64;
 Query Match 98.7%; Score 819; DB 2; Length 151;
 Best Local Similarity 97.4%; Pred. No. 1.2e-72;
 Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGPNY 60
 DB 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGPNY 60
 QY 61 AVXDKCLKFYSKISEYHYCYSVGTTLEEQYNKPLCDLLIRCTNXXKPLCPBEKQRHLD 120
 DB 61 AVCDKCLKFYSKISEYHYCYSLVGTTLLEQYNKPLCDLLIRCTNXXKPLCPBEKQRHLD 120
 QY 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151
 DB 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151
 RESULT 17
 ID Q89648.9PAPI PRELIMINARY; PRT; 151 AA.
 AC Q89648; O12653; O12928; O12929;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 21.
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC unclassified Papillomaviridae.
 OC NCB1_TaxID=10566;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT 12, and 14 coding segments.";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Farmer A.D.;
 RL Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.
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 CC -----
 DR EMBL; U34110; AAA91657.1; -; Genomic DNA.

DR EMBL; U34109; AAA91656.1; -; Genomic DNA.
 DR EMBL; U34113; AAA91660.1; -; Genomic DNA.
 DR EMBL; U34135; AAA91682.1; -; Genomic DNA.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;
 Query Match 98.7%; Score 819; DB 2; Length 151;
 Best Local Similarity 98.0%; Pred. No. 1.2e-72;
 Matches 148; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGPNY 60
 DB 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGPNY 60
 QY 61 AVXDKCLKFYSKISEYHYCYSVGTTLEEQYNKPLCDLLIRCTNXXKPLCPBEKQRHLD 120
 DB 61 AVCDKCLKFYSKISEYHYCYSLVGTTLLEQYNKPLCDLLIRCTNXXKPLCPBEKQRHLD 120
 QY 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151
 DB 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151
 RESULT 18
 ID Q9W931.HPV16 PRELIMINARY; PRT; 151 AA.
 AC Q9W931;
 DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1999, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC unclassified Papillomaviridae.
 OC NCB1_TaxID=333760;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorthorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
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 CC -----
 DR EMBL; AJ388059; CAB45110.1; -; Genomic DNA.
 DR EMBL; AJ388058; CAB45108.1; -; Genomic DNA.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18306 MW; 6FB3D9E0F24A5300 CRC64;
 Query Match 98.7%; Score 819; DB 2; Length 151;
 Best Local Similarity 97.4%; Pred. No. 1.2e-72;
 Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGPNY 60
 DB 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFDLCIVYRDGPNY 60
 QY 61 AVXDKCLKFYSKISEYHYCYSVGTTLEEQYNKPLCDLLIRCTNXXKPLCPBEKQRHLD 120
 DB 61 AVCDKCLKFYSKISEYHYCYSLVGTTLLEQYNKPLCDLLIRCTNXXKPLCPBEKQRHLD 120
 QY 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151
 DB 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151

```

RESULT 19
Q2PUN9 HPV16 PRELIMINARY; PRT; 158 AA.
ID Q2PUN9 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q2PUN9;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DE 07-FEB-2006, entry version 2.
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mischak H., Soletmanjahi H., Meskhat Z., Bamdad T.;
RT "Cloning and sequence analysis of human papillomavirus type 16 E6.";
RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; DQ333982; ABC48950.1; -; Genomic DNA.
SQ SEQUENCE 158 AA; 19074 MW; 9EBCF5BDB95D75E CRC64;

Query Match 98.7%; Score 819; DB 2; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.2e-72;
Matches 148; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTVYRDGNPY 60
DB 8 MFQDPQRPRLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTVYRDGNPY 67
QY 61 AVXDKCKLFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPSEKQRLD 120
DB 68 AVCDKCKLFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPSEKQRLD 127
QY 121 KKQRFHNIRGRWTCRSCSSRTRETOL 151
DB 128 KKQRFHNIRGRWTCRSCSSRTRETOL 158

RESULT 20
Q8OHT0 HPV16 PRELIMINARY; PRT; 158 AA.
ID Q8OHT0 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q8OHT0;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DE 07-FEB-2006, entry version 15.
DE Putative transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=As-P, and As-A178;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Chung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
RT for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AF486299; AAL96604.1; -; Genomic DNA.
DR EMBL; AF486300; AAL96605.1; -; Genomic DNA.
DR EMBL; AF486301; AAL96606.1; -; Genomic DNA.
DR EMBL; AF486302; AAL96607.1; -; Genomic DNA.
DR EMBL; AF486306; AAL96611.1; -; Genomic DNA.
DR EMBL; AF486308; AAL96613.1; -; Genomic DNA.
DR EMBL; AF534061; AAO10403.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19201 MW; 004EF5ADCEB375B CRC64;

Query Match 98.7%; Score 819; DB 2; Length 158;
Best Local Similarity 97.4%; Pred. No. 1.2e-72;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTVYRDGNPY 60
DB 8 MFQDPQRPRLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTVYRDGNPY 67
QY 61 AVXDKCKLFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPSEKQRLD 120
DB 68 AVCDKCKLFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRCIINXOKPLCPSEKQRLD 127
QY 121 KKQRFHNIRGRWTCRSCSSRTRETOL 151
DB 128 KKQRFHNIRGRWTCRSCSSRTRETOL 158

RESULT 21
Q80963 9PAPI PRELIMINARY; PRT; 151 AA.
ID Q80963 9PAPI PRELIMINARY; PRT; 151 AA.
AC Q80963;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DE 07-FEB-2006, entry version 22.
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
NCBI_Taxid=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jensen S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
J. Virol. 69:7743-7753(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; U34122; AAA91669.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;

Query Match 98.6%; Score 818; DB 2; Length 151;
Best Local Similarity 97.4%; Pred. No. 1.5e-72;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTVYRDGNPY 60
DB 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTVYRDGNPY 60

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Qy 61 AVXDKCLKFYSKISEYRHVCYVYGTTLBOQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 120
    |||
Db 61 AVCDKCLKFYSKISEYRHVCYVYGTTLBOQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 120
Qy 121 KKORFHNIRGWRGCMSCCRSSRTRETOL 151
    |||
Db 121 KKORFHNIRGWRGCMSCCRSSRTRETOL 151

RESULT 22
Q80HP5 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q80HP5;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E-6276T, and E-6276G42T;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RA "Human papillomavirus type 16 intracytic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC
DR EMBL; AF486315; AAL96620.1; -; Genomic DNA.
DR EMBL; AF486315; AAL96620.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19160 MW; AFD01553FCTFAF7 CRC64;

Query Match 98.4%; Score 818; DB 2; Length 158;
Best Local Similarity 97.4%; Pred. No. 1.5e-72;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
    |||
Db 8 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGPNY 67
Qy 61 AVXDKCLKFYSKISEYRHVCYVYGTTLBOQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 120
    |||
Db 68 AVCDKCLKFYSKISEYRHVCYVYGTTLBOQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 127
Qy 121 KKORFHNIRGWRGCMSCCRSSRTRETOL 151
    |||
Db 128 KKORFHNIRGWRGCMSCCRSSRTRETOL 158

RESULT 23
Q8B564 9PAPI PRELIMINARY; PRT; 151 AA.
ID Q8B564 9PAPI PRELIMINARY; PRT; 151 AA.
AC Q8B564;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE E6 protein.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxId=10566;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RA Ponglikitmongkol M., Vaeewooteacharn K.;
RL Submitted (sep-2002) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AF548023; AAO16239.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18348 MW; FE3F2D5FCD7A69B2 CRC64;

Query Match 98.4%; Score 817; DB 2; Length 151;
Best Local Similarity 96.7%; Pred. No. 1.8e-72;
Matches 146; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
    |||
Db 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
Qy 61 AVXDKCLKFYSKISEYRHVCYVYGTTLBOQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 120
    |||
Db 61 AVCDKCLKFYSKISEYRHVCYVYGTTLBOQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 120
Qy 121 KKORFHNIRGWRGCMSCCRSSRTRETOL 151
    |||
Db 121 KKORFHNIRGWRGCMSCCRSSRTRETOL 151

RESULT 24
Q9W8C3 HPV16 PRELIMINARY; PRT; 151 AA.
ID Q9W8C3 HPV16 PRELIMINARY; PRT; 151 AA.
AC Q9W8C3;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duijn M., Smijders P.J., Vossen M.T., Klaassen E., Voorthorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC
DR EMBL; AJ388064; CAB45120.1; -; Genomic DNA.
DR EMBL; AJ388062; CAB45116.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18360 MW; FF9A2A3ADBBA7902 CRC64;

Query Match 98.4%; Score 817; DB 2; Length 151;
Best Local Similarity 97.4%; Pred. No. 1.8e-72;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
    |||
Db 1 MFODPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
Qy 61 AVXDKCLKFYSKISEYRHVCYVYGTTLBOQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 120
    |||

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Db      61 AVCDKCLKFYSKISEYHYCYSVYGTTLBEOQYNKPLCDLIRNCINQKPLCPBEKQRHLD 120
Qy      121 KKQRFHNIRGWRGCMSCCSSSRTTRETOL 151
Db      121 KKQRFHNIRGWRGCMSCCSSSRTTRETOL 151

RESULT 25
Q919D4 HPV16 PRELIMINARY; PRT; 161 AA.
ID Q919D4 HPV16 PRELIMINARY; PRT; 161 AA.
AC Q919D4;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jc.10103;
RA Watts K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL; AF404693; AAL01343.1; -, Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NCBI_TaxID=333760;
FT NON TER 1
SQ SEQUENCE 161 AA; 19624 MW; 10C72CDB14200460 CRC64;

Query Match 98.4%; Score 817; DB 2; Length 161;
Best Local Similarity 97.4%; Pred. No. 2e-72;
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREVYDFAFRDLCIVYRDGMPY 60
Db      11 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREVYDFAFRDLCIVYRDGMPY 70
Qy      61 AVXDKCLKFYSKISEYHYCYSVYGTTLBEOQYNKPLCDLIRNCINQKPLCPBEKQRHLD 120
Db      71 AVCDKCLKFYSKISEYHYCYSVYGTTLBEOQYNKPLCDLIRNCINQKPLCPBEKQRHLD 130
Qy      121 KKQRFHNIRGWRGCMSCCSSSRTTRETOL 151
Db      131 KKQRFHNIRGWRGCMSCCSSSRTTRETOL 161

RESULT 26
Q08RD9 HPV16 PRELIMINARY; PRT; 158 AA.
ID Q08RD9 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q08RD9;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
FT NON TER 1
SQ SEQUENCE 158 AA; 19187 MW; 005E2FCE1617C55B CRC64;

Query Match 98.3%; Score 816; DB 2; Length 158;
Best Local Similarity 96.7%; Pred. No. 2.4e-72;
Matches 146; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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RT      "Human papillomavirus type 16 intra-tytic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DR EMBL; AF486309; AAL96614.1; -, Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NCBI_TaxID=333760;
FT NON TER 1
SQ SEQUENCE 158 AA; 19173 MW; 161AD3EFAA4D636B CRC64;

Query Match 98.3%; Score 816; DB 2; Length 158;
Best Local Similarity 96.7%; Pred. No. 2.4e-72;
Matches 146; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREVYDFAFRDLCIVYRDGMPY 60
Db      8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREVYDFAFRDLCIVYRDGMPY 67
Qy      61 AVXDKCLKFYSKISEYHYCYSVYGTTLBEOQYNKPLCDLIRNCINQKPLCPBEKQRHLD 120
Db      68 AVCDKCLKFYSKISEYHYCYSVYGTTLBEOQYNKPLCDLIRNCINQKPLCPBEKQRHLD 127
Qy      121 KKQRFHNIRGWRGCMSCCSSSRTTRETOL 151
Db      128 KKQRFHNIRGWRGCMSCCSSSRTTRETOL 158

RESULT 27
Q08RE0 HPV16 PRELIMINARY; PRT; 158 AA.
ID Q08RE0 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q08RE0;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intra-tytic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DR EMBL; AF486307; AAL96612.1; -, Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NCBI_TaxID=333760;
FT NON TER 1
SQ SEQUENCE 158 AA; 19187 MW; 005E2FCE1617C55B CRC64;

Query Match 98.3%; Score 816; DB 2; Length 158;
Best Local Similarity 96.7%; Pred. No. 2.4e-72;
Matches 146; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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Db 68 AVCDKCLFYSKISEYRHVYCSLVGTTLEQYKPLCDLLIRCIINCQKPLCPBEKQRLD 127
Qy 121 KKORFHNIRGWTGCMSCCRSSRRRTTOL 151
Db 128 KKORFHNIRGWTGCMSCCRSSRRRTTOL 158

RESULT 28
Q0Q0H9 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q0Q0H9;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SSP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=As-C442;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DR EMBL; AF187866; AAF13392.1; -; Genomic DNA.
DR EMBL; AF486304; AAL96609.1; -; Genomic DNA.
DR EMBL; AF486305; AAL96610.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19187 MW; 155BF5ADCE6836F0 CRC64;

Query Match 98.3%; Score 816; DB 2; Length 158;
Best Local Similarity 96.7%; Pred. No. 2.4e-72;
Matches 146; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOEPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPRDLCTIVRDGNPY 60
Db 8 MFODPOEPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPRDLCTIVRDGNPY 67
Qy 61 AVXCKCLFYSKISEYRHVYCSLVGTTLEQYKPLCDLLIRCIINCQKPLCPBEKQRLD 120
Db 68 AVXCKCLFYSKISEYRHVYCSLVGTTLEQYKPLCDLLIRCIINCQKPLCPBEKQRLD 127
Qy 121 KKORFHNIRGWTGCMSCCRSSRRRTTOL 151
Db 128 KKORFHNIRGWTGCMSCCRSSRRRTTOL 158

RESULT 29
Q08887 HPV16 PRELIMINARY; PRT; 151 AA.
AC Q08887;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
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OX NCBI_TaxID=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; U34108; AAA91655.1; -; Genomic DNA.
DR EMBL; U34107; AAA91654.1; -; Genomic DNA.
DR EMBL; U34112; AAA91659.1; -; Genomic DNA.
DR EMBL; U34116; AAA91663.1; -; Genomic DNA.
DR EMBL; U34119; AAA91666.1; -; Genomic DNA.
DR EMBL; U34132; AAA91679.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18355 MW; 4695A0D5F34F9908 CRC64;

Query Match 98.2%; Score 815; DB 2; Length 151;
Best Local Similarity 97.4%; Pred. No. 2.9e-72;
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MFODPOEPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPRDLCTIVRDGNPY 60
Db 1 MFODPOEPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPRDLCTIVRDGNPY 60
Qy 61 AVXCKCLFYSKISEYRHVYCSLVGTTLEQYKPLCDLLIRCIINCQKPLCPBEKQRLD 120
Db 61 AVXCKCLFYSKISEYRHVYCSLVGTTLEQYKPLCDLLIRCIINCQKPLCPBEKQRLD 120
Qy 121 KKORFHNIRGWTGCMSCCRSSRRRTTOL 151
Db 121 KKORFHNIRGWTGCMSCCRSSRRRTTOL 151

RESULT 30
Q080R5 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q080R5;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NA1;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=QV15351AA; and QV15321AA;
RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
RA Chen Z., Teraï M., Fu L., Herrero R., Desalle R., Burk R.D.;
```

"Diversifying selection in human papillomavirus type 16 lineages based on complete genome analyses." J. Virol. 79:7014-7023 (2005).

RT on complete genome analyses."
RL J. Virol. 79:7014-7023 (2005).
RN
RP NUCLEOTIDE SEQUENCE.
RA Teraai M., Burk R.D.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN
RN NUCLEOTIDE SEQUENCE.
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN
RN NUCLEOTIDE SEQUENCE.
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN
RN NUCLEOTIDE SEQUENCE.
RA Cruz M.R., Martins C.R.F.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL: AF486325; AAL96630.1; -; Genomic DNA.
DR EMBL: AY686582; AAV91668.1; -; Genomic DNA.
DR EMBL: AF402678; AAO85408.1; -; Genomic DNA.
DR EMBL: AY098923; AAM29171.1; -; Genomic DNA.
DR EMBL: AY112662; AAM51953.1; -; Genomic DNA.
DR EMBL: AY686579; AAV91644.1; -; Genomic DNA.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; B6.
DR Pfam: PF00518; B6; 1.
SQ SEQUENCE 158 AA; 19208 MW; BBE47F57F22EC2E1 CRC64;

Query Match 98.1%; Score 815; DB 2; Length 158;
Best Local Similarity 97.4%; Pred. No. 3e-72;
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 60
DB 8 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 67

QY 61 AYXDKCLKFYSKISEYRHVYCYVYGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 120
DB 68 AVCDKCLKFYSKISEYRHVYCYVYGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 127

QY 121 KKQRFNIRGRWGTGRMCSCRSSRTRETOL 151
DB 128 KKQRFNIRGRWGTGRMCSCRSSRTRETOL 158

RESULT 31
ID Q8QRD6_HPV16 PRELIMINARY; PRT; 158 AA.
AC Q8QRD6;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE B6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E-T360T;
RX MEDLINE=2182962; Pubmed=12195358; DOI=10.1086/342046;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk

for cervical neoplasia in southern China." J. Infect. Dis. 186:686-700 (2002).

RT J. Infect. Dis. 186:686-700 (2002).
RL
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DR EMBL: AF486319; AAL96624.1; -; Genomic DNA.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; B6.
DR Pfam: PF00518; B6; 1.
SQ SEQUENCE 158 AA; 19246 MW; 01FEF70F45F137EB CRC64;

Query Match 98.1%; Score 814; DB 2; Length 158;
Best Local Similarity 97.4%; Pred. No. 3.8e-72;
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 60
DB 8 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 67

QY 61 AYXDKCLKFYSKISEYRHVYCYVYGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 120
DB 68 AVCDKCLKFYSKISEYRHVYCYVYGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 127

QY 121 KKQRFNIRGRWGTGRMCSCRSSRTRETOL 151
DB 128 KKQRFNIRGRWGTGRMCSCRSSRTRETOL 158

RESULT 32
ID Q9QDH3_HPV16 PRELIMINARY; PRT; 158 AA.
AC Q9QDH3;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE B6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
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DR EMBL: AF187869; AAF13398.1; -; Genomic DNA.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; B6.
DR Pfam: PF00518; B6; 1.
SQ SEQUENCE 158 AA; 19210 MW; 004FE5ADD6FA8B5B CRC64;

Query Match 98.1%; Score 814; DB 2; Length 158;
Best Local Similarity 96.7%; Pred. No. 3.8e-72;
Matches 146; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 60
DB 8 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYVDFAFRDLCIYVRDGNPY 67

QY 61 AYXDKCLKFYSKISEYRHVYCYVYGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 120
DB 68 AVCDKCLKFYSKISEYRHVYCYVYGTTLBOQYNNKPLCDLLIRCNQKPLCPBEKQRHLD 127

QY 121 KKQRFNIRGRWGTGRMCSCRSSRTRETOL 151
DB 128 KKQRFNIRGRWGTGRMCSCRSSRTRETOL 158

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RESULT 33
ID Q919B1_HPV16 PRELIMINARY; PRT; 161 AA.
AC Q919B1;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE E6 protein (fragment) type 16.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jc.10103;
RA Watts K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL; AF404705; AL013366.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 161 AA; 19616 MW; E4722F0F134104DC CRC64;

Query Match 98.1%; Score 814; DB 2; Length 161;
Best Local Similarity 96.7%; Pred. No. 3.9e-72;
Matches 146; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIVYRDGPNY 60
DB 11 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIVYRDGPNY 70

QY 61 AYXDKCLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 71 AYXDKCLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 130

QY 121 KKQRFNHRGRMTGRCMSCCRSSRTTRRETOL 151
DB 131 KKQRFNHRGRMTGRCMSCCRSSRTTRRETOL 161

RESULT 34
ID Q90RE1_HPV16 PRELIMINARY; PRT; 158 AA.
AC Q90RE1;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DE 07-FEB-2006, entry version 14.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=As-C131;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.-S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DR EMBL; AF486303; AA196608.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19146 MW; CB6EF5A91548727C CRC64;

Query Match 98.0%; Score 813; DB 2; Length 158;
Best Local Similarity 96.7%; Pred. No. 4.8e-72;
Matches 146; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIVYRDGPNY 60
DB 8 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIVYRDGPNY 67

QY 61 AYXDKCLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 68 AYXDKCLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 127

QY 121 KKQRFNHRGRMTGRCMSCCRSSRTTRRETOL 151
DB 128 KKQRFNHRGRMTGRCMSCCRSSRTTRRETOL 158

RESULT 35
ID Q12335_HPV16 PRELIMINARY; PRT; 151 AA.
AC Q12335;
DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT 01-JUL-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97437474; PubMed=9292007;
RA Tomecello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
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CC -----
DR EMBL; AF003015; AB070732.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B01CC88B CRC64;

Query Match 97.8%; Score 812; DB 2; Length 151;
Best Local Similarity 96.7%; Pred. No. 5.7e-72;
Matches 146; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIVYRDGPNY 60
DB 1 MFQDPQERPRKLPDLCTELQTTIHDIILCEVCYKQQLRREYVDFAFRDLCTIVYRDGPNY 60

QY 61 AYXDKCLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 61 AYXDKCLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120

QY 121 KKQRFNHRGRMTGRCMSCCRSSRTTRRETOL 151
DB 121 KKQRFNHRGRMTGRCMSCCRSSRTTRRETOL 151
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RESULT 36
Q9WMP4_HPV16 PRELIMINARY; PRT; 151 AA.
ID Q9WMP4_HPV16
AC Q9WMP4
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DE 07-FEB-2006, entry version 18.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
CC -----
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DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18387 MW; E2244784BBA6C02 CRC64;

Query Match 97.7%; Score 811; DB 2; Length 151;
Best Local Similarity 97.4%; Pred. No. 7.2e-72;
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTIVRDGNY 60
DB 1 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTIVRDGNY 60
QY 61 AVXDCKLKFYSKISEYHRYCYVYGTLEQYNNKPLCDLLIRINCXKPLCPBEKQRRLD 120
DB 61 AVXDCKLKFYSKISEYHRYCYVYGTLEQYNNKPLCDLLIRINCXKPLCPBEKQRRLD 120
QY 121 KKQRFNIRGRWTRGMSCCSSSTRRETOL 151
DB 121 KKQRFNIRGRWTRGMSCCSSSTRRETOL 151
QY 121 KKQRFNIRGRWTRGMSCCSSSTRRETOL 151
DB 121 KKQRFNIRGRWTRGMSCCSSSTRRETOL 151

RESULT 37
O12336_HPV16 PRELIMINARY; PRT; 151 AA.
ID O12336_HPV16
AC O12336
DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT 01-JUL-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
CC -----
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DR EMBL: AF003016; AAB70733.1; -, Genomic_DNA.

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DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 97.6%; Score 810; DB 2; Length 151;
Best Local Similarity 96.0%; Pred. No. 9e-72;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTIVRDGNY 60
DB 1 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTIVRDGNY 60
QY 61 AVXDCKLKFYSKISEYHRYCYVYGTLEQYNNKPLCDLLIRINCXKPLCPBEKQRRLD 120
DB 61 AVXDCKLKFYSKISEYHRYCYVYGTLEQYNNKPLCDLLIRINCXKPLCPBEKQRRLD 120
QY 121 KKQRFNIRGRWTRGMSCCSSSTRRETOL 151
DB 121 KKQRFNIRGRWTRGMSCCSSSTRRETOL 151
QY 121 KKQRFNIRGRWTRGMSCCSSSTRRETOL 151
DB 121 KKQRFNIRGRWTRGMSCCSSSTRRETOL 151

RESULT 38
Q9QDH7_HPV16 PRELIMINARY; PRT; 158 AA.
ID Q9QDH7_HPV16
AC Q9QDH7
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 17.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (Sep-1999) to the EMBL/Genbank/DBJ databases.
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DR EMBL: AF187867; AAF13394.1; -, Genomic_DNA.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19215 MW; FCSBF2B06576864B CRC64;

Query Match 97.5%; Score 809; DB 2; Length 158;
Best Local Similarity 96.0%; Pred. No. 1.2e-71;
Matches 145; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTIVRDGNY 60
DB 8 MFODPQRPRLPOLCTELQTTIHDIILBCYCKQQLLRREVDFAFRDLCTIVRDGNY 67
QY 61 AVXDCKLKFYSKISEYHRYCYVYGTLEQYNNKPLCDLLIRINCXKPLCPBEKQRRLD 120
DB 68 AVXDCKLKFYSKISEYHRYCYVYGTLEQYNNKPLCDLLIRINCXKPLCPBEKQRRLD 127
QY 121 KKQRFNIRGRWTRGMSCCSSSTRRETOL 151
DB 128 KKQRFNIRGRWTRGMSCCSSSTRRETOL 158
QY 121 KKQRFNIRGRWTRGMSCCSSSTRRETOL 151
DB 121 KKQRFNIRGRWTRGMSCCSSSTRRETOL 151

RESULT 39
Q8BB21_HPV16 PRELIMINARY; PRT; 151 AA.
ID Q8BB21_HPV16
AC Q8BB21
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.

```

DT 07-FEB-2006, entry version 13.
DE Early transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22424222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA Derlijpits V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
but not E7 oncogenes."
RL J. Mol. Evol. 55:491-499(2002).
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CC -----
CC EMBL; AY089952; AAM1877.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18398 MW; 4695B485FC1F8208 CRC64;
Query Match 97.3%; Score 808; DB 2; Length 151;
Best Local Similarity 96.7%; Pred. No. 1.4e-71;
Matches 146; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCCKQQLRREVDFAFRDLCTVRRDNPY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCCKQQLRREVDFAFRDLCTVRRDNPY 60
QY 61 AVXDKCLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRNCINXOKPLCPBEKQRLD 120
DB 61 AVXDKCLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRNCINXOKPLCPBEKQRLD 120
QY 121 KKQRFHNIRGRWTCRSCSSSTRRETOL 151
DB 121 KKQRFHNIRGRWTCRSCSSSTRRETOL 151
RESULT 40
Q9NMP2_HPV16 PRELIMINARY; PRT; 151 AA.
AC Q9NMP2;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 18.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2011892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis."
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
CC EMBL; AJ388067; CAB45126.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18306 MW; 5E71B4EF44993C34 CRC64;
Query Match 97.3%; Score 808; DB 2; Length 151;

Best Local Similarity 96.0%; Pred. No. 1.4e-71;
Matches 145; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCCKQQLRREVDFAFRDLCTVRRDNPY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCCKQQLRREVDFAFRDLCTVRRDNPY 60
QY 61 AVXDKCLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRNCINXOKPLCPBEKQRLD 120
DB 61 AVXDKCLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRNCINXOKPLCPBEKQRLD 120
QY 121 KKQRFHNIRGRWTCRSCSSSTRRETOL 151
DB 121 KKQRFHNIRGRWTCRSCSSSTRRETOL 151
RESULT 41
Q919A9_HPV16 PRELIMINARY; PRT; 161 AA.
AC Q919A9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 16.
DE E6 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia."
RL Int. J. Cancer 97:868-874(2002).
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CC -----
CC EMBL; AF04706; AL001368.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 161 AA; 19692 MW; ACC9B1A52045EA6A CRC64;
Query Match 97.3%; Score 808; DB 2; Length 161;
Best Local Similarity 96.7%; Pred. No. 1.5e-71;
Matches 146; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCCKQQLRREVDFAFRDLCTVRRDNPY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCCKQQLRREVDFAFRDLCTVRRDNPY 70
QY 61 AVXDKCLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRNCINXOKPLCPBEKQRLD 120
DB 71 AVXDKCLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRNCINXOKPLCPBEKQRLD 130
QY 121 KKQRFHNIRGRWTCRSCSSSTRRETOL 151
DB 131 KKQRFHNIRGRWTCRSCSSSTRRETOL 161
RESULT 42
Q76TS0_9PAPI PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 11.
DE Early transforming protein E6.
OS Human papillomavirus.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
NC NCB1_TaxID=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RL Farmer A.D.;
RU Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
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DR EMBL; U34114; AAA91661.1; -; Genomic DNA.
DR EMBL; U34125; AAA91672.1; -; Genomic DNA.
DR EMBL; U34130; AAA91677.1; -; Genomic DNA.
DR EMBL; U34131; AAA91678.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; B6.
DR Pfam; PF00518; B6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 97.1%; Score 806; DB 2; Length 151;
Best Local Similarity 96.0%; Pred. No. 2.2e-71;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCCKQQLRREVDYFARFDLCIVRDGDPY 60
DB 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCCKQQLRREVDYFARFDLCIVRDGDPY 60

QY 61 AVXKCLKFYSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXKQPLCPBEKORHLD 120
DB 61 AVCKCKLKFYSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXKQPLCPBEKORHLD 120

QY 121 KKQRFNIRGRWTRGCMSCCRSSRTRETQL 151
DB 121 KKQRFNIRGRWTRGCMSCCRSSRTRETQL 151

RESULT 43
Q80966 HPV16 PRELIMINARY; PRT; 151 AA.
AC Q80966; O12650; O12651; O12652; O12925; O12926; O12927; Q80962;
AC Q80964; Q80965;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCB1_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97437474; PubMed=9292007;
RA Tomecello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Terafi M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA Van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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DR EMBL; AF003014; AAB70731.1; -; Genomic DNA.
DR EMBL; AF003017; AAB70734.1; -; Genomic DNA.
DR EMBL; AF472508; AAO15697.1; -; Genomic DNA.
DR EMBL; AJ388068; CAB45128.1; -; Genomic DNA.
DR EMBL; AF003013; AAB70730.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; B6.
DR Pfam; PF00518; B6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 97.1%; Score 806; DB 2; Length 151;
Best Local Similarity 96.0%; Pred. No. 2.2e-71;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCCKQQLRREVDYFARFDLCIVRDGDPY 60
DB 1 MFQDPQRPRLPOLCTELQTTIHDIIECYCCKQQLRREVDYFARFDLCIVRDGDPY 60

QY 61 AVXKCLKFYSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXKQPLCPBEKORHLD 120
DB 61 AVCKCKLKFYSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXKQPLCPBEKORHLD 120

QY 121 KKQRFNIRGRWTRGCMSCCRSSRTRETQL 151
DB 121 KKQRFNIRGRWTRGCMSCCRSSRTRETQL 151

RESULT 44
Q80966 HPV16 PRELIMINARY; PRT; 158 AA.
AC Q80966; O12650; O12651; O12652; O12925; O12926; O12927; Q80962;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCB1_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cruz M.R., Queiroz D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.P.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Terafi M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY098922; AAO19170.1; -; Genomic DNA.
DR EMBL; AF536180; AAO10720.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; B6.
DR Pfam; PF00518; B6; 1.
SQ SEQUENCE 158 AA; 19145 MW; CB70F51C00F867DC CRC64;

Query Match 97.1%; Score 806; DB 2; Length 158;

Best Local Similarity 96.0%; Pred. No. 2.4e-71;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPFDLCIVRDGMPY 60
DB 8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPFDLCIVRDGMPY 67
QY 61 AVXDKCLKFYSKISEYRHVCYVYGTTLLEQYKNPCLDLLIRICINXQKPLCPBEKQRLHD 120
DB 68 AVXDKCLKFYSKISEYRHVCYVYGTTLLEQYKNPCLDLLIRICINXQKPLCPBEKQRLHD 127
QY 121 KKQRFHNIRGRWTRCSCCSSRTRRETOL 151
DB 128 KKQRFHNIRGRWTRCSCCSSRTRRETOL 158

RESULT 45

Q77E16 HPV16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;

RN NUCLEOTIDE SEQUENCE.
RA Ponglikitmongkol M., Vaeteewootacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RP [2]

CC NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).

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CC -----
DB EMBL: AF469197; AAO15691.1; -: Genomic DNA.
DR EMBL: AJ388063; CAB45118.1; -: Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBACF1F CRC64;

Query Match 96.9%; Score 804; DB 2; Length 151;
Best Local Similarity 96.0%; Pred. No. 3.5e-71;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPFDLCIVRDGMPY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPFDLCIVRDGMPY 60
QY 61 AVXDKCLKFYSKISEYRHVCYVYGTTLLEQYKNPCLDLLIRICINXQKPLCPBEKQRLHD 120
DB 61 AVXDKCLKFYSKISEYRHVCYVYGTTLLEQYKNPCLDLLIRICINXQKPLCPBEKQRLHD 120
QY 121 KKQRFHNIRGRWTRCSCCSSRTRRETOL 151
DB 121 KKQRFHNIRGRWTRCSCCSSRTRRETOL 151

RESULT 46

Q89708 9PAPI PRELIMINARY; PRT; 151 AA.
ID Q89708 9PAPI
AC Q89708;

DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 24.

DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxID=10566;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT E2, and L1 coding segments";
RL J. Virol. 69:7743-7753(1995).

RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

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CC -----

DB EMBL: U34128; AAA91675.1; -: Genomic DNA.
DR EMBL: U34117; AAA91664.1; -: Genomic DNA.
DR EMBL: U34118; AAA91665.1; -: Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBACF1F CRC64;

Query Match 96.9%; Score 804; DB 2; Length 151;
Best Local Similarity 96.0%; Pred. No. 3.5e-71;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPFDLCIVRDGMPY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPFDLCIVRDGMPY 60
QY 61 AVXDKCLKFYSKISEYRHVCYVYGTTLLEQYKNPCLDLLIRICINXQKPLCPBEKQRLHD 120
DB 61 AVXDKCLKFYSKISEYRHVCYVYGTTLLEQYKNPCLDLLIRICINXQKPLCPBEKQRLHD 120
QY 121 KKQRFHNIRGRWTRCSCCSSRTRRETOL 151
DB 121 KKQRFHNIRGRWTRCSCCSSRTRRETOL 151

RESULT 47

Q9WMP3 HPV16 PRELIMINARY; PRT; 151 AA.
ID Q9WMP3 HPV16
AC Q9WMP3;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).

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CC EMBL; AJ88065; CAB45122.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; B6.
DR Pfam; PF00518; B6; 1.
SQ SEQUENCE 151 AA; 18412 MW; E794A494F0D8E209 CRC64;

Query Match 96.9%; Score 804; DB 2; Length 151;
Best Local Similarity 96.0%; Pred. No. 3.5e-71;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTTHDILLECVCYCKQQLLRREYDFAFRDLCIVYRDGPNY 60
DB 1 MFODPOERPRKLPOLCTELQTTTHDILLECVCYCKQQLLRREYDFAFRDLCIVYRDGPNY 60
QY 61 AVXDCKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 120
DB 61 AVXDCKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 120
QY 121 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 121 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 48
Q08QNO HPV16 PRELIMINARY; PRT; 158 AA.
ID Q08QNO HPV16
AC Q08QNO;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Transforming protein B6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-350G, and Af2-a;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 integrative variant infection and risk
for cervical neoplasia in southern China."
RT J. Infect. Dis. 186:696-700(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Teral M., Ma Z., Burk R.D.;
RN Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Cruz M.R., Cerveira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
Martins C.R.F.;
RN Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AF486314; AAU96619.1; -; Genomic DNA.
DR EMBL; AF472509; AAO15705.1; -; Genomic DNA.
DR EMBL; AF486314; AAU96629.1; -; Genomic DNA.
DR EMBL; AY098918; AAM29166.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; B6.
DR Pfam; PF00518; B6; 1.
SQ SEQUENCE 158 AA; 19157 MW; F140F509DAC794F6 CRC64;

Query Match 96.9%; Score 804; DB 2; Length 158;
Best Local Similarity 96.0%; Pred. No. 3.7e-71;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTTHDILLECVCYCKQQLLRREYDFAFRDLCIVYRDGPNY 60
DB 8 MFODPOERPRKLPOLCTELQTTTHDILLECVCYCKQQLLRREYDFAFRDLCIVYRDGPNY 67
QY 61 AVXDCKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 120
DB 68 AVXDCKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 127
QY 121 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 128 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 158

Query Match 96.7%; Score 803; DB 2; Length 158;
Best Local Similarity 96.0%; Pred. No. 4.7e-71;
Matches 145; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTTHDILLECVCYCKQQLLRREYDFAFRDLCIVYRDGPNY 60
DB 8 MFODPOERPRKLPOLCTELQTTTHDILLECVCYCKQQLLRREYDFAFRDLCIVYRDGPNY 67
QY 61 AVXDCKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 120
DB 68 AVXDCKLKFYSKISEYHYCYSVYGTLEQOYNKPLCDLIRCTINXOKPLCPBEKORHLD 127
QY 121 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 128 KKORFHNIRGRWTRGCMSCCRSSRTRETOL 158

RESULT 50
Q019C4 HPV16 PRELIMINARY; PRT; 143 AA.
ID Q019C4 HPV16
AC Q019C4;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=21846229; PubMed=11857370; DOI=10.1002/13c.10103;
RX

```

RA  Wats K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT  "Sequence variation and physical state of human papillomavirus type 16
RL  Int. J. Cancer 97:868-874(2002).
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CC  -----
DR  EMBL; AF404698; AAL01353.1; -; Genomic DNA.
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
FT  NON TER
SQ  SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match      94.1%; Score 781; DB 2; Length 143;
Best Local Similarity 97.9%; Pred. No. 6.2e-69;
Matches 140; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  9 PRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLK 68
DB  1 PRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLK 60
QY  69 FYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLDDKKQRFHNI 128
DB  61 FYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLDDKKQRFHNI 120
QY  129 RGRWTRGCMSCCRSSRTRETOL 151
DB  121 RGRWTRGCMSCCRSSRTRETOL 143

RESULT 51
ID  Q919B6 HPV16 PRELIMINARY; PRT; 143 AA.
AC  Q919B6;
DT  01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT  01-DEC-2001, sequence version 1.
DT  07-FEB-2006, entry version 16.
DE  E6 protein (Fragment).
OS  Human papillomavirus type 16.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC  Alphapapillomavirus.
OX  NCBI_TaxID=333760;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;
RA  Wats K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT  "Sequence variation and physical state of human papillomavirus type 16
RL  Int. J. Cancer 97:868-874(2002).
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CC  -----
DR  EMBL; AF404702; AAL01361.1; -; Genomic DNA.
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
FT  NON TER
SQ  SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match      93.3%; Score 774; DB 2; Length 143;
Best Local Similarity 97.2%; Pred. No. 3e-66;
Matches 139; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY  9 PRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLK 68
DB  1 PRKLPOLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLK 60
QY  69 FYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLDDKKQRFHNI 128

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DB  61 FYSKISEYRHVCYSYVGTALAEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLDDKKQRFHNI 120
QY  129 RGRWTRGCMSCCRSSRTRETOL 151
DB  121 RGRWTRGCMSCCRSSRTRETOL 143

RESULT 52
ID  Q919D2 HPV16 PRELIMINARY; PRT; 138 AA.
AC  Q919D2;
DT  01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT  01-DEC-2001, sequence version 1.
DT  07-FEB-2006, entry version 16.
DE  E6 protein (Fragment).
OS  Human papillomavirus type 16.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC  Alphapapillomavirus.
OX  NCBI_TaxID=333760;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;
RA  Wats K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT  "Sequence variation and physical state of human papillomavirus type 16
RL  Int. J. Cancer 97:868-874(2002).
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CC  -----
DR  EMBL; AF404694; AAL01345.1; -; Genomic DNA.
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
FT  NON TER
SQ  SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match      90.8%; Score 754; DB 2; Length 138;
Best Local Similarity 98.6%; Pred. No. 2.8e-66;
Matches 136; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  14 QLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLKFYSKI 73
DB  1 QLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCTIYRDGNPYAVXDKCLKFYSKI 60
QY  74 SEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLDDKKQRFHNI RGRWT 133
DB  61 SEYRHVCYSYVGTTLLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLDDKKQRFHNI RGRWT 120
QY  134 GRWCMSCCRSSRTRETOL 151
DB  121 GRWCMSCCRSSRTRETOL 138

RESULT 53
ID  Q919C0 HPV16 PRELIMINARY; PRT; 130 AA.
AC  Q919C0;
DT  01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT  01-DEC-2001, sequence version 1.
DT  07-FEB-2006, entry version 16.
DE  E6 protein (Fragment).
OS  Human papillomavirus type 16.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC  Alphapapillomavirus.
OX  NCBI_TaxID=333760;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;
RA  Wats K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT  "Sequence variation and physical state of human papillomavirus type 16

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RT cervical cancer isolates from Australia and New Caledonia."
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL: AF404700; AL01357.1; -, Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; B6; 1.
FT NON TER
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 85.8%; Score 712; DB 2; Length 130;
Best Local Similarity 98.5%; Pred. No. 3.6e-62;
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 TIHHIIIECYVCKQOQLRREYVDFAFRDLCTVYRDGNFYAVXDKLKFYSKISEYRHICY 81
DB 1 TIHHIIIECYVCKQOQLRREYVDFAFRDLCTVYRDGNFYAVXDKLKFYSKISEYRHICY 60

QY 82 SVYGTLEQYNNKPLCDLLIRICINXQKPLCEBEKQRHLDKKQRFNIRGRTGRCMSCCR 141
DB 61 SVYGTLEQYNNKPLCDLLIRICINQKPLCEBEKQRHLDKKQRFNIRGRTGRCMSCCR 120

QY 142 SSRTRETOL 151
DB 121 SSRTRETOL 130

RESULT 54
QY 0919C2_HPV16 PRELIMINARY; PRT; 130 AA.
ID 0919C2_HPV16 PRELIMINARY; PRT; 130 AA.
AC 0919C2;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Watts K.U., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL: AF404699; AL01355.1; -, Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; B6; 1.
FT NON TER
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 85.8%; Score 712; DB 2; Length 130;
Best Local Similarity 98.5%; Pred. No. 3.6e-62;
Matches 128; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 TIHHIIIECYVCKQOQLRREYVDFAFRDLCTVYRDGNFYAVXDKLKFYSKISEYRHICY 81
DB 1 TIHHIIIECYVCKQOQLRREYVDFAFRDLCTVYRDGNFYAVXDKLKFYSKISEYRHICY 60

QY 82 SVYGTLEQYNNKPLCDLLIRICINXQKPLCEBEKQRHLDKKQRFNIRGRTGRCMSCCR 141
DB 61 SVYGTLEQYNNKPLCDLLIRICINQKPLCEBEKQRHLDKKQRFNIRGRTGRCMSCCR 120

QY 142 SSRTRETOL 151
DB 121 SSRTRETOL 130
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QY 142 SSRTRETOL 151
DB 121 SSRTRETOL 130

RESULT 55
QY 0919B8_HPV16 PRELIMINARY; PRT; 130 AA.
ID 0919B8_HPV16 PRELIMINARY; PRT; 130 AA.
AC 0919B8;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Watts K.U., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL: AF404701; AL01359.1; -, Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; B6; 1.
FT NON TER
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 85.2%; Score 707; DB 2; Length 130;
Best Local Similarity 98.4%; Pred. No. 1.1e-61;
Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 23 IHHIIIECYVCKQOQLRREYVDFAFRDLCTVYRDGNFYAVXDKLKFYSKISEYRHICY 82
DB 2 IHHIIIECYVCKQOQLRREYVDFAFRDLCTVYRDGNFYAVXDKLKFYSKISEYRHICY 61

QY 83 VYGTLEQYNNKPLCDLLIRICINXQKPLCEBEKQRHLDKKQRFNIRGRTGRCMSCCR 142
DB 62 VYGTLEQYNNKPLCDLLIRICINQKPLCEBEKQRHLDKKQRFNIRGRTGRCMSCCR 121

QY 143 SSRTRETOL 151
DB 122 SSRTRETOL 130

RESULT 56
QY 0919C8_HPV16 PRELIMINARY; PRT; 130 AA.
ID 0919C8_HPV16 PRELIMINARY; PRT; 130 AA.
AC 0919C8;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Watts K.U., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL: AF404696; AAL01349.1; -, Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378BDDC9 CRC64;

Query Match 85.2%; Score 707; DB 2; Length 130;
Best Local Similarity 97.7%; Pred. No. 1.1e-61;
Matches 127; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 22 TIHDIIECVYCKQOLLRREYDFAFRDLCTVYRGNPVAAXDKLKFYSKISRYHYCY 81
Db 1 TIHNIILCEVCYCKQOLLRREYDFAFRDLCTVYRGNPVAACDKLKFYSKISRYHYCY 60

Qy 82 SVYGTLEEQYNKPLCDLLIRICINQKPLCEBEKORHLDKKQRFHNIRGRTGRCMSCCR 141
Db 61 SVYGTLEEQYNKPLCDLLIRICINQKPLCEBEKORHLDKKQRFHNIRGRTGRCMSCCR 120

Qy 142 SSRTRRETOL 151
Db 121 SSRTRRETOL 130

RESULT 57
Q919B4_HPV16 PRELIMINARY; PRT; 130 AA.
ID Q919B4_HPV16
AC Q919B4;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jc.10103;
RA Watters K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
CC -----
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CC -----
DR EMBL: AF404703; AAL01363.1; -, Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;

Query Match 84.8%; Score 704; DB 2; Length 130;
Best Local Similarity 96.9%; Pred. No. 2.2e-61;
Matches 126; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 22 TIHDIIECVYCKQOLLRREYDFAFRDLCTVYRGNPVAAXDKLKFYSKISRYHYCY 81
Db 1 TIHNIILCEVCYCKQOLLRREYDFAFRDLCTVYRGNPVAACDKLKFYSKISRYHYCY 60

Qy 82 SVYGTLEEQYNKPLCDLLIRICINQKPLCEBEKORHLDKKQRFHNIRGRTGRCMSCCR 141
Db 61 SVYGTLEEQYNKPLCDLLIRICINQKPLCEBEKORHLDKKQRFHNIRGRTGRCMSCCR 120

Qy 142 SSRTRRETOL 151
```

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Db 121 SSRTRRETOL 130

RESULT 58
Q919D0_HPV16 PRELIMINARY; PRT; 130 AA.
ID Q919D0_HPV16
AC Q919D0;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jc.10103;
RA Watters K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
CC -----
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CC -----
DR EMBL: AF404695; AAL01347.1; -, Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30BEDCA21AF3 CRC64;

Query Match 84.6%; Score 702; DB 2; Length 130;
Best Local Similarity 96.9%; Pred. No. 3.5e-61;
Matches 126; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 22 TIHDIIECVYCKQOLLRREYDFAFRDLCTVYRGNPVAAXDKLKFYSKISRYHYCY 81
Db 1 TIHNIILCEVCYCKQOLLRREYDFAFRDLCTVYRGNPVAACDKLKFYSKISRYHYCY 60

Qy 82 SVYGTLEEQYNKPLCDLLIRICINQKPLCEBEKORHLDKKQRFHNIRGRTGRCMSCCR 141
Db 61 SVYGTLEEQYNKPLCDLLIRICINQKPLCEBEKORHLDKKQRFHNIRGRTGRCMSCCR 120

Qy 142 SSRTRRETOL 151
Db 121 SSRTRRETOL 130

RESULT 59
Q4TUF9_HPV35 PRELIMINARY; PRT; 149 AA.
ID Q4TUF9_HPV35
AC Q4TUF9;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 35.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=10587;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=NM1215, NM1301, NM2760, and NM3793;
RX PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
RX Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantar M., Allan B.,
RX Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,
RX Chu T.Y., Cudde H.A., Cuschieri K., von Kubeel-Deebertz M.,
RX Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
```


"Worldwide genomic diversity of the high-risk human papillomavirus
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus
RT type 16." J. Virol. 79:13630-13640(2005).

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DR EMBL: DQ057309; AAY58340.1; -; Genomic DNA.
DR EMBL: DQ057310; AAY58341.1; -; Genomic DNA.
DR EMBL: DQ057311; AAY58342.1; -; Genomic DNA.
DR EMBL: DQ057312; AAY58343.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 149 AA; 18015 MW; 8354D5CFA2935026 CRC64;

Query Match 69.9%; Score 580; DB 2; Length 149;
Best Local Similarity 71.5%; Pred. No. 4.4e-49;
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFODPQPRPKLPOLCTELQTTIHDIILECYCKQQLRREVDYFAPRDLCTVYRDGNPY 60
DB 1 MFODPARPRPKLHDLCHVESEIHEICLNCYCKQQLRSEVDYFACVYDLCTVYREGQPY 60
QY 61 AYXDKCLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCLNKKPLCPREKORHLD 120
DB 61 GVCCKCLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCLNKKPLCPREKORHLD 120
QY 121 KKQRFNHRGWRGRCSCCRSSRTRETO 151
DB 121 KKQRFNHRGWRGRCSCCRSSRTRETO 151

RESULT 60
Q84298 9PAPI PRELIMINARY; PRT; 149 AA.
ID O84298 9PAPI PRELIMINARY; PRT; 149 AA.
AC O84298
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE E6 protein.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxID=10566;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RP Fujinaga K.;
RL Submitted (FEB-1992) to the EMBL/Genbank/DBJ databases.

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DR EMBL: D10597; BAA01447.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 149 AA; 18015 MW; 8354D5CFA2935026 CRC64;

Query Match 69.9%; Score 580; DB 2; Length 149;
Best Local Similarity 71.5%; Pred. No. 4.4e-49;
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFODPQPRPKLPOLCTELQTTIHDIILECYCKQQLRREVDYFAPRDLCTVYRDGNPY 60
DB 1 MFODPARPRPKLHDLCHVESEIHEICLNCYCKQQLRSEVDYFACVYDLCTVYREGQPY 60
QY 61 AYXDKCLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCLNKKPLCPREKORHLD 120
DB 61 GVCCKCLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCLNKKPLCPREKORHLD 120
QY 121 KKQRFNHRGWRGRCSCCRSSRTRETO 151
DB 121 KKQRFNHRGWRGRCSCCRSSRTRETO 151

DB 121 EKGRFNHIGRWGRGRCSCCRSSRTRETO 149

RESULT 61
V66 HPV35 STANDARD; PRT; 149 AA.
ID V66 HPV35 STANDARD; PRT; 149 AA.
AC P27228;
DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1992, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE Protein E6.
GN Name=E6;
OS Human papillomavirus type 35.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10587;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Isolate 35H;
RX MEDLINE=94265501; PubMed=8205838;
RA Deline H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).

CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded
CC DNA (by similarity).
CC -1- FUNCTION: This protein may be involved in the oncogenic potential
CC of this virus (associated with cancer of the uterine cervix).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (by similarity).
CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.

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DR EMBL: X74477; CA52561.1; -; Genomic DNA.
DR EMBL: M74117; AAA46966.1; -; Genomic DNA.
DR PIR: E40824; W6W135.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
KW Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
KW Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger.
FT CHAIN 1 149 /FTID=PRO_0000133355.
FT ZN_FING 30 66 Potential.
FT ZN_FING 103 139 Potential.
SQ SEQUENCE 149 AA; 18045 MW; C605D19AF3935021 CRC64;

Query Match 69.6%; Score 578; DB 1; Length 149;
Best Local Similarity 71.5%; Pred. No. 6.9e-49;
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFODPQPRPKLPOLCTELQTTIHDIILECYCKQQLRREVDYFAPRDLCTVYRDGNPY 60
DB 1 MFODPARPRPKLHDLCHVESEIHEICLNCYCKQQLRSEVDYFACVYDLCTVYREGQPY 60
QY 61 AYXDKCLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCLNKKPLCPREKORHLD 120
DB 61 GVCCKCLKFYSKISEYRHYCYVGTTLLEQYKPLCDLLIRCLNKKPLCPREKORHLD 120
QY 121 KKQRFNHRGWRGRCSCCRSSRTRETO 151
DB 121 EKGRFNHIGRWGRGRCSCCRSSRTRETO 149

RESULT 62
Q4TUF4_HPV35

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ID O4TUF4 HPV35 PRELIMINARY; PRT; 149 AA.
AC O4TUF4;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DE E6 protein.
DE E6 protein.
GN Name=E6;
OS Human Papillomavirus type 35.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10587;
OX NCBI_TaxID=10587;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=SA1505, and TW4232;
RC PubMed=16227263; DOI=10.1128/JVI.79.21.13630-13640.2005;
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalandari M., Allan B.,
RA Williamson A.L., Chung H.A., Collins R.J., Zuna R.E., Dunn S.T.,
RA Chu T.Y., Cubie H.A., Guschleri K., von Knebel-Doeberitz M.,
RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
RT "Worldwide genomic diversity of the high-risk human papillomavirus
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus
RT type 16."
RL J. Virol. 79:13630-13640(2005).
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CC -----
DR EMBL; DQ057314; AA158345.1; -; Genomic DNA.
DR EMBL; DQ057313; AA158344.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 149 AA; 18045 MW; C605D19AF3935021 CRC64;

Query Match 69.6%; Score 578; DB 2; Length 149;
Best Local Similarity 71.5%; Pred. No. 6.9e-49;
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFQDPQERPRKLPLQCTELQTTIHDIIECYCKQQLRRREYDPAFRLDCIVYRDGPNY 60
DB 1 MFQDPARPRFYLHLDCNVESEIHETICNVCYCKQQLRRREYDPAFRLDCIVYREGOPY 60

QY 61 AVXDKLKFYSKISEYRHYCYSVYGTLEEQYNKPLCDLLIRNCINXQKPLCPBEKQRLD 120
DB 61 GVCMCKLKFYSKISEYRHYCYSVYGTLEEQYNKPLCDLLIRNCINXQKPLCPBEKQRLD 120

QY 121 KKQRFHNRGRWTCGSCCSSRRRRETOL 151
DB 121 EKRRFHNIGRWTCGSCSSRRRRETOL 151

RESULT 63
Q919D6 HPV16 PRELIMINARY; PRT; 103 AA.
ID Q919D6 HPV16 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE E6 protein (Fragment).
DE E6 protein (Fragment).
GN Human papillomavirus type 16.
OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=333760;
OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Watts K.U., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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DR EMBL; AF404692; AA101342.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1 1
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAR1F25449B CRC64;

Query Match 67.5%; Score 560; DB 2; Length 103;
Best Local Similarity 96.1%; Pred. No. 2.8e-47;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 49 DLCTVYRDGPNYAVXDKLKFYSKISEYRHYCYSVYGTLEEQYNKPLCDLLIRNCINXQK 108
DB 1 DLCTVYRDGPNYAVXDKLKFYSKISEYRHYCYSVYGTLEEQYNKPLCDLLIRNCINXQK 60

QY 109 PLCPBEKQRLDKKQRFHNRGRWTCGSCCSSRRRRETOL 151
DB 61 PLCPBEKQRLDKKQRFHNRGRWTCGSCCSSRRRRETOL 103

RESULT 64
Q919B2 HPV16 PRELIMINARY; PRT; 99 AA.
ID Q919B2 HPV16 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE E6 protein (Fragment).
DE E6 protein (Fragment).
GN Human papillomavirus type 16.
OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=333760;
OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Watts K.U., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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CC -----
DR EMBL; AF404704; AA101365.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1 1
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match 64.1%; Score 532; DB 2; Length 99;
Best Local Similarity 97.0%; Pred. No. 1.6e-44;
Matches 96; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 25 DIIIECYCKQQLRRREYDPAFRLDCIVYRDGPNYAVXDKLKFYSKISEYRHYCYSVY 84
DB 1 DIIIECYCKQQLRRREYDPAFRLDCIVYRDGPNYAVXDKLKFYSKISEYRHYCYSVY 60

QY 85 GTTLEEQYNKPLCDLLIRNCINXQKPLCPBEKQRLDKKQ 123
DB 61 GTTLEEQYNKPLCDLLIRNCINXQKPLCPBEKQRLDKKQ 99

RESULT 65
Q4TUG1 HPV31 PRELIMINARY; PRT; 149 AA.
ID Q4TUG1 HPV31 PRELIMINARY; PRT; 149 AA.
AC Q4TUG1;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DE E6 protein (Fragment).
DE E6 protein (Fragment).
GN Human papillomavirus type 31.
OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10587;
OX NCBI_TaxID=10587;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=SA1505, and TW4232;
RC PubMed=16227263; DOI=10.1128/JVI.79.21.13630-13640.2005;
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalandari M., Allan B.,
RA Williamson A.L., Chung H.A., Collins R.J., Zuna R.E., Dunn S.T.,
RA Chu T.Y., Cubie H.A., Guschleri K., von Knebel-Doeberitz M.,
RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
RT "Worldwide genomic diversity of the high-risk human papillomavirus
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus
RT type 16."
RL J. Virol. 79:13630-13640(2005).
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CC -----

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DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 31.
OC Viruses; deDNA viruses; no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=10585;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=BR1213, BR1692, and MR9917;
RA Callega-Macias I.E., Villa L.B., Prado J.C., Kalantari M., Allan B.,
RA Williams A.L., Chung L.P., Collins R.U., Zuna R.E., Dunn S.T.,
RA Chu T.Y., Gubie H.A., Guschietti K., von Knebel-Dobbert M.,
RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
RT "Worldwide genomic diversity of the high-risk human papillomavirus
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus
RT type 16".
RL J. Virol. 79:13630-13640 (2005).

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DR EMBL; DQ057307; AAY58338.1; -; Genomic DNA.
DR EMBL; DQ057308; AAY58339.1; -; Genomic DNA.
DR EMBL; DQ057305; AAY58336.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 149 AA; 17768 MW; 61C2A96EAC2677D8 CRC64;

Query Match 63.3%; Score 525; DB 2; Length 149;
Best Local Similarity 65.6%; Pred. No. 1.2e-43;
Matches 99; Conservative 16; Mismatches 34; Indels 2; Gaps 1;

QY 1 MFODPOEPRRLPOLCTELQTTIIIECVYCKOQLRRREYDFAFDLCIVRDGNPY 60
Db 1 MFQKPAERPRKLHLSALBEPYDELRLNLCVYCKQKQLRETEVLDPAFDLTVRADDPPY 60
1 MFQKPAERPRKLHLSALBEPYDELRLNLCVYCKQKQLRETEVLDPAFDLTVRADDPPY 60

QY 61 AVXDKCLFKYKISYRHYCHSVYGTTLLEQYKRLCDLLRLCINXKQPLCPPEKQRHLD 120
Db 61 GVCTKCLAFYKSVSEFRWRYSVYGTLEKLTNKQICDLLRLCINCPQPLCPPEKQRHLD 120
1 GVCTKCLAFYKSVSEFRWRYSVYGTLEKLTNKQICDLLRLCINCPQPLCPPEKQRHLD 120

QY 121 KKQRFNIRGRWYTGRCSCSSSFRRTETQL 151
Db 121 KKQRFNIRGRWYTGRCSCSSSFRRTETQL 151
1 KKQRFNIRGRWYTGRCSCSSSFRRTETQL 151

RESULT 66
ID V66 HPV31 STANDARD; PRT; 149 AA.
AC P17386;
DT 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1990, sequence version 1.
DT 07-FEB-2006, entry version 37.
DE Protein E6.
NN Name=E6;
OS Human papillomavirus type 31.
OC Viruses; deDNA viruses; no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=10585;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=89299478; PubMed=12545036;
RA Goldsborough M.D., Dislvestre D.; Temple G.F., Lorincz A.T.;
RT "Nucleotide sequence of human papillomavirus type 31: a cervical
RT neoplasia-associated virus.";
RL Virology 171:306-311 (1989).
[2]
RN [2]
RP INTERACTION WITH HUMAN PBLN1, AND INHIBITION OF E6-MEDIATED
RP TRANSFORMATION.
RX MEDLINE=22188366; PubMed=13200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.J.;
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1";
RL Biochem. Biophys. Res. Commun. 296:962-969 (2002).

RN P08679 | PDZ DOMAIN-BINDING MOTIF.
RA PubMed:15507623; DOI=10.1128/JVI.78.22.12366-12377.2004;
RT Lee C., Laimins L.A.;
Role of the pdz domain-binding motif of the oncoprotein E6 in the pathogenesis of human papillomavirus type 31." ;
RL J. Virol. 78:12366-12377(2004).
CC -I- FUNCTION: Transcriptional transactivator. Binds double stranded DNA. Has transforming activity. Inactivates, with E6-AP ubiquitin-protein ligase, the human TP53/p53 tumor suppressor protein by targeting it to degradation. Binds and targets human MDM1/MDM2 protein to degradation. Those two functions presumably contribute to transforming activity (By similarity). Interaction with human FBXW1 protein also seems to be linked to cell transformation.

-I- SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which interacts with human p53. Binds to human FBXW1 and MPDZ (By similarity).

-I- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
--SIMILARITY: Belongs to the papillomaviruses E6 protein family.

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DR EMBL:J04353; AAAA6950.1; -, Genomic_DNA.
DR PIR:A32444; W6ML31.
DR InterPro:IPR001334; E6.
KW Pfam:PF00518; B6; I.
KW Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein; Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger.
FT CHAIN 1 149 Protein E6.
FT FT /FTRID=PRO_0000133351.
FT ZN_FING 30 Potential.
FT FT 103 Potential.
FT FT_MOTIF 146 149 PDZ-binding.
SQ SEQUENCE 149 AA; 61SD2A86C36267BD9 CRC64;

Query Match 63.0%; Score 523; DB 1; Length 149;
Best local Similarity 64.9%; Pred. No. 1.9e+43; Indels 2; Gaps 1;
Matches 98; Conservative 18; Mismatches 33;

OY 1 MFODPORPRKLPOLCTELQTTIHDIILECYCKOQLLRREVVDPFAERDLCIYYRDGNPY 60
DB 1 MKKNPARRPRHLHLSALRIPEYLDELNLNCVYGCGQTETFEVLDFPAFTDLLTYVRDDTPH 60
OY 61 AYAXKCLFKFSKSIEFYHYHCYSVGTLTBOGYMKPLCDLDIRLNMXKRPLECEKHORHD 120
DB 61 GVCHRCIKRFPSKYSEFPWFYRSYGVLTLEKLTKNGICIDLRLICTTCQRPLCEKEORHLD 120
OY 121 KGORFNHRGRMTGRCMSGCCSRSTRRETTOU 151
DB 121 KKGRFHNIIGRMWGRCIAWR-RPRETIQV 149

RESULT 67

ID QATUG5_HPV31 PRELIMINARY; PRt; 149 AA.
AC Qatug5_
DT 19-JUL-2005, integrated into UniproCk/B/TREMBL.
DT 19-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE E6 protein.
GE E6 protein.
GN Name=E6;
OS Human papillomavirus type 31.
OC Viruseae, dsDNA viruses, no RNA stage; Papillomaviridae;
OX Alphapapillomavirus.
RN NCBI_taxid=10585;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HK31B, HK31C, and TL2069;
RX PubMed:16327283; DOI=10.1128/JVI.79.21.13630-13640.2005;
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B., Williamson A.V., Chung T.P., Collins R.J., Zona R.E., Dunn S.T., Chu T.Y., Cubie H.A., Cuschieri K., von Knebel Doeberitz M.,

RA	Martinez C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
RB	"Worldwide genomic diversity of the high-risk human papillomavirus
RT	types 31, 35, 52, and 58, four close relatives of human papillomavirus
RL	type 16.";
RJ	J. Virol. 79:13630-13640(2005).
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CC	-----
DR	EMBL; DQ057303; AAY58334.1; -; Genomic_DNA.
DR	EMBL; DQ057304; AAY58335.1; -; Genomic_DNA.
DR	EMBL; DQ057306; AAY58337.1; -; Genomic_DNA.
DR	EMBL; DQ057302; AAY58333.1; -; Genomic_DNA.
DR	GO; GO:0042025; C:host cell nucleus; IEA.
DR	GO; GO:0003677; F:DNA binding; IEA.
SQ	SEQUENCE 149 AA; 17714 MW; 61D2AB6C362767D9 CRC64;
Query Match	63.0%; Score 523; DB 2; Length 149;
Best Local Similarity	64.9%; Pred. No. 1.9e-43;
Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;	
OY	1 MFQDPQERPRKLPLQCLTELQTTIHIIIECYCKQQQLLRREYDPAFADLCIVRDGMPY 60
DB	1 MFKNFAEPRKRKHLESSALEIPDYDLRLNCVYCKQLTELETEDLDPAFDLTITVRDDPH 60
OY	61 AVXDKCLFEYSKISSEYRHYCVSYGTLLTEOQYNKEPCLDLLIRCIYXQKPCLPEEKQRHLD 120
DB	61 GVCTKKLAFYKSVSFRMYRYRSVYTILEKTLNKKICDDLIRCIQCGRPLCEBKQRHLD 120
OY	121 KKQRFHNIRGRWTCRCMCCSCSSRTRETOL 151
DB	121 KKKRFHNIGRWTCRCIACMR--RPETSTOV 149
RESULT 68	
VE6_HP V3	STANDARD; PRT; 149 AA.
ID_VEG_HP V3	P06427;
DT	01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT	01-JAN-1988, sequence version 1.
DT	07-FEB-2006, entry version 38.
DE	Protein E6.
CN	Name=E6;
OS	Human papillomavirus type 33.
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC	Alphapapillomavirus.
OX	NCBI_Taxid=10586;
RN	[1]
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX	MEDLINE=86200464; PubMed=3009902;
RA	Cole S.T., Strecek R.E.;
RT	"Genome organization and nucleotide sequence of human papillomavirus
RT	type 33, which is associated with cervical cancer.";
RL	J. Virol. 58:991-995(1986).
CC	- FUNCTION: Transcriptional transactivator. Binds double stranded
CC	DNA (by similarity).
CC	- FUNCTION: This protein may be involved in the oncogenic potential
CC	of this virus (cervical neoplasia-associated virus).
CC	- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
CC	- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
CC	-----
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CC	-----
DR	EMBL; MI2732; AAA46958.1; -; Genomic_DNA.
DR	PIR; A03683; W6W133.
DR	InterPro; IPR001334; E6.
KM	Pfam; PF00518; E6; 1.
KW	Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
KW	Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger.
FT	CHAIN 1 149 Protein E6.
FT	/FTId=PRO_000013353.
ZN_FING	30 66 Potential.

FT	ZN	FINC	103	139	Potential
SO	SEQUENCE	149	AA; 17652	MM; EDDBT444P9C8B1AF	CRC64;
	Query Match		62.7%	Score 520; DB 1;	Length 149;
	Best Local Similarity		62.6%	Pred. No. 3.7e-43;	
	Matches	96;	Conservative 19;	Mismatches 34;	Indels 2; Gaps 1;
OY		1	MFQOPORPRRLPOLCTELQTTINDILLECVCYCKQOILREBYVPFARPLDCTIVYRDGPNY	60	
DB		1	MFQDAEBPRRLDLCALLETTHNIEIQCECKKPLQRESEVDFAPADLTIVYRDGNPF	60	
OY		61	AVXDKCLKFYSKISSEYRHYCYSVYGTLEQOYNKPLCDLLIRCNXOKPLCPREKORHLD	120	
DB		61	GICLCLARFLSKISEYRHHYNSVYGNTLEQVKKPLMEILIRCIICQRLPCPCKKHVD	120	
OY		121	KKORFNNIRGWTGRCMSCCRSSSTRRETOL	151	
DB		121	LNKRFNNISGRWTCACWMP--RRRQTOV	149	
RESULT 69					
OQ0S57	HPV58		PRELIMINARY;	PRT;	149
AC	OQ0S57				
DT	01-JUN-2002,		integrated into UniProtKB/TrEMBL.		
DT	01-JUN-2002,		sequence version 1.		
DT	07-FEB-2006,		entry version 14.		
DE	E6 protein.				
OS	Human papillomavirus type 58.				
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;				
CC	Alphapapillomavirus.				
OX	NCBI_TaxID=10598;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=EG/E7-HK-8;				
RX	MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;				
RA	Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,				
RT	Cheung J.L.K., Cheng A.F.;				
RT	"Association of human papillomavirus type 58 variant with the risk of				
RT	cervical cancer";				
RL	J. Natl. Cancer Inst. 94:1249-1253(2002).				
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CC	Distributed under the Creative Commons Attribution-NonDerivs License				
CC	EMBL; AF478157; AAL85402.1; -; Genomic DNA.				
DR	GO; GO:0042025; C:host cell nucleus; IEA.				
DR	GO; GO:0003677; F:DNA binding; IEA.				
DR	InterPro; IPR001334; E6.				
DR	Pfam; PF00518; E6; 1.				
SO	SEQUENCE 149 AA; 17793 MW; 8D06DD69ED3EDC4 CRC64;				
	Query Match		60.6%	Score 503; DB 2;	Length 149;
	Best Local Similarity		62.3%	Pred. No. 1.7e-41;	
	Matches	94;	Conservative 20;	Mismatches 35;	Indels 2; Gaps 1;
OY		1	MFQOPORPRRLPOLCTELQTTINDILLECVCYCKQOILREBYVPFARPLDCTIVYRDGPNY	60	
DB		1	MFQDAEBPRRLDLCALLETTHNIEIQCECKKPLQRESEVDFAPADLTIVYRDGNPF	60	
OY		61	AVXDKCLKFYSKISSEYRHYCYSVYGTLEQOYNKPLCDLLIRCNXOKPLCPREKORHLD	120	
DB		61	AVCKVCARLRLSKISEYRHHYNSVYGNTLEQVKKPLMEILIRCIICQRLPCPCKKHVD	120	
OY		121	KKORFNNIRGWTGRCMSCCRSSSTRRETOL	151	
DB		121	LNKRFNNISGRWTCACWMP--RRRQTOV	149	
RESULT 70					
O91ZG6	HPV58		PRELIMINARY;	PRT;	149
AC	O91ZG6				
DT	091ZG6				
DT	091ZG6				
DT	091ZG6				
DE	E6 protein.				
OS	Human papillomavirus type 58.				
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;				
CC	Alphapapillomavirus.				
OX	NCBI_TaxID=10598;				
RN	[1]				

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DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE E6 protein.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Chan P.K.S., Lam C.W., Li W.H., Chan M.Y.M., Cheung J.L.K.,
RA Cheng A.P.,
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BE/ET-HK-3, and E6/ET-HK-14;
RX MEDLINE=2216796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Cheng A.P.,
RT "Association of human papillomavirus type 58 variant with the risk of
RT cervical cancer.";
RT J. Natl. Cancer Inst. 94:1249-1253(2002).
CC -----
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CC -----
DR EMBL: AF234530; AAF60306.1; -; Genomic DNA.
DR EMBL: AF478152; AAL85397.1; -; Genomic DNA.
DR EMBL: AF478153; AAL85408.1; -; Genomic DNA.
DR EMBL: AF478154; AAL85399.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 149 AA; 17780 MW; 7CB6DCC5D31B158 CRC64;

Query Match 60.5%; Score 502; DB 2; Length 149;
Best Local Similarity 62.3%; Pred. No. 2.2e-41;
Matches 94; Conservative 20; Mismatches 35; Indels 2; Gaps 1;

QY 1 MFQDPOERPRKLTLPOLCTELQTTIHDIILCEVCYKQQLRREVDFAFRDLCTIVRDGPNY 60
DB 1 MFQDAEKPRKTHDLCALETSVHEILKVCCKKTQIRSEVYDFVADLRIVYRDGNPF 60
QY 61 AYXDKCLKFYSKISEYHNYCYVGTTLDEQYNNKPLCDLLIRCNKXKPLCPBEKQKHLD 120
DB 61 AVCKVCRLRLSKISEYHNYSLYGTLEQTLKNCLEIILIRCIICQRPICPQEKKHVD 120
QY 121 KKORFNIRGRMTGRCMSCCRSSRTRETL 151
DB 121 LNKRFNHSGRMTGRCAVCWRP-RRRQTOV 149

RESULT 71
OS0723 HPV67 PRELIMINARY; PRT; 149 AA.
AC 090723;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE ORF E6.
OS Human papillomavirus type 67.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=37120;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99073659; PubMed=9857984; DOI=10.1023/A:1008002905588;
RA Kiri T., Matsukura T.,
RT "Nucleotide sequence and phylogenetic classification of human
RT papillomavirus type 67.";
RL Virus Genes 17:117-121(1998).

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CC -----
DR EMBL: D21208; BAA28852.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 149 AA; 17833 MW; AAF28AC1BE75B197 CRC64;

Query Match 60.0%; Score 498; DB 2; Length 149;
Best Local Similarity 60.1%; Pred. No. 5.4e-41;
Matches 89; Conservative 22; Mismatches 37; Indels 0; Gaps 0;

QY 1 MFQDPOERPRKLTLPOLCTELQTTIHDIILCEVCYKQQLRREVDFAFRDLCTIVRDGPNY 60
DB 1 MFQDTEKPRKTHDLCALETSTVHEISLPCVQCKKTLDREVDVFLTDLKIYVRCGPNY 60
QY 61 AYXDKCLKFYSKISEYHNYCYVGTTLDEQYNNKPLCDLLIRCNKXKPLCPBEKQKHLD 120
DB 61 GVCKQCLRLSKISEYHNYSLYGTLEIIVHKPLNEITIRCIICQRPICPQEKKHVD 120
QY 121 KKORFNIRGRMTGRCMSCCRSSRTRE 148
DB 121 RKKRFNHSGRMTGRCAVCWRPQRTQ 148

RESULT 72
OS0723 HPV58 PRELIMINARY; PRT; 149 AA.
AC 04TUG8;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BD1813;
RX PubMed=16227283; DOI=10.1126/JVI.79.21.13630-13640.2005;
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalencic M., Allan B.,
RA Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,
RA Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Deberitz M.,
RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
RT "Worldwide genomic diversity of the high-risk human papillomavirus
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus
RT type 16.";
RL J. Virol. 79:13630-13640(2005).
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CC -----
DR EMBL: DQ057300; AAY5831.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 149 AA; 17807 MW; 8803DD6CE83BDCF4 CRC64;

Query Match 59.9%; Score 497; DB 2; Length 149;
Best Local Similarity 61.6%; Pred. No. 6.6e-41;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

QY 1 MFQDPOERPRKLTLPOLCTELQTTIHDIILCEVCYKQQLRREVDFAFRDLCTIVRDGPNY 60
DB 1 MFQDAEKPRKTHDLCALETSVHEILKVCCKKTQIRSEVYDFVADLRIVYRDGNPF 60
QY 61 AYXDKCLKFYSKISEYHNYCYVGTTLDEQYNNKPLCDLLIRCNKXKPLCPBEKQKHLD 120
DB 61 AVCKVCRLRLSKISEYHNYSLYGTLEQTLKNCLEIILIRCIICQRPICPQEKKHVD 120

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Qy      121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151
Db      121 LNKRFHNISGRWTRCAVCWMP--RRQTQV 149

RESULT 73
091ZGS_HPV58      PRELIMINARY; PRT; 149 AA.
ID 091ZGS_HPV58
AC 091ZGS;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE B6 protein.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E6HK3.
RA Chan P.K.S., Lam C.W., Li W.H., Chan M.Y.M., Cheung J.L.K.,
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AF234531; AAF60307.1; -; Genomic_DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 149 AA; 17863 MW; 4C6A61AD3CEC302D CRC64;

Query Match      59.9%; Score 497; DB 2; Length 149;
Best Local Similarity 61.6%; Pred. No. 6.8e-41;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

Qy      1 MFOQPQRPRLPOLCTELQTTIHDIILECYCKQQLRREVPFAPRDLCTIVRDGPNY 60
Db      1 MFOQAEKPRTHLDCQALETSVHIELKVCCKKTLQRSEVDFVADLRIVRDGNPF 60
Qy      61 AVXDKCKFKYSKISEYHACYSVYGTLEQOYNKPLCDLIRCIINXOKPLCPBEKQRHLD 120
Db      61 AVCVCLRLSKISEYHNYNSLYGDTLEQTLKKCLNEILIRCIICQRLCPQEKGRHVD 120
Qy      121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151
Db      121 LNKRFHNISGRWTRCAVCWMP--RRQTQV 149

RESULT 74
VE6_HPV58      STANDARD; PRT; 149 AA.
ID VE6_HPV58
AC P26555;
DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1992, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Protein E6.
OS Name=E6;
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=92024102; PubMed=1656594;
RA Kiril' Y., Iwamoto S., Matsukura T.;
RT "Human papillomavirus type 58 DNA sequence.";
RL Virology 185:424-427(1991).
CC -!- FUNCTION: Transcriptional transactivator. Binds double stranded
CC DNA (by similarity).

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CC      -!- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
CC      -!- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
CC      -----
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CC      -----
CC      EMBL; D90400; BAA31845.1; -; Genomic_DNA.
DR PIR; E36779; W6W158.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KM Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
KM Transcription; Transcription regulation; Zinc; Zinc-finger.
FT CHAIN 1
FT /Ftrd=PRO_0000133374.
FT ZN_FING 30
FT ZN_FING 103 Potential.
SQ SEQUENCE 149 AA; 17794 MW; 79B3DC95831B158 CRC64;

Query Match      59.8%; Score 496; DB 1; Length 149;
Best Local Similarity 61.6%; Pred. No. 8.5e-41;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

Qy      1 MFOQPQRPRLPOLCTELQTTIHDIILECYCKQQLRREVPFAPRDLCTIVRDGPNY 60
Db      1 MFOQAEKPRTHLDCQALETSVHIELKVCCKKTLQRSEVDFVADLRIVRDGNPF 60
Qy      61 AVXDKCKFKYSKISEYHACYSVYGTLEQOYNKPLCDLIRCIINXOKPLCPBEKQRHLD 120
Db      61 AVCVCLRLSKISEYHNYNSLYGDTLEQTLKKCLNEILIRCIICQRLCPQEKGRHVD 120
Qy      121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151
Db      121 LNKRFHNISGRWTRCAVCWMP--RRQTQV 149

RESULT 75
0547M1_HPV58      PRELIMINARY; PRT; 149 AA.
ID 0547M1_HPV58
AC 0547M1;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE B6 protein.
OS Name=E6;
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E6/E7-HK-1, E6/E7-HK-10, E6/E7-HK-11, E6/E7-HK-12, E6/E7-HK-13,
RC E6/E7-HK-15, E6/E7-HK-16, E6/E7-HK-2, E6/E7-HK-4, E6/E7-HK-6,
RC E6/E7-HK-7, and E6/E7-HK-9;
RX MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Cheng A.F.;
RT "Association of human papillomavirus type 58 variant with the risk of
RT cervical cancer.";
RL J. Natl. Cancer Inst. 94:1249-1253(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ED1710, ED1767, ED6197, HK2178, and OK332;
RX PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalamantari M., Allan B.,
RA Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,
RA Chu T.Y., Cudde H.A., Cuschieri K., von Knebel-Doeberitz M.,
RA Martinez C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
RT "Worldwide genomic diversity of the high-risk human papillomavirus
RT types 31, 35, 52, and 58, four close relatives of human papillomavirus
RT type 16.";
RL J. Virol. 79:13630-13640(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN-B6HK1;
RA Chan P.K.S., Lam C.W., Li W.H., Chan M.Y.M., Cheung J.L.K.,
RA Cheng A.F.;
RT "Nucleotide sequence variation of the E6 gene of human papillomavirus
RT type 58 from Chinese women with normal cervixes and cancerous
RT lesions";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AF478150; AAL85395.1; -; Genomic DNA.
DR EMBL: DQ057297; AAY58328.1; -; Genomic DNA.
DR EMBL: DQ057298; AAY58329.1; -; Genomic DNA.
DR EMBL: DQ057299; AAY58330.1; -; Genomic DNA.
DR EMBL: DQ057301; AAY58332.1; -; Genomic DNA.
DR EMBL: AF234529; AAF60305.1; -; Genomic DNA.
DR EMBL: AF478151; AAL85396.1; -; Genomic DNA.
DR EMBL: AF478153; AAL85398.1; -; Genomic DNA.
DR EMBL: AF478155; AAL85400.1; -; Genomic DNA.
DR EMBL: AF478156; AAL85401.1; -; Genomic DNA.
DR EMBL: AF478159; AAL85403.1; -; Genomic DNA.
DR EMBL: AF478159; AAL85404.1; -; Genomic DNA.
DR EMBL: AF478160; AAL85405.1; -; Genomic DNA.
DR EMBL: AF478161; AAL85406.1; -; Genomic DNA.
DR EMBL: AF478162; AAL85407.1; -; Genomic DNA.
DR EMBL: AF478164; AAL85409.1; -; Genomic DNA.
DR EMBL: AF478165; AAL85410.1; -; Genomic DNA.
DR EMBL: DQ057296; AAY58327.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 149 AA; 17794 MW; 79B3DCC95831B158 CRC64;
Query Match 59.8%; Score 496; DB 2; Length 149;
Best Local Similarity 61.6%; Pred. No. 8.5e-41;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;
QY 1 MFQDPERPRKLPOLCTELQTTTHDILIECYCQQLRREYVDFARFDLCIVRDGPNP 60
DB 1 MFQDAEKPRTLHDLCOALETSVHEILKCECKTQRSSEYDFVADLRIVRDGNPF 60
QY 61 AVXDKCKFKYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLIRCTNKKPLCPCEKORHLD 120
DB 61 AVCVKCLRLSKISEYHYNYSLYGTLEQTLKCLNIEILIRCTICQRPLOPKKHVD 120
QY 121 KKQRFNIRGRWTCRCSCCSSRTRETOL 151
DB 121 LNKRFNHSGRWTCRCACWCRP--RRRQTV 149
RESULT 76
Q8QHO3 HPV58
ID Q8QHO3 HPV58 PRELIMINARY; PRT; 149 AA.
AC Q8QHO3;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE E6 protein.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E6/E7-HK-17, and E6/E7-HK-18;
RX MEDLINE=2217696; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Cheng A.F.;
RT "Association of human papillomavirus type 58 variant with the risk of
RT cervical cancer";
RL J. Natl. Cancer Inst. 94:1249-1253(2002).
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CC -----
CC EMBL: AF478166; AAL85411.1; -; Genomic DNA.
CC EMBL: AF478167; AAL85412.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 149 AA; 17808 MW; 7803DD78E831B159 CRC64;
Query Match 59.8%; Score 496; DB 2; Length 149;
Best Local Similarity 61.6%; Pred. No. 8.5e-41;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;
QY 1 MFQDPERPRKLPOLCTELQTTTHDILIECYCQQLRREYVDFARFDLCIVRDGPNP 60
DB 1 MFQDAEKPRTLHDLCOALETSVHEILKCECKTQRSSEYDFVADLRIVRDGNPF 60
QY 61 AVXDKCKFKYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLIRCTNKKPLCPCEKORHLD 120
DB 61 AVCVKCLRLSKISEYHYNYSLYGTLEQTLKCLNIEILIRCTICQRPLOPKKHVD 120
QY 121 KKQRFNIRGRWTCRCSCCSSRTRETOL 151
DB 121 LNKRFNHSGRWTCRCACWCRP--RRRQTV 149
RESULT 77
Q80887 9PAPI
ID Q80887 9PAPI PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE E6 protein (fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxID=10586;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galurita D.F., Youngusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: U14516; AAB60570.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 91 AA; 11136 MW; 22FD3EA185ACBA7 CRC64;
Query Match 59.6%; Score 495; DB 2; Length 91;
Best Local Similarity 96.7%; Pred. No. 6.4e-41;
Matches 88; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 42 VYDFARFDLCIVRDGPNYAVXDKCKFKYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLI 101
DB 1 VYDFARFDLCIVRDGPNYAVXDKCKFKYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLI 60
QY 102 RCINXQKPLCPCEKORHLDKKQRFNIRGRM 132
DB 61 RCINXQKPLCPCEKORHLDKKQRFNIRGRM 91
RESULT 78
Q4TUN6 HPV52
ID Q4TUN6 HPV52 PRELIMINARY; PRT; 148 AA.
CC -----
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AC Q4TUH6;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE E6 protein.
 GN Name=E6;
 OS Human papillomavirus type 52.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 CC Alphapapillomavirus.
 NX NCBI_TaxID=10618;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HK1151;
 RX PubMed:16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
 RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B.,
 RA Williamson A.-L., Chung L.-P., Collins R.J., Zuna R.E., Dunn S.T.,
 RA Chu T.-Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.,
 RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
 RT "Worldwide genomic diversity of the high-risk human papillomavirus
 RT types 31, 35, 52, and 58, four close relatives of human papillomavirus
 RT type 16".
 RL J. Virol. 79:13630-13640 (2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HK1151;
 RA Calleja-Macias I.E., Kalantari M., Villa L.L., Prado J.C., Allan B.,
 RA Williamson A.-L., Chung L.-P., Collins R.J., Zuna R.E., Dunn T.,
 RA Chu T.-Y., Cubie H.A., Cuschieri K., Knebel-Doeberitz M.V.,
 RA Sanchez G.I., Bosch X., Bernard H.-U.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: DQ057292; AAY58323.1; -; Genomic DNA.
 DR GO: GO:0042025; C:nuc cell nucleus; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 SQ SEQUENCE 148 AA; 17913 MW; 2BE9D590611AB0D4 CRC64;

Query Match 59.3%; Score 492; DB 2; Length 148;
 Best Local Similarity 62.4%; Pred. No. 2,1e-40;
 Matches 88; Conservative 19; Mismatches 34; Indels 0; Gaps 0;

QY 1 MFODPOBRPKLPOLCTELQTTIHDIIECYVCKQQLRREVDPAFRLDCTVYRDGPNPY 60
 AC P36814; DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-1994, sequence version 1.
 DT 07-FEB-2006, entry version 27.
 DE Protein E6.
 GN Name=E6;
 OS Human papillomavirus type 52.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 CC Alphapapillomavirus.
 NX NCBI_TaxID=10618;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RX MEDLINE:9426501; PubMed:8205838;
 RA Delius H., Hofmann B.;

RT "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded
 CC DNA (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
 CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
 CC -----
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 CC -----
 DR EMBL: X74481; CA52585.1; -; Genomic DNA.
 DR PIR: S36573; S36573.
 DR InterPro: IPR001334; E6.
 DR Pfam: PF00518; E6; 1.
 KW Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
 KW Transcription; Transcription regulation; Zinc; Zinc-finger.
 FT CHAIN 1 148
 FT ZN FING 30 66
 FT ZN FING 103 139
 FT SEQUENCE 148 AA; 17898 MW; C5E9DEC341AB0DE CRC64;

Query Match 50.7%; Score 487; DB 1; Length 148;
 Best Local Similarity 61.7%; Pred. No. 6,6e-40;
 Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 1 MFODPOBRPKLPOLCTELQTTIHDIIECYVCKQQLRREVDPAFRLDCTVYRDGPNPY 60
 DB 1 MFEDPATRPRTLHLCVLESVHEIRLQCVCKKEIQRREVYKFLFTDLRIYRDNNPY 60
 QY 61 AVXDCKLFYSKISSEYRHYCSYVGTTLLEQYNNKPLCDLLIRCIYNKQKPLCPBEKQRLD 120
 DB 61 GVCIMCLRFPSKISSEYRHYCSYVGTTLLEBKVKEPLSEITRCCIQTPLCPBEKERRVN 120
 QY 121 KKORFHNIRGRWGRCSCCR 141
 DB 121 AKKRFHNIMGRWGRCSCCR 141

RESULT 80
 Q4TUH4_HPV52 PRELIMINARY; PRT; 148 AA.
 ID Q4TUH4; AC Q4TUH4;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE E6 protein.
 GN Name=E6;
 OS Human papillomavirus type 52.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 CC Alphapapillomavirus.
 NX NCBI_TaxID=10618;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HK1243; and HK2571;
 RX PubMed:16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
 RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B.,
 RA Williamson A.-L., Chung L.-P., Collins R.J., Zuna R.E., Dunn S.T.,
 RA Chu T.-Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.,
 RA Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
 RT "Worldwide genomic diversity of the high-risk human papillomavirus
 RT types 31, 35, 52, and 58, four close relatives of human papillomavirus
 RT type 16".
 RL J. Virol. 79:13630-13640 (2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HK1243; and HK2571;
 RA Calleja-Macias I.E., Kalantari M., Villa L.L., Prado J.C., Allan B.,
 RA Williamson A.-L., Chung L.-P., Collins R.J., Zuna R.E., Dunn T.,
 RA Chu T.-Y., Cubie H.A., Cuschieri K., Knebel-Doeberitz M.V.,
 RA Sanchez G.I., Bosch X., Bernard H.-U.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -----

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DR1 EMBL; DQ057294; AA58325.1; -; Genomic DNA.
DR EMBL; DQ057293; AA58324.1; -; Genomic DNA.
DR GO; GO:0042023; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 148 AA; 17926 MW; 0CE9C7D7341AB0CD CRC64;

Query Match 58.7%; Score 487; DB 2; Length 148;
Best Local Similarity 61.7%; Pred. No. 6.6e-40;
Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

Qy 1 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAPRDLCTIVRDGPNY 60
Db 1 MFEDPARRPRTLHLCVLEESVHEIRLQCVQCKKELRRREVYFLFDLRIYVRDNNPY 60
Qy 61 AVXDKLKFYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLIRCNXKPLCPSEKORHL 120
Db 61 GVCIMCLRFSLKISEYHYCYSVYGTTLLEQYNNKPLCDLLIRCNXKPLCPSEKORHL 120
Qy 121 KQRFHNIRGWRGRCMSCR 141
Db 121 ANKRFHNIRGWRGRCSCWR 141

RESULT 81
Q4TUH7 HPV52 PRELIMINARY; PRT; 148 AA.
AC Q4TUH7;
DT 19-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE B6 protein.
GN Name=B6;
OS Human papillomavirus type 52.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxId=10618;
RX STRAIN=BR0258, ED123, and ED18604;
RP NUCLEOTIDE SEQUENCE.
RA Calleja-Macias I.E., Villa L.L., Prado J.C., Kalandari M., Allan B.,
Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.,
Martinez G.I., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
RT "Worldwide genomic diversity of the high-risk human papillomavirus
types 31, 35, 52, and 58, four close relatives of human papillomavirus
type 16." J. Virol. 79:13630-13640(2005).
RL J. Virol. 79:13630-13640(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BR0258, ED123, and ED18604;
RA Calleja-Macias I.E., Kalandari M., Villa L.L., Prado J.C., Allan B.,
Williams A.-L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,
Chu T.Y., Cubie H.A., Cuschieri K., Knebel-Doeberitz M.,
Sanchez G.I., Bosch F.X., Bernard H.U.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; DQ057291; AA58322.1; -; Genomic DNA.
DR EMBL; DQ057290; AA58321.1; -; Genomic DNA.
DR EMBL; DQ057289; AA58320.1; -; Genomic DNA.
DR GO; GO:0042023; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 148 AA; 17898 MW; C5E9DECE341AB0DE CRC64;

Query Match 58.7%; Score 487; DB 2; Length 148;
Best Local Similarity 61.7%; Pred. No. 6.6e-40;
Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

Qy 1 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAPRDLCTIVRDGPNY 60
Db 1 MFEDPARRPRTLHLCVLEESVHEIRLQCVQCKKELRRREVYFLFDLRIYVRDNNPY 60
Qy 61 AVXDKLKFYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLIRCNXKPLCPSEKORHL 120
Db 61 GVCIMCLRFSLKISEYHYCYSVYGTTLLEQYNNKPLCDLLIRCNXKPLCPSEKORHL 120
Qy 121 KQRFHNIRGWRGRCMSCR 141
Db 121 ANKRFHNIRGWRGRCSCWR 141

RESULT 82
VE6 HPV34 STANDARD; PRT; 148 AA.
ID VE6 HPV34
AC P36811;
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1994, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Protein E6.
DE Protein E6.
GN Name=E6;
OS Human papillomavirus type 34.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxId=333764;
RX MEDLINE=94265501; PubMed=8205838;
RN [1]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RA Deline H., Hofmann B.;
RT Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded
DNA (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
CC
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DR EMBL; X74476; CAAS255.1; -; Genomic DNA.
DR PIR; S36515; S36515.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
KW Transcription; Transcription regulation; Zinc; Zinc-finger.
FT CHAIN 1 148 /FTId=PRO_0000133354.
FT ZN_FING 31 67 Potential.
FT ZN_FING 104 140 Potential.
SQ SEQUENCE 148 AA; 17735 MW; E2FCC6B62BAF0DA CRC64;

Query Match 58.3%; Score 484; DB 1; Length 148;
Best Local Similarity 60.4%; Pred. No. 1.3e-39;
Matches 87; Conservative 17; Mismatches 40; Indels 0; Gaps 0;

Qy 2 FQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAPRDLCTIVRDGPNY 61
Db 3 FPNDEPRPYKLPALCEVNIISIHIEBLDVCYCEQRLRYCEYDPIFDLCTVYARKKPYLG 62
Qy 62 VXDCKLKFYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLIRCNXKPLCPSEKORHL 121
Db 63 VQPCCLLFYSKISEYHYCYSVYGTTLLEQYNNKPLCDLLIRCNXKPLCPSEKORHL 122
Qy 122 KQRFHNIRGWRGRCMSCR 145
Db 123 NKRPHQIADQWGTGRCQKRPST 146

RESULT 83
Q82005 HPV73 PRELIMINARY; PRT; 148 AA.
ID Q82005 HPV73

RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Youngsband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; U14513; AAB60567.2; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; B6.
DR Pfam; PF00518; B6; 1.
FT NON_TER 1 1
FT SEQUENCE 90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;
SQ
Query Match 57.3%; Score 476; DB 2; Length 90;
Best Local Similarity 95.6%; Pred. No. 4.7e-39;
Matches 86; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 42 VYDFAPFDLCIVRDGNPYAVXDKLKYSKISRYRHCYSVYGTTLLEQYNNKPLCDLLI 101
DB 1 VYDFAPFDLWIVYRDGNPYAVCDKLKYSKISRYRHCYSVYGTTLLEQYNNKPLCDLLI 60
QY 102 RCINXOKPLCPBEKORHLDKKORFHNIRGR 131
DB 61 RCINXOKPLCPBEKORHLDKKORFHNIRGR 90
RESULT 87
VE6 HPV68 STANDARD; PRT; 158 AA.
ID V66 HPV68
AC PS4667;
DT 01-OCT-1996, integrated into UniprotKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Protein B6.
GN Name=B6;
OS Human papillomavirus type 68.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=45240;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=97060129; PubMed=8904450;
RA Longuet M., Beaudenon S., Orth G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
RT related to the potentially oncogenic HPV39.";
RL J. Clin. Microbiol. 34:738-744(1996).
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded
CC DNA (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
CC -1- SIMILARITY: Belongs to the papillomaviruses B6 protein family.
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CC -----
DR EMBL; X67160; CAA47632.1; -; Genomic DNA.
DR InterPro; IPR001334; B6.
DR Pfam; PF00518; B6; 1.
DR Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
KM Transcription; Transcription regulation; Zinc; Zinc-finger.
FT CHAIN 1 158
FT ZN_FING 32 68
FT ZN_FING 105 141
FT SEQUENCE 158 AA; 18796 MW; 46B37939CFBA6596 CRC64;
SQ
Query Match 56.4%; Score 468.5; DB 1; Length 158;
Best Local Similarity 55.1%; Pred. No. 4.7e-38;
Matches 86; Conservative 23; Mismatches 42; Indels 5; Gaps 1;
QY 1 MFQDPOBRPRRLPOLCTELQTTIHDIIECVYCKQQLRREVPYAFAPFDLCIVRDGNPY 60.

DB 3 LFHNPEBRPYKLPDLCTLTDTTTLHDVTIDCVYCRQQRQREVEYEFASDLCVYRDGVPF 62
QY 61 AYVXDKLKYSKISRYRHCYSVYGTTLLEQYNNKPLCDLLIRCNXOKPLCPBEKORHL 120
DB 63 AACQSCIKFYAKIRELHYSESVAATLTETITWTKLVNLLIRGMSCLKPLCPAEKLRHVT 122
QY 121 KKQRFHNIRGRWTCRMSCCRSS-----RTRRRQQL 151
DB 123 TKRLHKRIAGNFTGQCRHCWTSKRDRRRRIQETQV 158
RESULT 88
VE6 HPV70 STANDARD; PRT; 158 AA.
ID V66 HPV70
AC PS0804;
DT 01-OCT-1996, integrated into UniprotKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Protein B6.
GN Name=B6;
OS Human papillomavirus type 70.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=39457;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=96249586; PubMed=8815087;
RA Forslund O., Hansson B.G.;
RT "Human papillomavirus type 70 genome cloned from overlapping PCR
RT products: complete nucleotide sequence and genomic organization.";
RL J. Clin. Microbiol. 34:802-809(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=97060129; PubMed=8904450;
RA Longuet M., Beaudenon S., Orth G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
RT related to the potentially oncogenic HPV39.";
RL J. Clin. Microbiol. 34:738-744(1996).
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded
CC DNA (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
CC -1- SIMILARITY: Belongs to the papillomaviruses B6 protein family.
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CC -----
DR EMBL; U21941; AAC54850.1; -; Genomic DNA.
DR EMBL; U22461; AAC54880.1; -; Genomic DNA.
DR InterPro; IPR001334; B6.
DR Pfam; PF00518; B6; 1.
DR Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
KM Transcription; Transcription regulation; Zinc; Zinc-finger.
FT CHAIN 1 158
FT ZN_FING 32 68
FT ZN_FING 105 141
FT CONFICT 100 100 N -> D (in Ref. 2).
FT SEQUENCE 158 AA; 18617 MW; 6B610800D923D6DE CRC64;
SQ
Query Match 56.4%; Score 468.5; DB 1; Length 158;
Best Local Similarity 56.8%; Pred. No. 4.7e-38;
Matches 88; Conservative 21; Mismatches 41; Indels 5; Gaps 1;
QY 2 FQDPOBRPRRLPOLCTELQTTIHDIIECVYCKQQLRREVPYAFAPFDLCIVRDGNPYA 61
DB 4 FPNPABRPRYLPLDCTLTDTTTLHDITIDCVYCKTQQLQGTVEYERAFSDLFIVRNGSPYA 63
QY 62 VXDCKLKYSKISRYRHCYSVYGTTLLEQYNNKPLCDLLIRCNXOKPLCPBEKORHL 121
DB 64 ACQSCIKFYAKIRELHYSESVAATLTETITWTKLVNLLIRGMSCLKPLCPAEKLRHVT 123
QY 122 KQRFHNIRGRWTCRMSCCRSS-----RTRRRQQL 151


```
FT  ZN_FING  32  68  Potential.
FT  ZN_FING  105 141  Potential.
FT  CONFLICT 10 10  R -> P (in Ref. 2).
FT  CONFLICT 30 30  I -> N (in Ref. 2).
FT  CONFLICT 118 118  R -> A (in Ref. 2).
SQ  SEQUENCE 158 AA; 18897 MW;  FICF10DD33AA4C3E CRC64;

Query Match 55.4%; Score 459.5; DB 1; Length 158;
Best Local Similarity 56.1%; Pred. No. 3.6e-37;
Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

QY 2 FODPQERPKLPOLCTELIQTTHDIIEECYCCKQOQLRREYVDPFADLCIVRDGPNYA 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4 FDDPKQPKYKLPDLCLELNTSLQVSIACVYCKATLRETEYQPAFDCLIVRDCTAYA 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 VDXKCLFYSKISEYRYCYSVVGTLEQOYNKPLCDLIRJCINXOKPLCPPEKQRLDK 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 64 ACHKICIDFYRIRRLRYYSNVGETLEKINTLTYLLIRCLACQKPLNPAEKRRRLKD 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 KQRFNIRGKWTGRCMCCRSS-----RTRRTEL 151
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 124 KRPHSIAQYRGQCNTCCDQARQERLRRRETGV 158
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 92
ID 080882_9PAPI PRELIMINARY; PRT; 84 AA.
AC 080882;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE E6 protein (fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxId=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Hegeert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL: U14511; AAB60565.2; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468B1CAA CRC64;

Query Match 55.1%; Score 457; DB 2; Length 84;
Best Local Similarity 97.6%; Pred. No. 3.3e-37;
Matches 82; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 45 FAFDLCIVRDGPNYVXDKLKFYSKISEYRYCYSVVGTLEQOYNKPLCDLIRCI 104
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 FAFDLCIVRDGPNYVXDKLKFYSKISEYRYCYSVVGTLEQOYNKPLCDLIRCI 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 105 NXQKPLCPPEKQRLDKKQRFNIR 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 NCQKPLCPPEKQRLDKKQRFNIR 84
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 93
VE6_HPV18 STANDARD; PRT; 158 AA.
ID _VE6_HPV18
AC P06463;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1988, sequence version 1.
```

RL	Biochem. Biophys. Res. Commun.	296:962-969(2002).
CC	-1- FUNCTION: Transcriptional transactivator. Binds double stranded DNA (By similarity). Has transforming activity. Inactivates, with E6-AP ubiquitin-protein ligase, the human TP53/p53 tumor suppressor protein by targeting it to degradation. Binds and targets human MDM1/MDM2 protein to transformation. Those two functions presumably contribute to transformation activity.	
CC	-1- Interaction with human FBXL1 protein also seems to be linked to cell transformation.	
CC	-1- SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which interacts with human P53. Binds to human FBXL1 and MPDZ.	
CC	-1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).	
CC	-1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.	
CC	-----	
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs license	
DR	EMBL; X04354; CAA27879.1; -; Genomic DNA.	
DR	EMBL; X05015; CAA28664.1; -; Genomic DNA.	
DR	EMBL; M20325; AAA99514.1; -; mRNA.	
DR	EMBL; M26798; AAA45946.1; -; Genomic DNA.	
DR	EMBL; X04773; CAA28466.1; -; Genomic DNA.	
DR	EMBL; A06324; CAA00539.1; -; Unassigned DNA.	
DR	EMBL; A06328; CAA00542.1; -; Unassigned RNA.	
DR	PIR; A26165; W6WU18.	
DR	InterPro; IPR001334; E6.	
KM	Pfam; PF00518; E6; 1.	
KM	Activator: DNA-binding; Early protein; Metal-binding; Nuclear protein; Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger.	
KM	OncoGene; Transcription; Transcription regulation; Zinc; Zinc-finger.	
FT	CHAIN	
FT	1	
FT	ZN_FING	
FT	32	
FT	ZN_FING	
FT	105	
FT	MOTIF	
FT	155	
FT	MUTAGEN	
FT	156	
FT	MUTAGEN	
FT	158	
FT	CONFLICT	
FT	22	
FT	SEQUENCE	
SO	158 AA; 18872 MW; 5BCF13CFA3D157FA CRC64;	
OY	Query Match	
Db	Beet Local Similarity	
OY	Matches	
OY	87; Conservative	
OY	21; Mismatches	
OY	42; Indels	
OY	5; Gaps	
OY	1	
OY	2 FQDPQERARKLPOLCTELQTTHIDHILECVCKQQQLLRREYVDFAFRDLCIYYRDGNPYA 61	
Db	4 FEDPTRRRYKLPDLCTELMTSLTODLEIRTCVCVTALBELTEVEEFAFKULFVVYRSISHA 63	
OY	62 VXDCLKAKYSKISEYRHCVSYVGTTLFOQYNKKPLCDLLIRCTNYOKPCLCPBEKORHLDK 121	
Db	64 ACHKCIDPSYRIELRHYSDSVYGDTLEKLTFYTGYNLLIRCLRCKPKLANPAEKURHINE 123	
OY	122 KQPFNINRGWTGRCMSCCRSR-----TRRETOL 151	
Db	124 KRFFNINGHYRGQCHSCCNRAQRRLQRRRETYV 158	
RESULT 94		
ID	Q76297_HPV18	
AC	Q76297_HPV18 PRELIMINARY; PRT; 158 AA.	
DT	10-MAY-2005, integrated into UniProtKB/TrEMBL.	
DT	10-MAY-2005, sequence version 1.	
DT	07-FEB-2006, entry version 4.	
DE	E6 protein.	
GN	Name=E6;	
OS	Human Papillomavirus type 18.	
OC	Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;	
OC	Alphapapillomavirus.	
NCBI	taxid=333761;	
NP	[1]	
NP	NUCLEOTIDE SEQUENCE.	

Query Match	54.9%	Score 455.5	DB 2	Length 158
Best Local Similarity	56.1%	Pred. No. 9e-37		
Matches	87	Conservative	21	Mismatches 42; Indels 5; Gaps 1
QY	2	FODPDEPRKLPOLCTELQTTIHDIILECYCQGOQLRREYVOPAPRDLCTVRRDGPVA	61	
DB	4	FEDTRRPVPLPDCTELNTSLQDIEITCYCKVLELTVEFEAFKDLVVRDLSLPA	63	
QY	62	VXDKCLFYSKISERYHYCVYGTTLQOYNKPLCDLLIRCIINXKPLCPPEKORHLK	121	
DB	64	ACHKCIDFYSRIRELRHYSDSVGDTLEKLTNTGLYVLLIRCLRCQPLNPAERLRLNE	123	
QY	122	KORFHNRGRMTGRCMCCRSSR-----TRRETOL	151	
DB	124	KRRFHNIAGHYRGQCHSCNRAQERLQRRETQV	158	
RESULT 95				
V66_HPVM6				
ID	V66_HPVM6	STANDARD;	PRT;	158 AA.
AC	P27962;			
DT	01-AUG-1992,	integrated into UniProtKB/Swiss-Prot.		
DT	01-AUG-1992,	sequence version 1.		
DT	07-FEB-2006,	entry version 28.		
DE	Protein E6.			
CN	Name=E6;			
OS	Human Papillomavirus type ME180.			
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;			
OC	unclassified Papillomaviridae.			
OX	NCBI_TaxID=10602;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE (GENOMIC DNA).			
RX	ME180=91374616, Pubmed=1716694.			
RA	Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;			
RT	"Characterization of a novel human papillomavirus DNA in the cervical			
RT	carcinoma cell line ME180."			
RL	J. Virol. 65:5564-5568(1991).			
CC	-1- FUNCTION: Transcriptional transactivator. Binds double stranded			
CC	DNA (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).			
CC	-1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NonDerivs License			
CC	-----			
DR	EMBL, M73258; -; NOT_ANNOTATED_CDS; Genomic_DNA.			
DR	PIR; C40509; W6WLP.			
DR	InterPro; IPR001334; E6.			
DR	Pfam; PF00518; E6; 1.			
KW	Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;			
KW	Transcription; Transcription regulation; Zinc; zinc-finger.			
FT	CHAIN	1	158	/Ftrid=PRO_0000133318.
FT	FT			/Ftrid=PRO_0000133318.
FT	ZN_FING	32	68	Potential.
FT	ZN_FING	106	141	Potential.
SO	SEQUENCE	158 AA;	18739 MW;	2B1F406B563F05FC CRC64;

Query Match	Similarity	Score	DB 1	Length	158
Best Local	54.1%	Pred. No. 2.2e-36			
Matches	86	Conservative	21	Mismatches	44
				Indels	5
				Gaps	1
Qy	1	MFODPQERPRKLPOLCTELQTTIHDIILIECYCKQOLLRRVYDPAFRLDLCIVRDGNPY	60		
Db	3	LFNHNEERPRYKLPDLCTRLDITLTHDVITDCYCRQQLQRTVEYEFAPFDLNVVRDGVPL	62		
Qy	61	AVXDKLKFYSKISEYRHVCYSVGTLEQQYNKPLCDLLRCINXOKPLCEEQKHLD	120		
Db	63	AACOSCICFYAKIRELRYSSSVATLTETINTKLYDLSIRCMCLKPLSPAEXLRHLN	122		
Qy	121	KKORFHNIRGWTGRCMSCCRSS-----RTRERQL	151		
Db	123	SKRPFHAKAGNFTGCRCHCWTSKREDRRTROETOV	158		
RESULT	96				
ID	07KXK8	HPV68	PRELIMINARY	PRT	158 AA.
AC	07KXK9				
DT	05-JUL-2004				integrated into UniProtKB/TrEMBL.
DT	05-JUL-2004				sequence version 1.
DT	07-FEB-2006				entry version 12.
DE	B6 protein.				
OS	Human papillomavirus type 68.				
OC	Viruses; deDNA viruses; no RNA stage; Papillomaviridae;				
OX	Alphapapillomavirus.				
NCBI	taxid=45240;				
LN	[1]				
RP	NCULEOTIDE SEQUENCE.				
RX	MEDLINE=91374616; PubMed=1716694;				
RA	Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;				
RT	"Characterization of a novel human papillomavirus DNA in the cervical				
RL	carcinoma cell line ME180."				
RN	J. Virol. 65:5564-5568(1991).				
RV	[2]				
RP	NCULEOTIDE SEQUENCE.				
RX	MEDLINE=98090644; PubMed=9427755; DOI=10.1093/emboj/17.1.215;				
RA	Reuter S., Bartelmann M., Vogt M., Geisen C., Napieraki I., Kahn T.,				
RT	Delius H., Lichten P., Weitz S., Korn B., Schwarz E.;				
RL	"APM-1, a novel human gene, identified by aberrant cotranscription				
RV	with papillomavirus oncogenes in aa cervical carcinoma cell line,				
RT	encodes a B7B/POZ-zinc finger protein with growth inhibitory				
RL	activity".				
EMBO	J. 17:215-222 (1998).				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
CC	Distributed under the Creative Commons Attribution-NonCommercial license				
CC	EMBL: Y14591; CAA74931.1; -; mRNA.				
DR	GO:0042025; C:host cell nucleus; IEA.				
DR	GO:0003677; F:DNA binding; IEA.				
DR	InterPro: IPR00134; E6.				
DR	Pfam: PF00518; E6; 1.				
SQ	SEQUENCE 158 AA; 18739 MW; 2B1F406B563F05FC CRC64;				
Query Match	54.4%	Score 451.5	DB 2	Length 158	
Best Local Similarity	55.1%	Pred. No. 2.2e-36			
Matches	86	Conservative	21	Mismatches	44
				Indels	5
				Gaps	1
Qy	1	MFODPQERPRKLPOLCTELQTTIHDIILIECYCKQOLLRRVYDPAFRLDLCIVRDGNPY	60		
Db	3	LFNHNEERPRYKLPDLCTRLDITLTHDVITDCYCRQQLQRTVEYEFAPFDLNVVRDGVPL	62		
Qy	61	AVXDKLKFYSKISEYRHVCYSVGTLEQQYNKPLCDLLRCINXOKPLCEEQKHLD	120		
Db	63	AACOSCICFYAKIRELRYSSSVATLTETINTKLYDLSIRCMCLKPLSPAEXLRHLN	122		
Qy	121	KKORFHNIRGWTGRCMSCCRSS-----RTRERQL	151		
Db	123	SKRPFHAKAGNFTGCRCHCWTSKREDRRTROETOV	158		

```

RESULT 97
OC0129_9PAPI PRELIMINARY; PRT; 162 AA.
ID 090129;
AC 090129;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxID=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91374616; PubMed=1716694;
RA Reuter S., Dalius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
RT "Characterization of a novel human papillomavirus DNA in the cervical
RT carcinoma cell line ME180."
RL J. Virol. 65:5564-5568(1991).
CC -----
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CC -----
CC EMBL: M73258; AAF1401.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR003334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 162 AA; 19167 MW; 2E40C128FEF7902C CRC64;

Query Match 54.4%; Score 451.5; DB 2; Length 162;
Best Local Similarity 55.1%; Pred. No. 2,36-36;
Matches 86; Conservative 21; Mismatches 44; Indels 5; Gaps 1;

OY 1 MFQDPQERPRKLPOLCTELQTTTHDILIECYCKCOQLRREYDFPARDLCTYRDGNPY 60
DB 7 LFHNPEERPYKLPLCLCTLDTHDVIDCYCRROLREVEYFAFDLNVVRDGVPL 66
OY 61 AVNOKCKEYKISBYRHYCQSVYGTLEQOYNPLCDLILRCINXOKPLCPPEKORHLD 120
DB 67 AACSCCIFPKYAKIELRYSQSVAYITLDTITNKLVDLSIRCMCKLPSPAEKRLHN 126
OY 121 KKQRFHNIRGWTGRCMSCCRSS-----RTRETRQL 151
DB 127 SKRRFHKIAGNFTGQCHRCWTSKXEDRRRTQGEYQV 162

RESULT 98
VE6 HPV39 STANDARD; PRT; 158 AA.
ID VE6 HPV39
AC P24835;
DT 01-MAR-1992, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-1992, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Protein E6.
OS Human papillomavirus type 39.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10588;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=91135017; PubMed=1847266;
RA Volpers C., Strebeck R.E.;
RT "Genome organization and nucleotide sequence of human papillomavirus
RT type 39."
RL Virology 181:419-423(1991).
CC -----
CC FUNCTION: Transcriptional transactivator. Binds double stranded
CC DNA (By similarity).
CC -!- FUNCTION: This protein may be involved in the oncogenic potential
CC of this virus (cervical neoplasia-associated virus).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).

```

CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
CC -----
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CC -----
DR EMBL; M62849; AAA47050.1; -; Genomic_DNA.
DR PIR; A38502; M6WL39.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
KW Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger.
FT CHAIN 1 158 /FtId=PRO_0000133358.
FT ZN FING 32 68 Potential.
FT ZN FING 105 141 Potential.
SQ SEQUENCE 158 AA; 18727 MW; 1B5E9D55BC1B662E CRC64;
Query Match 54.2%; Score 449.5; DB 1; Length 158;
Best Local Similarity 55.5%; Pred. No. 3.5e-36;
Matches 86; Conservative 19; Mismatches 45; Indels 5; Gaps 1;
QY 2 FODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAPRDLCTVYRDGNPYA 61
DB 4 FHNEAPRPYKLPDLCTLDITLQDTTACVYCRBPLOQTEVEYEFASDLYVYRDGEPLA 63
QY 62 VXDCKLFYSKISSEYRHYCVSVGTTLLEQYNNKPLCDLLIRGINXOKPLCPBEKORHLDK 121
DB 64 ACGSCIFPFAKIRRLRYSDSVVATLTLENITKLYNLLIRCMCKLRPLCAFKLRHLNS 123
QY 122 KORFNIRGRWTCRCMSCCRSSR-----TRRETQL 151
DB 124 KRPFHKLAGHYRGCHSCCRARQERQRRETV 158
RESULT 99
Q90NP8 HPV8 PRELIMINARY; PRT; 158 AA.
ID Q90NP8 HPV18
AC Q90NP8;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE E6 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333761;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Laaseri M., Gul'ko L., Vinokurova S., Kissel'jova N., Veiko V.,
RA Kissel'jev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RT Transformation Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Veiko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; Y18491; CAB53096.1; -; Genomic_DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 18886 MW; 5BECF13CF43D407AF CRC64;
Query Match 54.2%; Score 449.5; DB 2; Length 158;
Best Local Similarity 55.5%; Pred. No. 3.5e-36;
Matches 86; Conservative 21; Mismatches 43; Indels 5; Gaps 1;
QY 2 FODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAPRDLCTVYRDGNPYA 61

DB 4 FEDPTRRPYKLPDLCTELNTSLQDIEITCYCKVLELTVEFEAFKDLFVYRDSIPHA 63
QY 62 VXDCKLFYSKISSEYRHYCVSVGTTLLEQYNNKPLCDLLIRGINXOKPLCPBEKORHLDK 121
DB 64 ACHKCIDFPYRIRRLRYSDSVYGDITLTKLNGLYNLLIRCLRCQKPLNPAEKLRHLNE 123
QY 122 KORFNIRGRWTCRCMSCCRSSR-----TRRETQL 151
DB 124 KRPFHKLAGHYRGCHSCCRARQERQRRETV 158
RESULT 100
Q994A0 HPV82 PRELIMINARY; PRT; 151 AA.
ID Q994A0 HPV82
AC Q994A0;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Putative transforming protein E6.
GN Name=E6;
OS Human papillomavirus type 82.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=129724;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
RA Natchania A., Chen Z., Desalle R., Burk R.D.;
RT "Phylogenetic Inference among Oncogenic Genital Alpha Human
RT Papillomaviruses";
RL J. Virol. 79:15503-15510(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Teraï M., Burk R.D.;
RT "Cervical HPVs in Evolution; Genomic Sequence of IS39/AE2, a Subtype
RT of Oncogenic HPV 82 (W13B).";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AF293961; AAK28449.1; -; Genomic_DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18071 MW; 5BDC340E467CF5D CRC64;
Query Match 54.1%; Score 449; DB 2; Length 151;
Best Local Similarity 56.3%; Pred. No. 3.8e-36;
Matches 85; Conservative 24; Mismatches 42; Indels 0; Gaps 0;
QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAPRDLCTVYRDGNPY 60
DB 1 MFEDIRERPRPTLYELCAVYNTSMHNIQVLCVYCKEELCRADVYVNAFTETRIYRDMPY 60
QY 61 AYVDCKLFYSKISSEYRHYCVSVGTTLLEQYNNKPLCDLLIRGINXOKPLCPBEKORHL 120
DB 61 AVCKKCLMPYSRIREIRYRSYVGTATLEAITNKSLEYELLIRCHRCORPLGPEKQKRV 120
QY 121 KORFNIRGRWTCRCMSCCRSSRTRRETQL 151
DB 121 DKCRPFHKLARWVGQCANCRATARQSESTV 151
Search completed: May 27, 2006, 05:16:23
Job time : 238.867 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:33:17 ; Search time 157.064 Seconds
(without alignments)
445.330 Million cell updates/sec

Title: US-10-530-253-13ED
Perfect score: 830
Sequence: 1 MFQDPQERPRKLPQLCTELQ.....MTGRCMSCCRSRRTRETQL 151

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues
Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	828	99.8	248	5	US-10-530-253-3
2	828	99.8	248	5	US-10-530-253-5
3	826	99.5	151	5	US-10-484-063-20
4	826	99.5	151	5	US-10-484-063-27
5	826	99.5	151	5	US-10-530-253-13
6	826	99.5	151	5	US-10-530-253-1
7	823	99.2	158	5	US-10-858-384-2
8	823	99.2	158	5	US-10-367-057-16
9	823	99.2	158	6	US-11-021-949-13
10	823	99.2	158	6	US-11-021-949-13
11	823	99.2	171	4	US-10-472-724-2
12	823	99.2	248	5	US-10-530-253-9
13	823	99.2	248	5	US-10-530-253-11
14	823	99.2	256	6	US-11-192-923A-2
15	823	99.2	266	3	US-09-367-309A-1
16	823	99.2	273	4	US-10-000-903-4
17	823	99.2	273	5	US-10-899-771-4
18	823	99.2	292	4	US-10-000-903-10
19	823	99.2	321	4	US-10-899-771-10
20	823	99.2	371	5	US-10-000-903-6
21	823	99.2	371	5	US-10-899-771-6
22	823	99.2	390	4	US-10-000-903-14
23	823	99.2	390	5	US-10-899-771-14
24	821	98.7	248	5	US-10-530-253-7
25	819	98.7	151	4	US-10-177-390-6
26	779.5	93.9	243	6	US-11-072-288-1
27	578	69.6	149	5	US-10-530-253-18

28	578	69.6	149	6	US-11-021-949-14	Sequence 14, Appl
29	523	63.0	149	5	US-10-530-253-16	Sequence 16, Appl
30	523	63.0	149	5	US-11-021-949-18	Sequence 18, Appl
31	520	62.7	149	6	US-10-530-253-17	Sequence 17, Appl
32	520	62.7	149	6	US-11-021-949-16	Sequence 16, Appl
33	498	60.0	149	6	US-10-530-253-24	Sequence 24, Appl
34	496	59.8	149	6	US-11-021-949-15	Sequence 15, Appl
35	496	59.8	149	6	US-10-530-253-22	Sequence 22, Appl
36	487	58.7	148	5	US-11-021-949-11	Sequence 11, Appl
37	487	58.7	148	6	US-11-021-949-19	Sequence 19, Appl
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42	460	55.4	151	6	US-10-530-253-21	Sequence 21, Appl
43	460	55.4	151	6	US-11-021-949-24	Sequence 24, Appl
44	459.5	55.4	158	5	US-10-530-253-20	Sequence 20, Appl
45	459.5	55.4	158	6	US-11-021-949-29	Sequence 29, Appl
46	455.5	54.9	158	5	US-10-530-253-15	Sequence 15, Appl
47	455.5	54.9	158	6	US-11-021-949-28	Sequence 28, Appl
48	455.5	54.9	172	4	US-10-472-724-6	Sequence 6, Appl
49	455.5	54.9	278	4	US-10-000-903-21	Sequence 21, Appl
50	455.5	54.9	278	5	US-10-899-771-21	Sequence 21, Appl
51	455.5	54.9	383	4	US-10-000-903-23	Sequence 23, Appl
52	455.5	54.9	383	5	US-10-899-771-23	Sequence 23, Appl
53	451.5	54.4	162	6	US-11-021-949-31	Sequence 31, Appl
54	449.5	54.2	158	5	US-10-800-023-27	Sequence 27, Appl
55	449.5	54.2	158	5	US-10-530-253-19	Sequence 19, Appl
56	449.5	54.2	158	6	US-11-021-949-30	Sequence 30, Appl
57	449	54.1	151	6	US-11-021-949-25	Sequence 25, Appl
58	436.5	53.6	150	6	US-11-021-949-27	Sequence 27, Appl
59	426.5	51.4	155	5	US-10-530-253-23	Sequence 23, Appl
60	426.5	51.4	155	6	US-11-021-949-22	Sequence 22, Appl
61	421	50.7	152	5	US-10-530-253-39	Sequence 39, Appl
62	415.5	50.1	160	5	US-10-530-253-25	Sequence 25, Appl
63	415.5	50.1	160	6	US-11-021-949-32	Sequence 32, Appl
64	415	50.0	151	6	US-11-021-949-26	Sequence 26, Appl
65	385.5	46.4	153	6	US-11-021-949-20	Sequence 20, Appl
66	379	45.7	154	6	US-11-021-949-21	Sequence 21, Appl
67	372.5	44.9	155	6	US-11-021-949-23	Sequence 23, Appl
68	333	40.1	117	5	US-10-751-845-16	Sequence 16, Appl
69	333	40.1	236	5	US-10-751-845-157	Sequence 157, Appl
70	333	40.1	237	5	US-10-751-845-158	Sequence 158, Appl
71	333	40.1	261	5	US-10-751-845-160	Sequence 160, Appl
72	323	38.9	536	4	US-10-367-095-10	Sequence 10, Appl
73	323	38.9	536	4	US-10-368-046-10	Sequence 10, Appl
74	323	38.9	536	5	US-10-918-337-10	Sequence 10, Appl
75	323	38.9	536	5	US-10-367-057-11	Sequence 11, Appl
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77	189	22.8	119	5	US-10-476-570-19	Sequence 19, Appl
78	177	21.3	32	4	US-10-476-570-9	Sequence 9, Appl
79	172	20.7	32	4	US-10-476-570-53	Sequence 53, Appl
80	163	19.6	30	5	US-10-858-384-4	Sequence 4, Appl
81	163	19.6	30	5	US-10-476-570-55	Sequence 55, Appl
82	159	19.2	29	4	US-10-858-384-8	Sequence 8, Appl
83	159	19.2	29	5	US-10-476-570-13	Sequence 13, Appl
84	157	18.9	29	4	US-11-021-949-5	Sequence 5, Appl
85	146	17.6	24	6	US-11-021-949-23	Sequence 23, Appl
86	136.5	16.4	140	6	US-10-367-057-11	Sequence 11, Appl
87	136	16.4	25	6	US-10-476-570-40	Sequence 40, Appl
88	135	16.3	23	4	US-10-476-570-44	Sequence 44, Appl
89	135	16.3	24	4	US-10-751-845-65	Sequence 65, Appl
90	132	15.9	24	4	US-10-476-570-56	Sequence 56, Appl
91	130	15.7	22	5	US-10-751-845-10	Sequence 10, Appl
92	130	15.7	42	5	US-10-751-845-152	Sequence 152, Appl
93	130	15.7	23	5	US-10-751-845-66	Sequence 66, Appl
94	126	15.2	23	5	US-10-858-384-6	Sequence 6, Appl
95	124	14.9	22	5	US-11-021-949-3	Sequence 3, Appl
96	119	14.3	23	6	US-10-476-570-27	Sequence 27, Appl
97	115.5	13.9	23	4	US-10-938-249-513	Sequence 513, Appl
98	115	13.9	20	5	US-10-476-570-41	Sequence 41, Appl
99	114	13.7	22	4	US-10-612-818-4	Sequence 4, Appl
100	114	13.7	22	4		

ALIGNMENTS

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RESULT 1
US-10-530-253-3
; Sequence 3, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Cassecci, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhiney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-3

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Best Local Similarity 98.7%; Pred. No. 6.5e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 AYXDKCLKFYSKISSEYRHVCYVGTTLLEQYNNKPLCDLLIRICINXQKPLCEBEKQRHLD 120
DB 61 AYXDKCLKFYSKISSEYRHVCYVGTTLLEQYNNKPLCDLLIRICINXQKPLCEBEKQRHLD 120

QY 121 KQRFHNIRGWRGRCMSCCRSSRTRETEL 151
DB 121 KQRFHNIRGWRGRCMSCCRSSRTRETEL 151

RESULT 2
US-10-530-253-5
; Sequence 5, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Cassecci, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhiney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 66/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-5

Query Match          99.8%; Score 828; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 6.5e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 121 KQRFHNIRGWRGRCMSCCRSSRTRETEL 151
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Best Local Similarity 98.7%; Pred. No. 6.5e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 121 KQRFHNIRGWRGRCMSCCRSSRTRETEL 151
DB 121 KQRFHNIRGWRGRCMSCCRSSRTRETEL 151

RESULT 3
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILTERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match          99.5%; Score 826; DB 5; Length 151;
Best Local Similarity 98.7%; Pred. No. 6e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 AYXDKCLKFYSKISSEYRHVCYVGTTLLEQYNNKPLCDLLIRICINXQKPLCEBEKQRHLD 120
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QY 121 KQRFHNIRGWRGRCMSCCRSSRTRETEL 151
DB 121 KQRFHNIRGWRGRCMSCCRSSRTRETEL 151

RESULT 4
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILTERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
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; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match          99.5%; Score 826; DB 5; Length 151;
Best Local Similarity 98.7%; Pred. No. 6e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQQYNKPLCDLLIRCNXOKPLCPBEKQRHLD 120
DB 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQQYNKPLCDLLIRCNXOKPLCPBEKQRHLD 120
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DB 121 KKORFHNIRGWTGRCMSCCRSSRTRETOL 151

RESULT 5
US-10-530-253-13
; Sequence 13, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-13

Query Match          99.5%; Score 826; DB 5; Length 151;
Best Local Similarity 98.7%; Pred. No. 6e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQQLIRREYVDFAPRDLCTVYRDGMPY 60
QY 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQQYNKPLCDLLIRCNXOKPLCPBEKQRHLD 120
DB 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQQYNKPLCDLLIRCNXOKPLCPBEKQRHLD 120
QY 121 KKORFHNIRGWTGRCMSCCRSSRTRETOL 151
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RESULT 6
US-10-530-253-1
; Sequence 1, Application US/10530253
; Publication No. US20060014926A1
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; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-1

Query Match          99.5%; Score 826; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 1.1e-80;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQQYNKPLCDLLIRCNXOKPLCPBEKQRHLD 120
DB 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQQYNKPLCDLLIRCNXOKPLCPBEKQRHLD 120
QY 121 KKORFHNIRGWTGRCMSCCRSSRTRETOL 151
DB 121 KKORFHNIRGWTGRCMSCCRSSRTRETOL 151

RESULT 7
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match          99.2%; Score 823; DB 5; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQQLIRREYVDFAPRDLCTVYRDGMPY 60
DB 8 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQQLIRREYVDFAPRDLCTVYRDGMPY 67
QY 61 AVXDKCLKFYSKISEYHYCYSVYGTLEQQYNKPLCDLLIRCNXOKPLCPBEKQRHLD 120
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Db 68 AVCDKCLFKFSKISSEYRHYCYSLVGTTLLEQYCKQQLLRREYDFAFRDLCIVRDGNPY 127

Qy 121 KKQRFHNIRGRWTCGCMSCCRSSRTTRETOL 151
Db 128 KKQRFHNIRGRWTCGCMSCCRSSRTTRETOL 158

RESULT 8
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng;
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Curoseq1st version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 99.2%; Score 823; DB 5; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCIVRDGNPY 60
Db 8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCIVRDGNPY 67

Qy 61 AVXDCKLKFYSKISSEYRHYCYSLVGTTLLEQYCKQQLLRREYDFAFRDLCIVRDGNPY 120
Db 68 AVXDCKLKFYSKISSEYRHYCYSLVGTTLLEQYCKQQLLRREYDFAFRDLCIVRDGNPY 127

Qy 121 KKQRFHNIRGRWTCGCMSCCRSSRTTRETOL 151
Db 128 KKQRFHNIRGRWTCGCMSCCRSSRTTRETOL 158

RESULT 9
US-11-021-949-13
; Sequence 13, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARE, MICHAEL P.
; APPLICANT: DIAZ-SAMIENTO, CHAMORRO SOKOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FaalSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-13

Query Match 99.2%; Score 823; DB 6; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCIVRDGNPY 60
Db 8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCIVRDGNPY 67

Qy 61 AVXDCKLKFYSKISSEYRHYCYSLVGTTLLEQYCKQQLLRREYDFAFRDLCIVRDGNPY 120
Db 68 AVXDCKLKFYSKISSEYRHYCYSLVGTTLLEQYCKQQLLRREYDFAFRDLCIVRDGNPY 127

Qy 121 KKQRFHNIRGRWTCGCMSCCRSSRTTRETOL 151
Db 128 KKQRFHNIRGRWTCGCMSCCRSSRTTRETOL 158

RESULT 10
US-11-206-138-3
; Sequence 3, Application US/11206138
; Publication No. US20060039919A1
; GENERAL INFORMATION:
; APPLICANT: Healthbanc Biotech CO. LTD.
; TITLE OF INVENTION: Fusion protein for inhibiting cervical cancer
; FILE REFERENCE: P7819/0613
; CURRENT APPLICATION NUMBER: US/11/206,138
; CURRENT FILING DATE: 2005-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-11-206-138-3

Query Match 99.2%; Score 823; DB 6; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCIVRDGNPY 60
Db 8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCIVRDGNPY 67

Qy 61 AVXDCKLKFYSKISSEYRHYCYSLVGTTLLEQYCKQQLLRREYDFAFRDLCIVRDGNPY 120
Db 68 AVXDCKLKFYSKISSEYRHYCYSLVGTTLLEQYCKQQLLRREYDFAFRDLCIVRDGNPY 127

Qy 121 KKQRFHNIRGRWTCGCMSCCRSSRTTRETOL 151
Db 128 KKQRFHNIRGRWTCGCMSCCRSSRTTRETOL 158

RESULT 11
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-472-724-2

```

; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530_253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 248
; TYPE: PRF
; ORGANISM: Human papillomavirus type 16
US-10-530-253-11

Query Match      99.2%; Score 823; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 2,2e+80;
Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

YQ   2 FODPOERPRKLPOLCTELQTTHIDILLECVCYCKOQLLRREVDPAFRDLCTIVRDGNYA 61
Db    99 FODPOERPRKLPOLCTELQTTHIDILLECVCYCKOQLLRREVDPFAFRDLCIYVRDGNPYA 158

YQ   62 VDKLCLKFKYSKSIEVRYHYCYVGTTLEQQNKPICDLLIRCNXOKPLCPBEKHRLDK 121
Db   159 VDGLCLKFESKSISEVRYHCVSYGTTLDEQNPKPDCLLIRCINGOKPLCPBEKHRLDK 218

YQ   122 KORFHNIQRWTGRCMSCCRSSRTRETOL 151
Db   219 KORFHNIQRWTGRCMSCCRSSRTRETOL 248


RESULT 14
US-11-192-923A-2
; Sequence 2, Application US/11/92923A
; Publication No. US20060018928A1
; GENERAL INFORMATION:
; APPLICANT: PANQ, XIAOWU
; TITLE OF INVENTION: VIRUS-LIKE PARTICLE CONTAINING A DENGUE VIRUS
; FILE REFERENCE: 116620-003
; CURRENT APPLICATION NUMBER: US/11/192,923A
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: CN 03115272.4
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: CN 03115273.2
; PRIOR FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRF
; ORGANISM: Human papillomavirus
US-11-192-923A-2

Query Match      99.2%; Score 823; DB 6; Length 256;
Best Local Similarity 98.0%; Pred. No. 2,3e+80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

YQ   1 MFODPOERPRKLPOLCTELQTTHIDILLECVCYCKOQLLRREVDPAFRDLCTIVRGDNPY 60
Db   106 MFODPOERPRKLPOLCTELQTTHIDILLECVCYCKOQLLRREVDPAFRDLCTIVRDNPNY 165

YQ   61 AVXDCLCFKFSKISIEVRYHCYGVGTTLEQQNKKPCDLLIRCNXOKPLCPBEKHRLHD 120
Db   166 AVCDDCLCFKFSKISEVRYHCYSLGGTTLBQQNKPPCDLLIRCINCOKPLCPBEKHRLD 225

YQ   121 KQRFHNIRGRWTCRCMSCRSSRTRETOL 151
Db   226 KKQRFHNIRGRWTCRCMSCRSSRTRETOL 256


RESULT 15
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US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 99.2%; Score 823; DB 3; Length 266;
Best Local Similarity 98.0%; Pred. No. 2.4e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDFAFRDLCTVYRDGPNY 60
DB 8 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDFAFRDLCTVYRDGPNY 67
QY 61 AVXDCKLKFYSKISEYRHVCYVGTTLLEQYNNKPLCDLLIRINCXOKPLCEEKQRHLD 120
DB 68 AVCDCKLKFYSKISEYRHVCYVGTTLLEQYNNKPLCDLLIRINCXOKPLCEEKQRHLD 127
QY 121 KKQRFNIRGRWTRGRCMSCCRSSRTRETOL 151
DB 128 KKQRFNIRGRWTRGRCMSCCRSSRTRETOL 158

RESULT 16
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match 99.2%; Score 823; DB 4; Length 273;
Best Local Similarity 98.0%; Pred. No. 2.5e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDFAFRDLCTVYRDGPNY 60
DB 114 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDFAFRDLCTVYRDGPNY 173

QY 61 AVXDCKLKFYSKISEYRHVCYVGTTLLEQYNNKPLCDLLIRINCXOKPLCEEKQRHLD 120
DB 174 AVCDCKLKFYSKISEYRHVCYVGTTLLEQYNNKPLCDLLIRINCXOKPLCEEKQRHLD 233
QY 121 KKQRFNIRGRWTRGRCMSCCRSSRTRETOL 151
DB 234 KKQRFNIRGRWTRGRCMSCCRSSRTRETOL 264

RESULT 17
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeic protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and B6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match 99.2%; Score 823; DB 5; Length 273;
Best Local Similarity 98.0%; Pred. No. 2.5e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDFAFRDLCTVYRDGPNY 60
DB 114 MFQDQERPRKLPOLCTELQTTIHDIIECYCKQOLLREYVDFAFRDLCTVYRDGPNY 173
QY 61 AVXDCKLKFYSKISEYRHVCYVGTTLLEQYNNKPLCDLLIRINCXOKPLCEEKQRHLD 120
DB 174 AVCDCKLKFYSKISEYRHVCYVGTTLLEQYNNKPLCDLLIRINCXOKPLCEEKQRHLD 233
QY 121 KKQRFNIRGRWTRGRCMSCCRSSRTRETOL 151
DB 234 KKQRFNIRGRWTRGRCMSCCRSSRTRETOL 264

RESULT 18
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5

PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-10

Query Match 99.2%; Score 823; DB 4; Length 292;
Best Local Similarity 98.0%; Pred. No. 2.7e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVYRDGNY 60
DB 133 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVYRDGNY 192
QY 61 AVXDKLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLIRCTINXQKPLCPBEKQRHLD 120
DB 193 AVXDKLKFYSKISEYHYCTSLVGTLEQYNNKPLCDLIRCTINXQKPLCPBEKQRHLD 252
QY 121 KKQRFHNIRGRWTCGMSCCRSSRTRRETOL 151
DB 253 KKQRFHNIRGRWTCGMSCCRSSRTRRETOL 283

RESULT 19
US-10-899-771-10
Sequence 10, Application US/10899771
Publication No. US20050031638A1
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimaeic protein (Clyta from Streptococcus
OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
US-10-899-771-10

Query Match 99.2%; Score 823; DB 5; Length 292;
Best Local Similarity 98.0%; Pred. No. 2.7e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVYRDGNY 60
DB 133 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVYRDGNY 192
QY 61 AVXDKLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLIRCTINXQKPLCPBEKQRHLD 120
DB 193 AVXDKLKFYSKISEYHYCTSLVGTLEQYNNKPLCDLIRCTINXQKPLCPBEKQRHLD 252
QY 121 KKQRFHNIRGRWTCGMSCCRSSRTRRETOL 151
DB 253 KKQRFHNIRGRWTCGMSCCRSSRTRRETOL 283

RESULT 20
US-10-000-903-6
Sequence 6, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Bernarde
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 371
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-6

Query Match 99.2%; Score 823; DB 4; Length 371;
Best Local Similarity 98.0%; Pred. No. 3.6e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVYRDGNY 60
DB 114 MFODPOBPRRLPOLCTELQTTIHDIIECYCKQQLRRVYDFAFRDLCTVYRDGNY 173
QY 61 AVXDKLKFYSKISEYHYCYSVYGTLEQYNNKPLCDLIRCTINXQKPLCPBEKQRHLD 120
DB 174 AVXDKLKFYSKISEYHYCTSLVGTLEQYNNKPLCDLIRCTINXQKPLCPBEKQRHLD 233
QY 121 KKQRFHNIRGRWTCGMSCCRSSRTRRETOL 151
DB 234 KKQRFHNIRGRWTCGMSCCRSSRTRRETOL 264

RESULT 21
US-10-899-771-6
Sequence 6, Application US/10899771
Publication No. US20050031638A1
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 371
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimaeic protein (protein D from Haemophilus
OTHER INFORMATION: influenzae B and B6E7 fusion from Human papilloma
US-10-899-771-6

```
Query Match          99.2%; Score 823; DB 5; Length 371;
Best Local Similarity 98.0%; Pred. No. 3.8e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MFQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 60
DB 114 MFQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 173
OY 61 AVXDCKLFYKISSEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPBEKORHLD 120
DB 174 AVXDCKLFYKISSEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPBEKORHLD 233
OY 121 KKQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 151
DB 234 KKQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 264

RESULT 22
US-10-000-903-14
; Sequence 14, Application US/10000903
; Publication No. US2002018221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-14

Query Match          99.2%; Score 823; DB 4; Length 390;
Best Local Similarity 98.0%; Pred. No. 3.8e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MFQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 60
DB 133 MFQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 192
OY 61 AVXDCKLFYKISSEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPBEKORHLD 120
DB 193 AVXDCKLFYKISSEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPBEKORHLD 252
OY 121 KKQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 151
DB 253 KKQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 283

RESULT 23
US-10-899-771-14
; Sequence 14, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976

; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeic protein (CJyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-14

Query Match          99.2%; Score 823; DB 5; Length 390;
Best Local Similarity 98.0%; Pred. No. 3.8e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MFQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 60
DB 133 MFQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 192
OY 61 AVXDCKLFYKISSEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPBEKORHLD 120
DB 193 AVXDCKLFYKISSEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPBEKORHLD 252
OY 121 KKQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 151
DB 253 KKQRFHNIRGRWTGRCMSCCRSSRTTRRETOL 283

RESULT 24
US-10-530-253-7
; Sequence 7, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Cassecci, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-7

Query Match          98.9%; Score 821; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 3.7e-80;
Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 61
DB 99 FQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTVYRDGMPY 158
OY 62 VXDCKLFYKISSEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPBEKORHLD 121
DB 159 VXDCKLFYKISSEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPBEKORHLD 218
OY 122 KORFHNIRGRWTGRCMSCCRSSRTTRRETOL 151
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Db 219 KORFHNIRGRTGRCMCCRSSRTRRETOL 248

RESULT 25

US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerpse Innovatiecentrum
; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with linear
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match Best Local Similarity 98.7%; Score 819; DB 4; Length 151;

Matches 148; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLLRREVDPAFRDLCTIVRDGPNY 60

Db 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLLRREVDPAFRDLCTIVRDGPNY 60

Qy 61 AVXDKCLKFYSKISEYHRYCYSVYGTLEQOYNKPLCDLLIRCNXQKPLCPBEKORHLD 120

Db 61 AVXDKCLKFYSKISEYHRYCYSVYGTLEQOYNKPLCDLLIRCNXQKPLCPBEKORHLD 120

Qy 121 KORFHNIRGRTGRCMCCRSSRTRRETOL 151

Db 121 KORFHNIRGRTGRCMCCRSSRTRRETOL 151

RESULT 26

US-11-072-288-1
; Sequence 1, Application US/11072288
; Publication No. US20050159386A1
; GENERAL INFORMATION:
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: BALLOUT, Jean-Marc
; APPLICANT: BIZOUARNE, Nadine
; TITLE OF INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNOGENIC
; FILE REFERENCE: 017753-122
; CURRENT APPLICATION NUMBER: US/11/072,288
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US/09/462,993
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: PCT/FR98/01576
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: FR 97/09152
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 1
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
; OTHER INFORMATION: human papillomavirus, strain HPV-16, E6 protein
; OTHER INFORMATION: fused E protein signals, Clone E6*TWf.
US-11-072-288-1

Query Match Best Local Similarity 93.9%; Score 779.5; DB 6; Length 243;

Matches 94.7%; Pred. No. 1.1e-75;

Matches 143; Conservative 1; Mismatches 2; Indels 5; Gaps 1;

Qy 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLLRREVDPAFRDLCTIVRDGPNY 60

Db 36 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLLRREVDPAFRDLCTIVRDGPNY 95

Qy 61 AVXDKCLKFYSKISEYHRYCYSVYGTLEQOYNKPLCDLLIRCNXQKPLCPBEKORHLD 120

Db 96 AVXDKCLKFYSKISEYHRYCYSVYGTLEQOYNKPLCDLLIRCNXQKPLCPBEKORHLD 150

Qy 121 KORFHNIRGRTGRCMCCRSSRTRRETOL 151

Db 151 KORFHNIRGRTGRCMCCRSSRTRRETOL 181

RESULT 27

US-10-530-253-18
; Sequence 18, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Cassetti, Maria C.
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Human papillomavirus type 35
US-10-530-253-18

Query Match Best Local Similarity 69.6%; Score 578; DB 5; Length 149;

Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

Qy 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLLRREVDPAFRDLCTIVRDGPNY 60

Db 1 MFODPQERPRKLPOLCTELQTTTHDIIIECYCKQQLLRREVDPAFRDLCTIVRDGPNY 60

Qy 61 AVXDKCLKFYSKISEYHRYCYSVYGTLEQOYNKPLCDLLIRCNXQKPLCPBEKORHLD 120

Db 61 GVCCKCLKFYSKISEYHRYCYSVYGTLEQOYNKPLCDLLIRCNXQKPLCPBEKORHLD 120

Qy 121 KORFHNIRGRTGRCMCCRSSRTRRETOL 151

Db 121 KORFHNIRGRTGRCMCCRSSRTRRETOL 149

RESULT 28

US-11-021-949-14
; Sequence 14, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SABIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373

PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 149
TYPE: PRT
ORGANISM: human papilloma virus (HPV)
US-11-021-949-14

Query Match 69.6%; Score 578; DB 6; Length 149;
Best Local Similarity 71.5%; Pred. No. 3.6e-54;
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 60
QY 61 AVXDCKLRFYSKISSEYRHVYCVSGTTLTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 61 GVCCKLRFYSKISSEYRHVYCVSGTTLTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
QY 121 KKQRFHNIRGRWTCRCMSSCRSSRRRTETOL 151
DB 121 KKQRFHNIRGRWTCRCMSSCRSSRRRTETOL 151
QY 121 EKQRFHNIRGRWTCRCMSSCRSSRRRTETOL 149

RESULT 29
US-10-530-253-16
Sequence 16, Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:
APPLICANT: Casasetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
PRIOR FILING DATE: 2003-10-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 149
TYPE: PRT
ORGANISM: Human papillomavirus type 31
US-10-530-253-16

Query Match 63.0%; Score 523; DB 5; Length 149;
Best Local Similarity 64.9%; Pred. No. 3.2e-48;
Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 60
QY 61 AVXDCKLRFYSKISSEYRHVYCVSGTTLTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 61 GVCCKLRFYSKISSEYRHVYCVSGTTLTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
QY 121 KKQRFHNIRGRWTCRCMSSCRSSRRRTETOL 151
DB 121 KKQRFHNIRGRWTCRCMSSCRSSRRRTETOL 149

RESULT 30
US-11-021-949-18
Sequence 18, Application US/11021949
Publication No. US20050142541A1
GENERAL INFORMATION:

APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
PRIOR FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 149
TYPE: PRT
ORGANISM: human papilloma virus (HPV)
US-11-021-949-18

Query Match 63.0%; Score 523; DB 6; Length 149;
Best Local Similarity 64.9%; Pred. No. 3.2e-48;
Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 60
QY 61 AVXDCKLRFYSKISSEYRHVYCVSGTTLTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 61 GVCCKLRFYSKISSEYRHVYCVSGTTLTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
QY 121 KKQRFHNIRGRWTCRCMSSCRSSRRRTETOL 151
DB 121 KKQRFHNIRGRWTCRCMSSCRSSRRRTETOL 149

RESULT 31
US-10-530-253-17
Sequence 17, Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:
APPLICANT: Casasetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
PRIOR FILING DATE: 2003-10-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 149
TYPE: PRT
ORGANISM: Human papillomavirus type 33
US-10-530-253-17

Query Match 62.7%; Score 520; DB 5; Length 149;
Best Local Similarity 63.6%; Pred. No. 6.7e-48;
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 60
QY 61 AVXDCKLRFYSKISSEYRHVYCVSGTTLTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 61 GVCCKLRFYSKISSEYRHVYCVSGTTLTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120

Qy 121 KKORFHNIRGWTGRCSGCCSSRTRETOL 151
Db 121 LNKRFHNISGRWAGRCACWRS--RRRETAL 149

RESULT 32

US-11-021-949-16
; Sequence 16, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 149
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-16

Query Match 62.7%; Score 520; DB 6; Length 149;
Best Local Similarity 63.6%; Pred. No. 6.7e-48;
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

Qy 1 MFODPOBRPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFADLCIYYRDGPNY 60
Db 1 MFODTEKPRHLHLCALLETTHINIELQVCECKKPLRSEYDPAFADLVVYRREGNPF 60
Qy 61 AVXDCKLFYSKISEYRHHCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPPEKORHLD 120
Db 61 GICGLCLRLFSKISEYRHHCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPPEKORHLD 120
Qy 121 KKORFHNIRGWTGRCSGCCSSRTRETOL 151
Db 121 LNKRFHNISGRWAGRCACWRS--RRRETAL 149

RESULT 33

US-11-021-949-360
; Sequence 360, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 360
; LENGTH: 149
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-360

Query Match 60.0%; Score 498; DB 6; Length 149;
Best Local Similarity 60.1%; Pred. No. 1.6e-45;
Matches 89; Conservative 22; Mismatches 37; Indels 0; Gaps 0;

Qy 1 MFODPOBRPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFADLCIYYRDGPNY 60
Db 1 MFODTEKPRHLHLCALLETTHINIELQVCECKKPLRSEYDPAFADLVVYRREGNPF 60
Qy 61 AVXDCKLFYSKISEYRHHCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPPEKORHLD 120
Db 61 GVCCKCLRLFSKISEYRHHCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPPEKORHLD 120
Qy 121 KKORFHNIRGWTGRCSGCCSSRTRETOL 148
Db 121 LNKRFHNISGRWAGRCACWRS--RRRETAL 149

RESULT 34

US-10-530-253-24
; Sequence 24, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100MI37-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Human papillomavirus type 58
US-10-530-253-24

Query Match 59.8%; Score 496; DB 5; Length 149;
Best Local Similarity 61.6%; Pred. No. 2.6e-45;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

Qy 1 MFODPOBRPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFADLCIYYRDGPNY 60
Db 1 MFODTEKPRHLHLCALLETTHINIELQVCECKKPLRSEYDPAFADLVVYRREGNPF 60
Qy 61 AVXDCKLFYSKISEYRHHCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPPEKORHLD 120
Db 61 AVCKVCLRLFSKISEYRHHCYSVYGTLEQQYNKPLCDLLIRCIKXOKPLCPPEKORHLD 120
Qy 121 KKORFHNIRGWTGRCSGCCSSRTRETOL 151
Db 121 LNKRFHNISGRWAGRCACWRS--RRRETAL 149

RESULT 35

US-11-021-949-15
; Sequence 15, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949

```

; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 149
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-15

Query Match          59.8%; Score 496; DB 6; Length 149;
Best Local Similarity 61.6%; Pred. No. 2,4e-45;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

Qy 1 MFQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRDLCTVYRDGNPY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MFQDAERPRTLHDICQALETSVEHEILKVCCKKTLORSEYDVFADLRIVYRDGNPF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 AVXDCKLFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRICINXQKPLCPBEKORHLD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AVCKVCLRLSKISSEYRHVNSLYGDTLEQTLKKCLNELIRICICQPLCPBEKRRHVD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 KKQRFNIRGRWTGRCSGCCRSRRRTOTL 151
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 LNKRFHNISGRWTGRCAVCWMP--RRQTOV 149
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 36
US-10-530-253-22
; Sequence 22, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Human papillomavirus type 52
US-10-530-253-22

Query Match          58.7%; Score 487; DB 5; Length 148;
Best Local Similarity 61.7%; Pred. No. 2,4e-44;
Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

Qy 1 MFQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRDLCTVYRDGNPY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MFEDATPRRTLHELCVELESVHEIRLQCVCKKELRRREYKFLFTDLRIYVRDNNPY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 AVXDCKLFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRICINXQKPLCPBEKORHLD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GVCIMCLRLSKISSEYRHVQSLYKTLERVKKPLSEITIRICICQPLCPBEKERHVN 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 KKQRFNIRGRWTGRCSGCCR 141
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ANKRFHNIRGRWTGRCSGCCMR 141
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 37
US-11-021-949-17
; Sequence 17, Application US/11021949
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; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 148
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-17

Query Match          58.7%; Score 487; DB 6; Length 148;
Best Local Similarity 61.7%; Pred. No. 2,4e-44;
Matches 87; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

Qy 1 MFQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRDLCTVYRDGNPY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MFEDATPRRTLHELCVELESVHEIRLQCVCKKELRRREYKFLFTDLRIYVRDNNPY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 AVXDCKLFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRICINXQKPLCPBEKORHLD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GVCIMCLRLSKISSEYRHVQSLYKTLERVKKPLSEITIRICICQPLCPBEKERHVN 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 KKQRFNIRGRWTGRCSGCCR 141
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ANKRFHNIRGRWTGRCSGCCMR 141
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 38
US-11-021-949-359
; Sequence 359, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 359
; LENGTH: 148
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-359

Query Match          58.3%; Score 484; DB 6; Length 148;
Best Local Similarity 60.4%; Pred. No. 5,1e-44;
Matches 87; Conservative 17; Mismatches 40; Indels 0; Gaps 0;

Qy 2 FQDQERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRDLCTVYRDGNPY 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 FPNBERPRYKLPALCEVFNISIHIEILDVCYCEKQYLVCEVYDFIRDLCTVYRKGKRLG 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 62 VXDCKLFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRICINXQKPLCPBEKORHLDK 121
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Db 63 VCGPCLLFYSKAVQRYRNYNSVYGRTEJENLTNKLQCNILIRCGCKQKPLCELEKQRAVDE 122
QY 122 KORFNHNRGRWTCRMSCCSSSRT 145
Db 123 NKRFHQIADQWTCRCTRCWCRPSAT 146

RESULT 39
US-11-021-949-19
; Sequence 19, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 148
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-19

Query Match 58.2%; Score 483; DB 6; Length 148;
Best Local Similarity 61.4%; Pred. No. 6,6e-44;
Matches 89; Conservative 16; Mismatches 40; Indels 0; Gaps 0;

QY 1 MPDQPERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60
Db 2 LFPSEERPYKQLQCEVNIISHDINDVCFQGRGLYRSYVDFAFSDLCIVYRKQPY 61
QY 61 AVXDKCLFYSKISEYRHYCYSVYGTTLQOYNKPLCDLIRCNXOKPLCEPEKQRLD 120
Db 62 GVCOPCLAFYSKIREYRHYCYSVYGTTLQOYNKPLCDLIRCNXOKPLCEPEKQRLD 121
QY 121 KORFNHNRGRWTCRMSCCSSSRT 145
Db 122 EKRFHQIADQWTCRCTRCWCRPSAT 146

RESULT 40
US-10-530-253-26
; Sequence 26, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casaretti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human papillomavirus type 68
```

```
US-10-530-253-26
Query Match 56.4%; Score 468.5; DB 5; Length 158;
Best Local Similarity 55.1%; Pred. No. 2,6e-42;
Matches 86; Conservative 23; Mismatches 42; Indels 5; Gaps 1;

QY 1 MPDQPERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVYRDGNPY 60
Db 3 LFNPEERPYKLPDLCTLDITDITDIDVYCRQQLRTEYEFNFSDLCTIVYRDGVF 62
QY 61 AVXDKCLFYSKISEYRHYCYSVYGTTLQOYNKPLCDLIRCNXOKPLCEPEKQRLD 120
Db 63 AACQCIKFAKIRELRYSESVYATLTETITKYNLIRGMSCLKPLCPAEKRLHLT 122
QY 121 KORFNHNRGRWTCRMSCCSSSRT 145
Db 123 TKRHLKIAQNFQGCRCWTSNRDRRRIRRETQV 158

RESULT 41
US-11-021-949-361
; Sequence 361, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-361

Query Match 56.4%; Score 468.5; DB 6; Length 158;
Best Local Similarity 56.8%; Pred. No. 2,6e-42;
Matches 88; Conservative 21; Mismatches 41; Indels 5; Gaps 1;

QY 2 FQDQPERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVYRDGNPY 61
Db 4 FPNDAERPYKLPDLCTLDITDITDIDVYCKTQQLQTEYEFNFSDLCTIVYRNGEPYA 63
QY 62 VXDCKLAFYSKISEYRHYCYSVYGTTLQOYNKPLCDLIRCNXOKPLCEPEKQRLD 121
Db 64 ACQKCIKFAKIRELRYSESVYATLTETITKYNLIRGMSCLKPLCPAEKRLHVT 123
QY 122 KORFNHNRGRWTCRMSCCSSSRT 145
Db 124 KRPFHQIAGSYTGQCRHCVTSNRDRRRIRRETQV 158

RESULT 42
US-10-530-253-21
; Sequence 21, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casaretti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
```

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1 CURRENT FILING DATE: 2005-04-04
2
3 PRIOR APPLICATION NUMBER: PCT/US2003/031726
4
5 PRIOR FILING DATE: 2003-10-02
6
7 PRIOR APPLICATION NUMBER: US 60/415, 929
8
9 PRIOR FILING DATE: 2002-10-03
10
11 NUMBER OF SEQ ID NOS: 65
12
13 SOFTWARE: PatentIn version 3.1
14
15 SEQ ID NO 21
16
17 LENGTH: 151
18
19 TYPE: prt
20
21 ORGANISM: Human papillomavirus type 51
22
23 US-10-530-253-21

```

Query Match	55.4%	Score	460	DB	5	Length	151
Best Local Similarity	57.0%	Pred. No.	2.1e-41				
Matches	86	Conservative	24	Mismatches	41	Indels	0
						Gaps	0

```

QY      1 MFODQDERPRKLPOLCTELQTTIHDIILECYCKOOLRLREYVDFARDLCIYYRDNQPY 60
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1 MFEDKRERPRTHLCEALNVSMHNIQVVCYCKELCRADYVNAFTFEIKIIVYRDNQPY 60

```

QY AVXDCKLKFPSKISEYRHVCYVGTLLLEQYNKPLCDLLICINXKQPLCEEKQRHD 120
6 AVXDCKLKFPSKISEYRHVCYVGTLLLEQYNKPLCDLLICINXKQPLCEEKQRHD 120
Db 61 AVCKOCLFPSKIREYRYSVGTLLLEALTKKSLYDLSICRQGRPLGPEBKQYLD 120

```
QY      121 KKOREHINIRGRWTCRMSCCRSSRTRETOL 151  
        :|:|||||:|||||::|::|:|||||:  
DB      121 EKKRHEIAGRWTGCCANCWORTROBNETOV 151
```

RESULT 43
US-11-021-949-24

Sequence 24, Application 08/11022945
Publication No. US20050142541A1
GENERAL INFORMATION:
APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARENS, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHANORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HBV
TITLE OF INVENTION: AND METHODS OF THEIR USE

```

: FILE REFERENCE: VITA-012
: CURRENT APPLICATION NUMBER: US/11/021,949
: CURRENT FILING DATE: 2004-12-23
: PRIOR APPLICATION NUMBER: 60/532,373
: PRIOR FILING DATE: 2003-12-23
: NUMBER OF SEQ ID NOS: 361
: SOFTWARE: FastSeq for Windows Version 4.0.
: SEQ ID NO 24
: LENGTH: 151
: TYPE: PRT
: ORGANISM: human papilloma virus (HPV)
: US-11-021-949-24

```

Query Match	55.4%	Score 460;	DB 6;	Length 151;
Best Local Similarity	57.0%;	Pred. No. 2.1e-41;		
Matches 86; Conservative	41;	Mismatches 24;	Indels 0;	Gaps 0;

QY 1 MFQDQERPRKLPOLCTELQTTIHDIILBVCYCKQOLLREYVDFAPDLCIYRRDGNPY 60

Db 1 MFEDDKRERPRILHETCEALNVSMHNIQVVCYCKELCRADYVNAVEIKIYRRDNNPY 60

Qy 61 AVXDCKLFYSKISEYRHYCYSVYGTLLBEOQYNKPLCDLLRINCINXOKPLCBECKORHLD 120

Dp 61 AVCKOTLLFYSKIREYRYSRVSYGTTLEAFIRKKSIVDLSICRRCORPIGPECKOKLYD 120

RESULT 44

US-10-530-253-20

; Sequence 20, Application US/10530253
 ; Publication No. US20060014926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cassetti, Maria C.

1 APPLICANT: SMITH, LARRY
 2 APPLICANT: JEFFREY K. PULLEN
 3 APPLICANT: SUSAN P. McEHLNEY
 4 TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
 5 FILE REFERENCE: 00630/100M17-US2
 6 CURRENT APPLICATION NUMBER: US/10/530,253
 7 CURRENT FILING DATE: 2005-04-04
 8 PRIOR APPLICATION NUMBER: PCT/US2003/031726
 9 PRIOR FILING DATE: 2003-10-02
 10 PRIOR APPLICATION NUMBER: US 60/415,929

```

; PRIOR FILING DATE: 2002-10-03
;
; NUMBER OF SEQ ID NOS: 65
;
; SOFTWARE: PatentIn version 3.1

```

```
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 45
```

Query Match	55.4%	Score 459.5;	DB 5;	Length 158;
Best Local Similarity	56.1%	Pred. No. 2.5e-41;		
Best Local Containment	57.2%	Mismatches 41;	Totals	5.
Best Local Coverage	97.0%		Gaps	1

ay 2 FQDPRRPRKIPOLSTELQTTHIDIIIECVYCKOQLRR
:::| | | | | : : : | | |
nb 4 FDDPKRVYKIPLIETETNTSGIADVSLACVYSKATLEST

[illegible]

```

? Sequence 29, Application US/11021949
? Publication No. US20050142541A1
?
? GENERAL INFORMATION:
?
? APPLICANT: LU, PETER
?
? APPLICANT: GARMAN, JONATHAN DAVID
?
? APPLICANT: BELMARES, MICHAEL P.
?
? APPLICANT: DIAZ-SARMIENTO, CHANORRO SOMOZA
?
? APPLICANT: SCHWEIZER, JOHANNES
?
? TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
?
? TITLE OF INVENTION: ANTIBODIES FOR THEIR USE

```

```

? FILE REFERENCE: VITR-012
? CURRENT APPLICATION NUMBER: US/11/021,949
? CURRENT FILING DATE: 2004-12-23
? PRIOR APPLICATION NUMBER: 60/532,373
? PRIOR FILING DATE: 2003-12-23
? NUMBER OF SEQ ID NOS: 361
? SOFTWARE: FaastSeq for Windows Version 4.0
? SEQ ID NO 29
? LENGTH: 158
? TYPE: PRT
? ORGANISM: human papilloma virus (HPV)
US-11-021-949-29

```

Query Match	55.4%	Score 459.5	DB 6	Length 158
Best Local Similarity	56.1%	Pred. NO. 2.5e-41		
Matches 87	Conservative 22	Mismatches 41	Indels 5	Gaps 1


```

1  TITLE OF INVENTION: Vaccine
2  FILE REFERENCE: B45107
3  CURRENT APPLICATION NUMBER: US/10/000,903
4  CURRENT FILING DATE: 2001-10-01
5  PRIOR APPLICATION NUMBER: PCT/EP98/05285
6  PRIOR FILING DATE: 1998-08-17
7  PRIOR APPLICATION NUMBER: GB 971795.5
8  PRIOR FILING DATE: 1997-08-22
9  NUMBER OF SEQ ID NOS: 23
10 SOFTWARE: FastSeq for Windows Version 3.0
11 SEQ ID NO 21
12 LENGTH: 278
13 TYPE: prt
14 ORGANISM: Homo sapien
15 US-10-000-903-21

```

Query Match	54.9%	Score 455.5	DB 4	Length 278
Best Local Similarity	56.1%	Pred. No. 1.3e-40		
Matches 87, Conservative	21	Mismatches 42	Indels 5	Gaps 1

[illegible]

RESULT 50
US-10-899-771-21
; Sequence 21, Application US/10899771

```

1 Publication No. US20050031638A1
2
3 GENERAL INFORMATION:
4
5 APPLICANT: Dalemans, Wilfried L.J.
6
7 TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
8
9 TITLE OF INVENTION: and Fusion Proteins Adjuncted with a CpG Oligonucleotide
10 FILE REFERENCE: B45124
11
12 CURRENT APPLICATION NUMBER: US/10/899, 771
13
14 CURRENT FILING DATE: 2004-07-27
15
16 PRIOR APPLICATION NUMBER: US/09/581, 976
17
18 PRIOR FILING DATE: 2000-06-20
19
20 PRIOR APPLICATION NUMBER: PCT/EP98/08563
21
22 PRIOR FILING DATE: 1998-12-18
23
24 PRIOR APPLICATION NUMBER: GB 9727262.9
25
26 PRIOR FILING DATE: 1997-12-24
27
28 NUMBER OF SEQ ID NOS: 28
29
30 SOFTWARE: FastSeq for Windows Version 3.0
31
32 SEQ ID NO 21
33
34 LENGTH: 278
35
36 TYPE: PRT
37
38 ORGANISM: Artificial Sequence
39
40 FEATURE:
41
42 OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
43 OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
44 OTHER INFORMATION: 18)
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```

Query Match	54.9%	Score 455.5;	DB 5;	Length 278;
Best Local Similarity	56.1%	Pred. NO. 1.3e-40;		
Matches 87; Conservative	21;	Mismatches 42;	Indels 5;	Gaps 1;

QY 2 FODPOERPKALPOLCTELOTTHIDILBECVYCKOQULREBYDFAARDLCIVIRDGNPYA 61
 DB 115 FEDPRRBYKLPDCLCTELNTSLDIEITCYVCKTVELTEVEFEAFKDLFVVVRDSIPHA 174
 QY 62 VXDCKLKYYSKISEVRHVCYVYGTLLBEOQYNKPLCDLLIRCLNKKQPLCPBEKQHHDK 121

Db 175 ACHKCIDPFSRIRELHSHSDSVYGDPTLEKLTVTGLYNLLIRCLRQCPYLPNAEKLRLHANE 234

Qy 122 KQRFHNIKGMWYRCMCHSCCSSR-----TRRPTOL 151

Db 235 KRRPHNIAGYRQCHSCCNRRARQRLQRRRTPV 269

RESULT 51
US-10-000-903-23
; Sequence 23, Application US/10000903
; Publication No. US20020182221A1

```

GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Christaline
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 383
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-23

```

Query Match	54.9%;	Score 455.5;	DB 4;	Length 383;
Best Local Similarity	56.1%;	Pred. No. 1.8e-40;		
Matches	87;	Conservative 21;	Mismatches 42;	Indels 5;
				Gaps 1.

```

OY      2  FODPOEPRRLPOLCETLOTTIHDIILEBVCYCKOOLREAYVDAFRLCIVSDDGPA  61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      115 FBDPTRRPRYLPDLCTELNLTSLDIEILTCYVCKYLTBELTEVFBAFADLFPVYRDSIPA  174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      62  VXDCKLKFYSKISEYNNHCYSVYGTTLBQANNKPLCDLLIFCINXOKPPLCEBCKOBYLDK  121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      175 ACHCICIDFYSRIELHYSDSYAGTLELNTNLTGYNLLIRCLCQKPLNBAEKRLHNE  234
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      122 KORFHNRGRMTGRCMSCCRSSR-----TRRETOI  151
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      235 KRREFHNIAGHYRCOCHSCCNBARORLORRRRTQV  269
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 52
US-10-899-771-23
; Sequence 23, Application US/10899771

```

? Publication No.: US20050031638A1
? GENERAL INFORMATION:
? APPLICANT: Dalemans, Wilfried L.J.
? APPLICANT: Gerard, Catherine Marie Ghislaine
? TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
? TITLE OF INVENTION: and Fusion Proteins Adjuncted with a CpG Oligonucleotide
? FILE REFERENCE: B45124
? CURRENT APPLICATION NUMBER: US/10/899,771
? CURRENT FILING DATE: 2004-07-27
? PRIOR APPLICATION NUMBER: US/09/581,976
? PRIOR FILING DATE: 2000-06-20
? PRIOR APPLICATION NUMBER: PCT/EP98/08563
? PRIOR FILING DATE: 1998-12-18
? PRIOR APPLICATION NUMBER: GB 9727262.9
? PRIOR FILING DATE: 1997-12-24
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: fastSeq for Windows Version 3.0
? SEQ ID NO 23
? LENGTH: 383
? TYPE: PRT
?
?
?

```



```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chinaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 18)
US-10-899-771-23

Query Match      54.9%; Score 455.5; DB 5; Length 383;
Best Local Similarity 56.1%; Pred. No. 1.8e-40;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

Oy 2 FODPQERPRKLPOLCTELQTTIHDIIECYCKQOQLLRREYDPAFRLCIYVRDGNPYA 61
Db 115 FEDPTRRPYKLPDLCTELNTSLQDIETCYCKVLELTFEFAFADLPVVRDSDIPA 174
Oy 62 VDXKCLKFYKISEYRHYCYSVYGTLEQYKNPCLDLIRCNXQKPLCPBEKQRLDK 121
Db 175 ACHKCIDFYSRIRLEIRHYSVYGDLEKLTNTGLYNLIRCLRCQKPLPAEKLRLHNE 234
Oy 122 KQRFNIRGRMTGRCMSCCRSSR-----TRRETOL 151
Db 235 KRPFHNIAGHYRGQCHSCCNRAQERLQRRRETQV 269

RESULT 53
US-11-021-949-31
; Sequence 31, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 162
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-31

Query Match      54.4%; Score 451.5; DB 6; Length 162;
Best Local Similarity 55.1%; Pred. No. 1.8e-40;
Matches 86; Conservative 21; Mismatches 44; Indels 5; Gaps 1;

Oy 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQOQLLRREYDPAFRLCIYVRDGNPY 60
Db 7 LFHNPBRPRLPDLCTELTDTLTDVITIDCYCRQQRREYEFAGDLNVRDGVPL 66
Oy 61 AVXDKCLKFYKISEYRHYCYSVYGTLEQYKNPCLDLIRCNXQKPLCPBEKQRLDK 120
Db 67 AACQSCIKFYAKIRLEHYSESVAATLETTITNKLVDLSIRCMCCCKPSPAEKLAHLN 126
Oy 121 KQRFNIRGRMTGRCMSCCRSS-----RRRETOL 151
Db 127 SKRFHNIAGNFTGQCHCWTSKREDRRRTQETQV 162

RESULT 54
US-10-800-023-27
; Sequence 27, Application US/10800023
; Publication No. US20040258688A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Ralph
; APPLICANT: Nussenzweig, Michel
```

```

; APPLICANT: Hawiger, Daniel
; APPLICANT: Bonifaz, Laura
; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
; TITLE OF INVENTION: of the Immune Response Therefrom
; FILE REFERENCE: 600-1-081CONCIP1
; CURRENT APPLICATION NUMBER: US/10/800,023
; CURRENT FILING DATE: 2004-03-14
; PRIOR APPLICATION NUMBER: 09/925,284
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/586,704
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: PCT/US96/01383
; PRIOR FILING DATE: 1996-01-31
; PRIOR APPLICATION NUMBER: 08/381,528
; PRIOR FILING DATE: 1995-01-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus E6 protein
US-10-800-023-27

Query Match      54.2%; Score 449.5; DB 5; Length 158;
Best Local Similarity 55.5%; Pred. No. 3e-40;
Matches 86; Conservative 21; Mismatches 43; Indels 5; Gaps 1;

Oy 2 FODPQERPRKLPOLCTELQTTIHDIIECYCKQOQLLRREYDPAFRLCIYVRDGNPYA 61
Db 4 FEDPTRRPYKLPDLCTELNTSLQDIETCYCKVLELTFEFAFADLPVVRDSDIPA 63
Oy 62 VDXKCLKFYKISEYRHYCYSVYGTLEQYKNPCLDLIRCNXQKPLCPBEKQRLDK 121
Db 64 ACHKCIDFYSRIRLEIRHYSVYGDLEKLTNTGLYNLIRCLRCQKPLPAEKLRLHNE 123
Oy 122 KQRFNIRGRMTGRCMSCCRSSR-----TRRETOL 151
Db 124 KRPFHNIAGHYRGQCHSCCNRAQERLQRRRETQV 158
```

```

RESULT 55
US-10-530-253-19
; Sequence 19, Application US/105310253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-0S2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human papillomavirus type 39
US-10-530-253-19

Query Match      54.2%; Score 449.5; DB 5; Length 158;
Best Local Similarity 55.5%; Pred. No. 3e-40;
Matches 86; Conservative 19; Mismatches 45; Indels 5; Gaps 1;

Oy 2 FODPQERPRKLPOLCTELQTTIHDIIECYCKQOQLLRREYDPAFRLCIYVRDGNPYA 61
Db 4 FHNPAERPYKLPDLCTELTDTLTDVITIDCYCRQQRREYEFAGDLNVRDGVPLA 63
```

```

RESULT 59
US-10-530-253-23
; Sequence 23, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pallen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2

```

;; CURRENT APPLICATION NUMBER: US/10/530,253
;; PCT/US2003/031726
;; PRIOR FILING DATE: 2003-10-02
;; PRIOR APPLICATION NUMBER: US 60/415,929
;; PRIOR FILING DATE: 2002-10-03
;; NUMBER OF SEQ ID NOS: 65
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 23
;; LENGTH: 155
;; TYPE: PRT
;; ORGANISM: Human papillomavirus type 56
US-10-530-253-23

Query Match 51.4%; Score 426.5; DB 5; Length 155;
Best Local Similarity 56.4%; Pred. No. 8.8e-38;
Matches 84; Conservative 17; Mismatches 47; Indels 1; Gaps 1;

QY 2 FQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDPAFRLDLCIVYRDGNPYA 61
DB 5 FNNPQERPRSLHLSVLEIPLIDRLSCVYCKKELTAEVYNFACTELKLVYRDDPPYA 64
QY 62 VXDCKLFYKISIEYRYHCYVYGTTLQEQYNKPLCDLLIRCIYXQKPLCPPEEKQRLD 121
DB 65 VCRVCLLFYKSKVRKYRYDYSVIGATLESTIKQLCDLLIRCYCQSPLPPEEKQRLHCDR 124
QY 122 KQRFHNIRGWTGRCMCCR-SSRTRET 149
DB 125 KRPFHLIAHGWTGSLCGMROTSPRES 153

RESULT 60
US-11-021-949-22
;; Sequence 22, Application US/11021949
;; Publication No. US20050142541A1
;; GENERAL INFORMATION:
;; APPLICANT: LU PETER
;; APPLICANT: GARMAN, JONATHAN DAVID
;; APPLICANT: BELMARES, MICHAEL P.
;; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
;; APPLICANT: SCHWEIZER, JOHANNES
;; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
;; TITLE OF INVENTION: AND METHODS OF THEIR USE
;; FILE REFERENCE: VITA-012
;; CURRENT APPLICATION NUMBER: US/11/021,949
;; CURRENT FILING DATE: 2004-12-23
;; PRIOR APPLICATION NUMBER: 60/532,373
;; PRIOR FILING DATE: 2003-12-23
;; NUMBER OF SEQ ID NOS: 361
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 22
;; LENGTH: 155
;; TYPE: PRT
;; ORGANISM: human papilloma virus (HPV)
US-11-021-949-22

Query Match 51.4%; Score 426.5; DB 6; Length 155;
Best Local Similarity 56.4%; Pred. No. 8.8e-38;
Matches 84; Conservative 17; Mismatches 47; Indels 1; Gaps 1;

QY 2 FQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDPAFRLDLCIVYRDGNPYA 61
DB 5 FNNPQERPRSLHLSVLEIPLIDRLSCVYCKKELTAEVYNFACTELKLVYRDDPPYA 64
QY 62 VXDCKLFYKISIEYRYHCYVYGTTLQEQYNKPLCDLLIRCIYXQKPLCPPEEKQRLD 121
DB 65 VCRVCLLFYKSKVRKYRYDYSVIGATLESTIKQLCDLLIRCYCQSPLPPEEKQRLHCDR 124
QY 122 KQRFHNIRGWTGRCMCCR-SSRTRET 149
DB 125 KRPFHLIAHGWTGSLCGMROTSPRES 153

RESULT 61
US-10-530-253-39
;; Sequence 39, Application US/10530253
;; Publication No. US20060014926A1
;; GENERAL INFORMATION:
;; APPLICANT: Casasetti, Maria C.
;; APPLICANT: Smith, Larry
;; APPLICANT: Jeffrey K. Pullen
;; APPLICANT: Susan P. McElhinney
;; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
;; FILE REFERENCE: 00630/100M137-US2
;; CURRENT APPLICATION NUMBER: US/10/530,253
;; CURRENT FILING DATE: 2005-04-04
;; PRIOR APPLICATION NUMBER: PCT/US2003/031726
;; PRIOR FILING DATE: 2003-10-02
;; PRIOR APPLICATION NUMBER: US 60/415,929
;; PRIOR FILING DATE: 2002-10-03
;; NUMBER OF SEQ ID NOS: 65
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 39
;; LENGTH: 152
;; TYPE: PRT
;; ORGANISM: Human papillomavirus
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (1)-(152)
;; OTHER INFORMATION: where Xaa is any amino acid
US-10-530-253-39

Query Match 50.7%; Score 421; DB 5; Length 152;
Best Local Similarity 56.6%; Pred. No. 3.4e-37;
Matches 81; Conservative 5; Mismatches 57; Indels 0; Gaps 0;

QY 2 FQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLRREYDPAFRLDLCIVYRDGNPYA 61
DB 4 FQDPXERPKLXDLXCLXXHBIXXXCVCXZLREXEVYXFAFXDLIVYRDXXPX 63
QY 62 VXDCKLFYKISIEYRYHCYVYGTTLQEQYNKPLCDLLIRCIYXQKPLCPPEEKQRLD 121
DB 64 XCXXCLFYKISIEYRYHCYVYGTTLQEQYNKPLCDLLIRCIYXQKPLCPPEEKQRLD 123
QY 122 KQRFHNIRGWTGRCMCCR-SSR 144
DB 124 KRPFHNIRGWTGRCMCCR-SSR 146

RESULT 62
US-10-530-253-25
;; Sequence 25, Application US/10530253
;; Publication No. US20060014926A1
;; GENERAL INFORMATION:
;; APPLICANT: Casasetti, Maria C.
;; APPLICANT: Smith, Larry
;; APPLICANT: Jeffrey K. Pullen
;; APPLICANT: Susan P. McElhinney
;; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
;; FILE REFERENCE: 00630/100M137-US2
;; CURRENT APPLICATION NUMBER: US/10/530,253
;; CURRENT FILING DATE: 2005-04-04
;; PRIOR APPLICATION NUMBER: PCT/US2003/031726
;; PRIOR FILING DATE: 2003-10-02
;; PRIOR APPLICATION NUMBER: US 60/415,929
;; PRIOR FILING DATE: 2002-10-03
;; NUMBER OF SEQ ID NOS: 65
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 25
;; LENGTH: 160
;; TYPE: PRT
;; ORGANISM: Human papillomavirus type 59
US-10-530-253-25

Query Match 50.1%; Score 415.5; DB 5; Length 160;
Best Local Similarity 51.3%; Pred. No. 1.4e-36;


```

; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEITZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 154
; TYPE: PR1
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-21

```

[illegible]

```

RESULT 67
US-11-021-949-23
; Sequence 23, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P
; APPLICANT: DIAZ-SARMIENTO, CHANORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: ANTIBODIES FOR THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 155
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
; US-11-021-949-23

```

	44.9%; Score 372.5; DB 6, length 155;
Query Match	50.7%; Pred. No. 6e-23;
Best Local Similarity	Matches 76; Conservative 20; Mismatches 53; Indels 1; Gaps 1;
Dy	1 MFODPDRRLPLQCTETLTTHIDILIECYCQQQLLRREYVPAFADLCIVRDSNPY 60
Dz	4 IFSNTERPRSLHMLSEVLQIPLDLIRSCYCCKELTSLERACIELKLYHNMPY 63
Oy	61 AVXDCLKEYSKISEYRRHCYSVGTTLEEQYNRPCLDLIRICINXQKPCLPEEKRHLD 120
Ob	64 AVCRCVLLFEYSKVRYKYKSIVGATLESITRKQLSGLSIRCVNCOCPLPPEEKQACE 123

```

QY      121 KKQRFHNIGRWTCRCMSCCRSSRTRETO 150
          | : ||| | | | : | : | :
DB      124 HKRPFHYIAYWTGSCLOQWRHT-SQOATE 152

```

```

RESULT 68
US-10-751-845-126
Sequence 126, Application US/10/751845
Publication NO. US20050100928A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OR INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIORITY APPLICATION NUMBER: US/09/664,225
PRIORITY FILING DATE: 2000-08-18
PRIORITY APPLICATION NUMBER: US 60/165,846
PRIORITY FILING DATE: 1999-12-09
PRIORITY APPLICATION NUMBER: US 60/154,665
PRIORITY FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 126
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
US-10-751-845-126
OTHER INFORMATION: Artificial fusion sequence

```

Query Match	40.1%;	Score 333;	DB 5;	length 117;
Best Local Similarity	65.3%;	Pred. No. 8e-28;		
Matches	66;	Conservative %	4;	Mismatches 3; Indels 28; Gaps 2;

Oy	1	MFODPOBRPRKLPOLCTELQTTIHDIILECYCKQKQLLRVYVGFAPFDLCITVYRDGPY	60
Db	2	MFQDPQBRPRKLPOLCTEL-----LLRRVYVGFAPFDLCITVYRDGPY	44
Oy	61	AVNDKCLAFYSKISERHRYCYSVYGTLLLEQYNNKPLCDLLI	101
Db	45	-----KISEYRHRYCYSLVGTLLLEQYNNKPLTHEYML	74

```

RESULT 69
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence

```

US-10-751-845-157

Query Match 40.1%; Score 333; DB 5; Length 236;
Best Local Similarity 65.3%; Pred. No. 1.8e-27;
Matches 66; Conservative 4; Mismatches 3; Indels 28; Gaps 2;

Qy 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIVYRDGPNY 60
Db 2 MFODPQERPRKLPOLCTEL-----LLRREYVDFAFRDLCTIVYRDGPNY 44

Qy 61 AVXDCKLFYSKISEYRHVCYSVYGTTLLEQQYNKPLCDLLI 101
Db 45 -----KISEYRHVCYSVYGTTLLEQQYNKPLHEMYL 74

RESULT 70

US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; PRIOR FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 40.1%; Score 333; DB 5; Length 237;
Best Local Similarity 65.3%; Pred. No. 1.8e-27;
Matches 66; Conservative 4; Mismatches 3; Indels 28; Gaps 2;

Qy 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIVYRDGPNY 60
Db 3 MFODPQERPRKLPOLCTEL-----LLRREYVDFAFRDLCTIVYRDGPNY 45

Qy 61 AVXDCKLFYSKISEYRHVCYSVYGTTLLEQQYNKPLCDLLI 101
Db 46 -----KISEYRHVCYSVYGTTLLEQQYNKPLHEMYL 75

RESULT 71

US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; PRIOR FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665

; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Qy 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIVYRDGPNY 60
Db 27 MFODPQERPRKLPOLCTEL-----LLRREYVDFAFRDLCTIVYRDGPNY 69

Qy 61 AVXDCKLFYSKISEYRHVCYSVYGTTLLEQQYNKPLCDLLI 101
Db 70 -----KISEYRHVCYSVYGTTLLEQQYNKPLHEMYL 99

Query Match 40.1%; Score 333; DB 5; Length 261;
Best Local Similarity 65.3%; Pred. No. 2e-27;
Matches 66; Conservative 4; Mismatches 3; Indels 28; Gaps 2;

Qy 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIVYRDGPNY 60
Db 27 MFODPQERPRKLPOLCTEL-----LLRREYVDFAFRDLCTIVYRDGPNY 69

RESULT 72

US-10-367-095-10
; Sequence 10, Application US/10367095
; Publication No. US20030228696A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; TITLE OF INVENTION: No. US20030228696A1 Insect Cell Line
; FILE REFERENCE: 44149-1US1
; CURRENT APPLICATION NUMBER: US/10/367,095
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,123
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,113
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,154
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,135
; PRIOR FILING DATE: 2002-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-367-095-10

Query Match 38.9%; Score 323; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 5.5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIVYRDGPNY 59
Db 478 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREYVDFAFRDLCTIVYRDGPNY 536

RESULT 73
US-10-368-046-10
; Sequence 10, Application US/10368046
; Publication No. US20040063188A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; APPLICANT: Victoria Cioce
; TITLE OF INVENTION: Method for Isolation and Purification of
; TITLE OF INVENTION: Expressed Gene Products in Vitro
; FILE REFERENCE: 44149-3US1
; CURRENT APPLICATION NUMBER: US/10/368,046
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,123
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,113
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,154
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,135
; PRIOR FILING DATE: 2002-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-368-046-10
Query Match 38.9%; Score 323; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 5.5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFDDPQRRPKLQPLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCIYRDGNP 59
Db 478 MFDDPQRRPKLQPLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCIYRDGNP 536
RESULT 74
US-10-367-367-10
; Sequence 10, Application US/10367367
; Publication No. US20040121465A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; TITLE OF INVENTION: Optimization of Gene Sequences of
; TITLE OF INVENTION: Virus-Like Particles for Expression in Insect Cells
; FILE REFERENCE: 44149-2US1
; CURRENT APPLICATION NUMBER: US/10/367,367
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157

; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-367-367-10
Query Match 38.9%; Score 323; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 5.5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFDDPQRRPKLQPLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCIYRDGNP 59
Db 478 MFDDPQRRPKLQPLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCIYRDGNP 536
RESULT 75
US-10-918-337-10
; Sequence 10, Application US/10918337
; Publication No. US20050118191A1
; GENERAL INFORMATION:
; APPLICANT: NOVAVAX, INC., et al.
; TITLE OF INVENTION: Optimization of Gene Sequences of
; TITLE OF INVENTION: Chimeric Virus-Like Particles for Expression in Insect Cells
; FILE REFERENCE: 19065/2132
; CURRENT APPLICATION NUMBER: US/10/918,337
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: PCT/US03/04473
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,154
; PRIOR FILING DATE: 2002-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-918-337-10
Query Match 38.9%; Score 323; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 5.5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFDDPQRRPKLQPLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCIYRDGNP 59
Db 478 MFDDPQRRPKLQPLCTELQTTIHDIILCEVCYCKQQLLRREYVDFAFRDLCIYRDGNP 536


```
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9
```

```
Query Match      20.7%; Score 172; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 ERPRKLPQLCTELQTTIHDIILECVYCKQQL 38
Db      1 ERPRKLPQLCTELQTTIHDIILECVYCKQQL 32
```

```
RESULT 80
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: GUILLET, Jean-Gerard
; APPLICANT: POUVELLE-MORATILLE, Sandra
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT FILING DATE: 2003-11-04
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: FR 01 05980
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44
US-10-476-570-53
```

```
Query Match      19.6%; Score 163; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 RPRKLPQLCTELQTTIHDIILECVYCKQQL 37
Db      1 RPRKLPQLCTELQTTIHDIILECVYCKQQL 30
```

```
RESULT 81
US-10-858-384-4
; Sequence 4, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US/10/858,384
; PRIOR APPLICATION NUMBER: FR 9907012
```

```
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-4
```

```
Query Match      19.6%; Score 163; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 RPRKLPQLCTELQTTIHDIILECVYCKQQL 37
Db      1 RPRKLPQLCTELQTTIHDIILECVYCKQQL 30
```

```
RESULT 82
US-10-476-570-55
; Sequence 55, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT FILING DATE: 2003-11-04
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: FR 01 05980
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 55
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55
```

```
Query Match      19.2%; Score 159; DB 4; Length 29;
Best Local Similarity 96.6%; Pred. No. 1e-09;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      73 ISEYRHVCYSVYGTTLLEQYQNKPLCDLLI 101
Db      1 ISEYRHVCYSVYGTTLLEQYQNKPLCDLLI 29
```

```
RESULT 83
US-10-858-384-8
; Sequence 8, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
```

```
FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858.384
CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 8
LENGTH: 29
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
US-10-858-384-8

Query Match      19.2%; Score 159; DB 5; Length 29;
Best Local Similarity 96.6%; Pred. No. 1e-09;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 84

```
US-10-476-570-13
Sequence 13, Application US/10476570
Publication No. US20040170644A1
GENERAL INFORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLIERE, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 29
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of the artificial sequence: peptide E6 91-119
US-10-476-570-13
```

```
Query Match      18.9%; Score 157; DB 4; Length 29;
Best Local Similarity 96.6%; Pred. No. 1.7e-09;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      84 YGTTLEQQYNKPLCDLLIRCIINXKPLCP 112
Db      1 YGTTLEQQYNKPLCDLLIRCIINXKPLCP 29
```

```
RESULT 85
US-11-021-949-5
Sequence 5, Application US/11021949
Publication No. US20050142541A1
GENERAL INFORMATION:
APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
```

```
APPLICANT: SCHMEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 24
TYPE: PRT
ORGANISM: human papilloma virus (HPV)
US-11-021-949-5

Query Match      17.6%; Score 146; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 86

```
US-10-367-057-23
Sequence 23, Application US/10367057
Publication No. US20050100554A1
GENERAL INFORMATION:
APPLICANT: Cuthill, Scott;
APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Ooi, Chean Eng;
TITLE OF INVENTION: Complexes and Methods of Using Same
FILE REFERENCE: 21402-559
CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 198
SOFTWARE: Curoseqqlist version 0.1
SEQ ID NO 23
LENGTH: 140
TYPE: PRT
ORGANISM: Homo sapiens
US-10-367-057-23
```

```
Query Match      16.4%; Score 136.5; DB 5; Length 140;
Best Local Similarity 28.0%; Pred. No. 1.7e-06;
Matches 37; Conservative 21; Mismatches 73; Indels 1; Gaps 1;
```

```
QY      10 RKLPLCTELQTTIHDIILECVYCKQQLRREYDFAPRLCIYVRGPNFYAXDKCLKF 69
Db      6 RTVQQLSESLCIPYIDVLLPCNFCNPFLSNAEKLLFHPDLHLVWRNNTLVFGCCGGART 65
QY      70 YSKISEVRHYCVSYGGTTLEQQYNKPLCDLLIRCIINXKPLCEPEKORHLDKORFNIR 129
Db      66 VSLIEFVLYIQESIEVEVEIEIIDLRLQIETKCVTCIKLSVAEKLEVVNGERVHVR 125
QY      130 GRWTRCMSCCR 141
Db      126 NRLKAC-SLCR 136
```

```
RESULT 87
US-11-021-949-1
Sequence 1, Application US/11021949
Publication No. US20050142541A1
GENERAL INFORMATION:
APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
```

```

; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
; US-11-021-949-1

Query Match      16.4%; Score 136; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FQDPERPRRLPOLCTELQTTIHDI 26
Db      1 FQDPERPRRLPOLCTELQTTIHDI 25

RESULT 88
US-10-476-570-40
; Sequence 40, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-140
; US-10-476-570-40

Query Match      16.3%; Score 135; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      111 CPEKORHLDKKORFHNIRGRWT 133
Db      1 CPEKORHLDKKORFHNIRGRWT 23

RESULT 89
US-10-476-570-44
; Sequence 44, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
```

```

; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 24
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 135-158
; US-10-476-570-44

Query Match      16.3%; Score 135; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      128 IGRWTRGCMSCCRSRTTRRRTQL 151
Db      1 IGRWTRGCMSCCRSRTTRRRTQL 24

RESULT 90
US-10-751-845-65
; Sequence 65, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human Papilloma virus
; US-10-751-845-65

Query Match      15.9%; Score 132; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      37 LIRREYVDPAFRLDCLIVRDGNPY 60
Db      1 LIRREYVDPAFRLDCLIVRDGNPY 24

RESULT 91
US-10-476-570-56
; Sequence 56, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
```

```
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 22
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-139
US-10-476-570-56
```

```
Query Match 15.7%; Score 130; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 111 CPEKQRLDKKQRFHNIRGW 132
Db 1 CPEKQRLDKKQRFHNIRGW 22
```

```
RESULT 92
US-10-858-384-10
; Sequence 10, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIS, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDE PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
US-10-858-384-10
```

```
Query Match 15.7%; Score 130; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 111 CPEKQRLDKKQRFHNIRGW 132
Db 1 CPEKQRLDKKQRFHNIRGW 22
```

```
RESULT 93
US-10-751-845-152
; Sequence 152, Application US/10751845
```

```
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-152
```

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Query Match 15.7%; Score 130; DB 5; Length 42;
Best Local Similarity 58.5%; Pred. No. 2.1e-06;
Matches 24; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 8 RPRKLPOLCTELTTHIDILCEVCCKQDLREVDPAFR 48
Db 2 RPRKLPOLCTELTTHIDILCEVCCKQDLREVDPAFR 42
```

```
RESULT 94
US-10-751-845-66
; Sequence 66, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66
```

```
Query Match 15.2%; Score 126; DB 5; Length 23;
Best Local Similarity 95.7%; Pred. No. 2.9e-06;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 72 KISEYRHVCYSVGTLEQYRK 94
Db 1 KISEYRHVCYSVGTLEQYRK 23
```

```
RESULT 95
US-10-858-384-6
; Sequence 6, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
```

```

; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; US-10-858-384-6

Query Match      14.9%; Score 124; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      39 RREYDFAFRDLCTIVRDGNPY 60
DB      1 RREYDFAFRDLCTIVRDGNPY 22

RESULT 96
US-11-021-949-3
; Sequence 3, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
; APPLICANT: BELMARES, MICHAEL P.
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
; US-11-021-949-3

Query Match      14.3%; Score 119; DB 6; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e-05;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      99 LIRICINQKPLCPPEKORHLDK 121
DB      1 LIRICINQKPLCPPEKORHLDK 23

RESULT 97
US-10-476-570-27
; Sequence 27, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
```

```

; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 44-67
; US-10-476-570-27

Query Match      13.9%; Score 115.5; DB 4; Length 23;
Best Local Similarity 95.8%; Pred. No. 3.9e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      37 LIRREYDFAFRDLCTIVRDGNPY 60
DB      1 LIRREYDFAFRDLCTIVRDGNPY 23

RESULT 98
US-10-938-249-513
; Sequence 513, Application US/10938249
; Publication No. US20050037969A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 020054-001130US
; CURRENT APPLICATION NUMBER: US/10/938,249
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US/09/724,553
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 543
; SOFTWARE: FaestSeq for Windows Version 3.0
; SEQ ID NO 513
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: HPV16 E6 C-terminal
US-10-938-249-513

Query Match      13.9%; Score 115; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      132 WTGRCMSCCRSSRRRTRETOL 151
Db      1 WTGRCMSCCRSSRRRTRETOL 20

RESULT 99
US-10-476-570-41
; Sequence 41, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MATILERE, Bernard
; APPLICANT: BOURCAULT-VILLADA, Isabelle
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 41
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 121-140
US-10-476-570-41

Query Match      13.7%; Score 114; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      114 EKQRHLDKORFHNIRGRWT 133
Db      1 EKQRHLDKORFHNIRGRWT 20

RESULT 100
US-10-612-818-4
; Sequence 4, Application US/10612818
; Publication No. US20040110925A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Pap
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/10/612,818
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 22
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
US-10-612-818-4

Query Match      13.7%; Score 114; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.4e-05;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      55 RDGNPYAVXDCKLKFSKISEY 76
Db      1 RDGNPYAVXDCKLKFSKISEY 22
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Search completed: May 27, 2006, 05:37:51
Job time : 161.064 secs

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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:33:42 ; Search time 10.3092 Seconds

(Without alignments)
163.129 Million cell updates/sec

Title: US-10-530-253-13ED

Perfect score: 830
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 1113735 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US09_NEW_PUB pep:*
- 2: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US06_NEW_PUB pep:*
- 3: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US07_NEW_PUB pep:*
- 4: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US08_NEW_PUB pep:*
- 5: /EMC_Celerra_SIDS3/prodata/1/pubppaa/PC7_NEW_PUB pep:*
- 6: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US10_NEW_PUB pep:*
- 7: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US11_NEW_PUB pep:*
- 8: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74.5	9.0	591	US-10-933-854-4	Sequence 4, Appl1
2	74.5	9.0	591	US-10-933-854-6	Sequence 6, Appl1
3	74.5	9.0	609	US-10-933-854-2	Sequence 2, Appl1
4	72.5	8.7	800	US-10-953-349-33871	Sequence 33871, A
5	72.5	8.7	809	US-10-953-349-33870	Sequence 33870, A
6	72.5	8.7	867	US-10-953-349-33869	Sequence 33869, A
7	71	8.6	531	US-11-293-697-2762	Sequence 2762, Ap
8	65	7.8	359	US-10-953-349-17182	Sequence 17182, A
9	63.5	7.7	419	US-10-953-349-6306	Sequence 6306, Ap
10	63.5	7.7	515	US-10-953-349-6305	Sequence 6305, Ap
11	63.5	7.6	540	US-10-953-349-6304	Sequence 6304, Ap
12	63	7.6	247	US-10-953-349-32521	Sequence 32521, A
13	63	7.6	276	US-10-953-349-32520	Sequence 32520, A
14	63	7.6	307	US-10-953-349-32519	Sequence 32519, A
15	62.5	7.5	278	US-11-293-697-4876	Sequence 4876, Ap
16	62.5	7.5	472	US-11-106-014-8	Sequence 8, Appl1
17	62	7.5	417	US-10-196-749-474	Sequence 474, App
18	62	7.5	1056	US-10-505-928-825	Sequence 225, App
19	61.5	7.4	176	US-10-953-349-18091	Sequence 18091, A
20	61.5	7.4	208	US-10-953-349-18090	Sequence 18090, A
21	61.5	7.4	220	US-10-953-349-18089	Sequence 18089, A
22	61.5	7.4	705	US-11-293-697-4346	Sequence 4346, Ap
23	61	7.3	259	US-10-953-349-19918	Sequence 19918, A
24	61	7.3	355	US-10-953-349-19917	Sequence 19917, A
25	60.5	7.3	267	US-10-953-349-28497	Sequence 28497, A

26	60.5	7.3	314	US-10-538-066-365	Sequence 365, App
27	60.5	7.3	706	US-11-293-697-3919	Sequence 3919, Ap
28	60.5	7.3	971	US-10-505-928-397	Sequence 397, App
29	60.5	7.3	1085	US-10-505-928-175	Sequence 175, App
30	60	7.2	867	US-11-293-697-33034	Sequence 3034, Ap
31	59	7.1	233	US-10-953-349-13389	Sequence 13389, A
32	59	7.1	258	US-10-953-349-1032	Sequence 1032, Ap
33	59	7.1	369	US-10-953-349-1031	Sequence 1031, Ap
34	59	7.1	376	US-10-953-349-1030	Sequence 1030, Ap
35	59	7.1	385	US-10-953-349-13388	Sequence 13388, A
36	59	7.1	400	US-10-953-349-13387	Sequence 13387, A
37	59	7.1	428	US-10-953-349-25008	Sequence 25008, A
38	59	7.1	433	US-10-953-349-25007	Sequence 25007, A
39	59	7.1	436	US-10-953-349-25006	Sequence 25006, A
40	58.5	7.0	204	US-10-953-349-37463	Sequence 37463, A
41	58.5	7.0	251	US-10-953-349-38140	Sequence 38140, A
42	58.5	7.0	280	US-10-953-349-38139	Sequence 38139, A
43	58.5	7.0	421	US-10-953-349-22153	Sequence 22153, A
44	58.5	7.0	471	US-10-953-349-22152	Sequence 22152, A
45	58.5	7.0	482	US-10-953-349-22151	Sequence 22151, A
46	58.5	7.0	708	US-11-170-482-16	Sequence 16, Appl
47	58	7.0	152	US-10-953-349-24130	Sequence 24130, A
48	58	7.0	177	US-10-953-349-24129	Sequence 24129, A
49	57.5	6.9	284	US-10-953-349-22949	Sequence 22949, A
50	57.5	6.9	359	US-10-953-349-22948	Sequence 22948, A
51	57.5	6.9	380	US-10-953-349-22947	Sequence 22947, A
52	57.5	6.9	393	US-10-953-349-22947	Sequence 22947, A
53	57.5	6.9	423	US-10-953-349-22311	Sequence 22311, A
54	57.5	6.9	429	US-10-953-349-21322	Sequence 21322, A
55	57.5	6.9	487	US-10-953-349-21321	Sequence 21321, A
56	57.5	6.9	495	US-10-953-349-22310	Sequence 22310, A
57	57.5	6.9	485	US-10-953-349-22310	Sequence 22310, A
58	57	6.9	320	US-10-953-349-12540	Sequence 12540, A
59	56.5	6.8	166	US-11-318-156-6	Sequence 6, Appl1
60	56.5	6.8	185	US-11-293-697-3341	Sequence 3341, Ap
61	56.5	6.8	293	US-11-318-156-2	Sequence 2, Appl1
62	56.5	6.8	516	US-10-953-349-3991	Sequence 3991, Ap
63	56.5	6.8	528	US-10-953-349-3990	Sequence 3990, Ap
64	56.5	6.8	547	US-10-953-349-3989	Sequence 3989, Ap
65	56.5	6.8	840	US-11-293-697-3121	Sequence 3121, Ap
66	56.5	6.8	968	US-11-293-697-3838	Sequence 3838, Ap
67	56	6.7	233	US-10-953-349-19251	Sequence 19251, A
68	56	6.7	279	US-11-259-950-95	Sequence 95, Appl
69	56	6.7	291	US-10-953-349-19822	Sequence 19822, A
70	56	6.7	303	US-10-953-349-19821	Sequence 19821, A
71	56	6.7	309	US-10-953-349-19820	Sequence 19820, A
72	56	6.7	355	US-10-953-349-6767	Sequence 6767, Ap
73	56	6.7	385	US-10-953-349-19249	Sequence 19249, A
74	56	6.7	410	US-10-953-349-19248	Sequence 19248, A
75	55.5	6.7	179	US-10-953-349-8916	Sequence 8916, Ap
76	55.5	6.7	274	US-10-953-349-34190	Sequence 34190, A
77	55.5	6.7	278	US-10-953-349-34189	Sequence 34189, A
78	55.5	6.7	280	US-10-953-349-34188	Sequence 34188, A
79	55.5	6.7	403	US-10-953-349-938	Sequence 938, App
80	55.5	6.7	436	US-10-953-349-937	Sequence 937, App
81	55.5	6.7	456	US-10-953-349-9969	Sequence 9969, App
82	55.5	6.7	508	US-10-953-349-936	Sequence 936, App
83	55.5	6.7	508	US-10-953-349-9968	Sequence 9968, App
84	55.5	6.7	538	US-10-953-349-9967	Sequence 9967, App
85	55.5	6.7	744	US-11-293-697-4338	Sequence 4398, Ap
86	55.5	6.7	969	US-10-505-928-94	Sequence 9685, Ap
87	55	6.6	466	US-10-953-349-9685	Sequence 9685, Ap
88	55	6.6	433	US-10-953-349-9684	Sequence 9684, Ap
89	55	6.6	541	US-11-293-697-3101	Sequence 3101, Ap
90	55	6.6	541	US-11-293-697-3790	Sequence 3790, Ap
91	55	6.6	560	US-10-953-349-9683	Sequence 9683, Ap
92	54.5	6.6	167	US-10-953-349-21080	Sequence 21080, A
93	54.5	6.6	201	US-10-953-349-21079	Sequence 21079, A
94	54.5	6.6	308	US-10-953-349-21078	Sequence 21078, A
95	54.5	6.6	337	US-10-953-349-33223	Sequence 33223, A
96	54.5	6.6	358	US-10-953-349-33222	Sequence 33222, A
97	54.5	6.6	386	US-10-953-349-33222	Sequence 33222, A
98	54.5	6.6	393	US-10-953-349-36844	Sequence 36844, A

RESULT 8
US-10-953-349-17182
; Sequence 17182, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17182
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-17182

Query Match 7.8%; Score 65; DB 6; Length 369;
Best Local Similarity 22.2%; Pred. No. 9.5;
Matches 39; Conservative 24; Mismatches 59; Indels 54; Gaps 10;
QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREV-----YDFAFRD 41
DB 62 LKSPLSRP-----LFTAESGIPETIVIELLYSPDLIMKVDGQNRSLFHIAIMHRQEKI 116
QY 42 ---YDFDLCIVYRDGNPVAVDKCLKFKYSKI--SEYRHYCYSVYGTTLBOQYN-- 93
DB 117 FNLIYDIDGAKHDLITTSYRDNNNNHNI-----LHLAKGLAPSEQLHY---VSGAALQMORELL 169
QY 94 -----KELCDLLIRFCINXQKPLCE-----EKQRHLDDKQRHNRGRWTCGMSCC 140
DB 170 WPKREVERKIQPLFKFKIDSGRTPQMLFTEBHEKELAGE-----KWLKNTASSC 219

RESULT 9
US-10-953-349-6306
; Sequence 6306, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6306
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6306

Query Match 7.7%; Score 63.5; DB 6; Length 419;
Best Local Similarity 21.0%; Pred. No. 16;
Matches 37; Conservative 19; Mismatches 69; Indels 51; Gaps 6;
QY 7 ERPRKLPOLCTELQTTIHDIIECVYCKQQLRREV-----YDFAFRD 49
DB 194 ESVYKIPNVVGSITVTHIPIAPKRVHVAAYFNKRHTERNOKTSYSITVGQVNVADGIFTD 253
QY 50 LCTIYRDGNPVAVDKCLKFKYSKISEYRHYCYSVYGTTLBOQYNKPLCDLLIRFCINXQKP 109
DB 254 VCI-----GNPGLSLDDQILEKSSLSRQRAARGMLRDSWIVGNSGFPPLTDYL----- 300
QY 110 LCEPEKQ-----RHLDDKQ-----RFHNIRGRWTCGMSCCRSRTRRETQ 150
DB 301 LVPTTRQNLWTQHAFFNESIGETIGIATAFAFERLKGW-----ACLOKRTVEYKLO 350

RESULT 10
US-10-953-349-6305
; Sequence 6305, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6305
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6305

Query Match 7.7%; Score 63.5; DB 6; Length 515;
Best Local Similarity 21.0%; Pred. No. 19;
Matches 37; Conservative 19; Mismatches 69; Indels 51; Gaps 6;
QY 7 ERPRKLPOLCTELQTTIHDIIECVYCKQQLRREV-----YDFAFRD 49
DB 290 ESVYKIPNVVGSITVTHIPIAPKRVHVAAYFNKRHTERNOKTSYSITVGQVNVADGIFTD 349
QY 50 LCTIYRDGNPVAVDKCLKFKYSKISEYRHYCYSVYGTTLBOQYNKPLCDLLIRFCINXQKP 109
DB 350 VCI-----GNPGLSLDDQILEKSSLSRQRAARGMLRDSWIVGNSGFPPLTDYL----- 396
QY 110 LCEPEKQ-----RHLDDKQ-----RFHNIRGRWTCGMSCCRSRTRRETQ 150
DB 397 LVPTTRQNLWTQHAFFNESIGETIGIATAFAFERLKGW-----ACLOKRTVEYKLO 446

RESULT 11
US-10-953-349-6304
; Sequence 6304, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6304
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6304

Query Match 7.7%; Score 63.5; DB 6; Length 540;
Best Local Similarity 21.0%; Pred. No. 20;
Matches 37; Conservative 19; Mismatches 69; Indels 51; Gaps 6;
QY 7 ERPRKLPOLCTELQTTIHDIIECVYCKQQLRREV-----YDFAFRD 49
DB 315 ESVYKIPNVVGSITVTHIPIAPKRVHVAAYFNKRHTERNOKTSYSITVGQVNVADGIFTD 374
QY 50 LCTIYRDGNPVAVDKCLKFKYSKISEYRHYCYSVYGTTLBOQYNKPLCDLLIRFCINXQKP 109
DB 375 VCI-----GNPGLSLDDQILEKSSLSRQRAARGMLRDSWIVGNSGFPPLTDYL----- 421
QY 110 LCEPEKQ-----RHLDDKQ-----RFHNIRGRWTCGMSCCRSRTRRETQ 150
DB 422 LVPTTRQNLWTQHAFFNESIGETIGIATAFAFERLKGW-----ACLOKRTVEYKLO 471

RESULT 12

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RESULT 16
US-11-106-014-8
; Sequence 8, Application US/11106014
; Publication No. US20060088846A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chaur, Dah Sharim
; APPLICANT: Lactes, Bether
; APPLICANT: Srivastava, Promod
; APPLICANT: Chandrasekar, Rajiv
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-106-999
; CURRENT APPLICATION NUMBER: US/11/106_014

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; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 10/633,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1997-03-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-014-8
```

```

Query Match      7.5%; Score 62.5; DB 7; Length 472;
Best Local Similarity 26.3%; Pred. No. 22;
Matches 26; Conservative 14; Mismatches 40; Indels 19; Gaps 5;
```

```

QY      36 QLR---EYVDFAPRDLCTIYRDNPNYA--VXDCKLKFYSSEYRHYC-----YSV 83
Db      122 QILKRPISVSDGAFPDYMAVYLMCCPTTRASSSRMYCAVTSPLHSILIEPPPAL 181
QY      84 YGTTLEQYNNKPLCDLLIRCNXKQPLCPPE--KORHLD 120
Db      182 FGPRLEQ-----LMTSLVLSLSSEBELCPTAGLPQRFQD 215
```

```

RESULT 17
US-10-196-749-474
; Sequence 474, Application US/10196749
; Publication No. US2006094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyere, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACTIS ENCODING THE SAME
; FILE REFERENCE: P343ORIC340
; CURRENT APPLICATION NUMBER: US/10/196, 749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
```

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; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-474
```

```

Query Match      7.5%; Score 62; DB 6; Length 417;
Best Local Similarity 26.2%; Pred. No. 22;
Matches 17; Conservative 18; Mismatches 22; Indels 8; Gaps 4;
```

```

QY      15 LCTELQTTIHDIIECY-YKQQLRREYVDFAPRDLCTIYRDNPNYA--VDKCKLKFYSKI 73
Db      174 ICSALATVLLALILLCVYCKRFMEKRP--SWLSRSQDIQY--NGSELSCFDR-----POL 226
QY      74 SEYRH 78
Db      227 HEYAH 231
```

```

RESULT 18
US-10-505-928-225
; Sequence 225, Application US/10505928
; Publication No. US20060086532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig, Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505, 928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363, 019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 225
; LENGTH: 1056
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-225
```

```

Query Match      7.5%; Score 62; DB 6; Length 1056;
Best Local Similarity 26.3%; Pred. No. 60;
Matches 15; Conservative 12; Mismatches 14; Indels 16; Gaps 2;
```

```

QY      87 TLEQYNNKPLCDLL-----IRCNXKQPLCP---BEKORHLDKORFHN 127
Db      713 TIKQTHSQELCKLMNLTWTERFCALIEKCEINIQKPLSSVQENIOOKSKDQVNMKTFHS 769
```

```

RESULT 19
US-10-953-349-18091
; Sequence 18091, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nicholas et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18091
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18091
```

```

Query Match      7.4%; Score 61.5; DB 6; Length 176;
Best Local Similarity 21.6%; Pred. No. 9.9;
```

	Matches	27;	Conservative	11;	Mismatches	44;	Indels	43;	Gaps	5;
QY	33	CKQQLRREV-----	-YDPAPRLDLCIVRDGNPVAVDKCLKFYSKISRYHRCYSV	:	:	:	:	:	:	83
Dd	36	CKRKQRKRRTVIVNELGSGYEDTFEDV-----	KAQMNFYFYKA	:	:	:	:	:	:	74
QY	84	YGTLLEQQY--NKPLCDLLIRCIINXQKPELCPBEKORHLDDKQ----	RFINIGRR	:	:	:	:	:	:	131
Dd	75	VRIALHQIYYEMNPPKYTWFFYNFVASNKPADGGFRFSLSGKEQDELAERVMTTRLI-LYGK		:	:	:	:	:	:	133
QY	132	WTGRC	136	:	:	:	:	:	:	
Dd	134	WVKKC	138	:	:	:	:	:	:	

Db 381 PHSPPKDNNAVYKCVKCNKSTPEALEHNLQTATHN--PSPCHQKVFPCERYLRRLP 438
Qy 43 -YFAPRDLCTIVYRDGNPVAVDKLFK-----YSKISEYRH-----YCYSYVG-- 85
Db 439 THSGGGFKQCV-----CKKFFREHRLKJLHAHSHGEKPKYKCSVCESAFNRK 486
Qy 86 -----TTLEQYNNKPLCDLLIRCIYNQK-----PLCPE-- 113
Db 487 DKLKRNHLIHEPRKVKCPSTHTGCSKEFRNP--DLKXAHILSHSGMKLHKALCKSKSF 544
Qy 114 EKQPHLDKQRFNINRGWTRGCMSCCR 141
Db 545 SRAHLAEHQRAHT--GNVYKFCAGCAK 570

RESULT 28
US-10-505-928-397
; Sequence 397, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 397
; LENGTH: 971
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-397

Query Match 7.3%; Score 60.5; DB 6; Length 971;
Best Local Similarity 18.2%; Pred. No. 79;
Matches 30; Conservative 22; Mismatches 56; Indels 57; Gaps 8;

Qy 16 CTEPLQTTIHDIIEC-VYCKQ-----QLLRREYVDFAFRDLCIVYRDGNPVAVDK 66
Db 104 CCELA-----IALECRQACKQASSKNDISKVCRKEYNALFS--CISRNE-----MGSVC 151
Qy 67 LKPYSKISEYRYHYGYVGTLE-----QQYNKPLCDLLIRCI-----X 106
Db 152 CSTAGHHTNCREYCOALFRIDSSGFSQIKAVENYCASISPQLHCVNNYTOGYPMENPT 211
Qy 107 OKPLCPEKORHLDKQRFNINRGWTRGCMSCCRSRTRETOL 151
Db 212 DSLYCCBRADH-----ACONACKRIIMSKTIEM 240

RESULT 29
US-10-505-928-175
; Sequence 175, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 175
; LENGTH: 1085
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-175

Query Match 7.3%; Score 60.5; DB 6; Length 1085;

Best Local Similarity 24.4%; Pred. No. 89;
Matches 20; Conservative 14; Mismatches 27; Indels 21; Gaps 3;
Qy 25 DILIECYCKQQLRREVYDFAFRDLCIVYRDGNPVAVDKLFK-----ISRYRH 78
Db 230 DVEQVWYCKEKIRGE--SEFSFEEL-----RAQKYNGRRHGEQWVNEBDR 274
Qy 79 YCYSVGTLEQQYNNKPLCDLL 100
Db 275 YMKRKNAAFEEQLKQKXDEL 296

RESULT 30
US-11-293-697-3034
; Sequence 3034, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3034
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3034

Query Match 7.2%; Score 60; DB 7; Length 867;
Best Local Similarity 20.9%; Pred. No. 79;
Matches 29; Conservative 18; Mismatches 34; Indels 58; Gaps 7;

Qy 12 LPOLCTELQTTIHDIIECYCKQQLRREVYDFAFRDLCIVYRDGNPVAVDKLFKYS 71
Db 474 LPOLCTIMEQYKGD-----KQVC-----TNIAKIFS 499
Qy 72 KISEYR-----HYCYSVGTLEQQYNNKPLCDLLIRCI-----NXQKPLCP 112
Db 500 KLTSYRDCCTALASYSYCVLFL--LNLINKYQKQ--DLVAVVVFILGULTAKNNQARQOFS 557
Qy 113 EER---ORHLDKQRFNIN 128
Db 558 KEGKSIQTLTLSPQTFHQ 576

RESULT 31
US-10-953-349-13389
; Sequence 13389, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nicholas et al.
; TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13389
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13389

Query Match 7.1%; Score 59; DB 6; Length 233;
Best Local Similarity 23.9%; Pred. No. 24;
Matches 37; Conservative 21; Mismatches 53; Indels 44; Gaps 9;
Qy 11 KLPQLCTELQTTIHDIIECYCKQQLRREVYDFA-----FRDL-----CTIV 54

```

Db      26 KLVQIGSNLELKIH--TLQFVEVLQGTADALKYARYLAFPASLNGEFPKMGCLLY 83
Oy      55 R---DGNFYAVXDKCLKFKFSKISEY-RHYCVSVYGTTLLEQOYNKPL-----CDLL 100
Db      84 AGRLESSYSELSTSIHMETTEELARQPC-----TLIGQSTYENPLSVAVAGVGLPL 138
Oy      101 IRCIN---XQKPLCEKQKOR---HLDKKQREHNT 128
Db      139 LKLAVMAAKKQEWQEMKQLPVVELGKEFCQHSI 173

RESULT 32
US-10-953-349-1032
; Sequence 1032, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patencin version 3.3
; SEQ ID NO 1032
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1032

Query Match      7.1%; Score 59; DB 6; Length 258;
Best Local Similarity 29.7%; Pred. No. 27;
Matches 27; Conservative 14; Mismatches 32; Indels 18; Gaps 7;

Oy      1 MFQDQERPRKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDNXY 60
Db      52 MAPDPEP-QQDLPEIC-----RDVWME--YSKQVMILGE--FLF-ELLSEALGLNPN 97
Oy      61 AVXD-KCLKFKYSKISEYRHYCVS---VYGT 87
Db      98 HLKDMELCKGLRMLCHYFPFPCPEPDLTFTS 128

RESULT 33
US-10-953-349-1031
; Sequence 1031, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patencin version 3.3
; SEQ ID NO 1031
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1031

Query Match      7.1%; Score 59; DB 6; Length 369;
Best Local Similarity 29.7%; Pred. No. 40;
Matches 27; Conservative 14; Mismatches 32; Indels 18; Gaps 7;

Oy      1 MFQDQERPRKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDNXY 60
Db      163 MAPDPEP-QQDLPEIC-----RDVWME--YSKQVMILGE--FLF-ELLSEALGLNPN 208
Oy      61 AVXD-KCLKFKYSKISEYRHYCVS---VYGT 87

```

[illegible]


```

Query Match Similarity   7.1%; Score 59; DB 6; Length 428;
Best Local Similarity    28.9%; Pred. No. 47;
Matches      13; Conservative     9; Mismatches    13; Indels    10; Gaps     2;

Oy          16 CTELOTTTHDILLEC-----VYCKQQLRREYDPAPFDLC 51
             |||:::||:|||||||
Db          171 CT-LKDTAKPVLIPTCYDLVTGRAAFVFSSRADALEVDGDFPKMRDVC 214

RESULT 38
US-10-953-349-25007
: Sequence 25007, Application US/10953349
: Publication No., US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nikolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1579F0S2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30

```

Query Match	7.0%	Score 58.5	DB 6	Length 204
Best Local Similarity	34.9%	Pred. No. 24		
Matches	15	Conservative	4	Mismatches 7
				Indels 17
				Gaps 2
QY	121	KKORFHNIRGRWTG	-----CMSCCKSSRRRR	147
		:::::		
Db	94	QORGDH-FARGTSRGRGRCSPASPRCSCLSCRCRCRRR	135	

RESULT 41
US-10-953-349-38140
; Sequence 38140, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38140
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38140

Query Match 7.0%; Score 58.5; DB 6; Length 251;
Best Local Similarity 34.9%; Pred. No. 30;
Matches 15; Conservative 4; Mismatches 7; Indels 17; Gaps 2;

Qy 121 KKQRFHNIRGRWTR-----CMSCCRSSRTTR 147
Db 141 QQRQGH-H-RAAGTSRGRWRCSPASPRCSCSLCCRCRCRRR 182

RESULT 42
US-10-953-349-38139
; Sequence 38139, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38139
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38139

Query Match 7.0%; Score 58.5; DB 6; Length 280;
Best Local Similarity 34.9%; Pred. No. 33;
Matches 15; Conservative 4; Mismatches 7; Indels 17; Gaps 2;

Qy 121 KKQRFHNIRGRWTR-----CMSCCRSSRTTR 147
Db 170 QQRQGH-H-RAAGTSRGRWRCSPASPRCSCSLCCRCRCRRR 211

RESULT 43
US-10-953-349-22153
; Sequence 22153, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22153
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22153

US-10-953-349-22153

Query Match 7.0%; Score 58.5; DB 6; Length 421;
Best Local Similarity 22.9%; Pred. No. 52;
Matches 22; Conservative 11; Mismatches 32; Indels 31; Gaps 5;

Qy 45 PAFRDLCTIVYRDGNPVAVDKCLKFYKISEYHHY-C-YSVYGTTLLEQQYKKPLCDLLIRC 103
Db 137 FSCENLC-----GNPVCGN-----HYCTKTHALENQLQSGQPCEDCYLSC 178
Qy 104 INXKPLCPREKQRHLDKKQRFHNIRGRWTRGCMSC 139
Db 179 QKEREPACPHHCPR-----RCH-----PGDCPPC 202

RESULT 44
US-10-953-349-22152
; Sequence 22152, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22152
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22152

Query Match 7.0%; Score 58.5; DB 6; Length 471;
Best Local Similarity 22.9%; Pred. No. 59;
Matches 22; Conservative 11; Mismatches 32; Indels 31; Gaps 5;

Qy 45 PAFRDLCTIVYRDGNPVAVDKCLKFYKISEYHHY-C-YSVYGTTLLEQQYKKPLCDLLIRC 103
Db 187 FSCENLC-----GNPVCGN-----HYCTKTHALENQLQSGQPCEDCYLSC 228

Qy 104 INXKPLCPREKQRHLDKKQRFHNIRGRWTRGCMSC 139
Db 229 QKEREPACPHHCPR-----RCH-----PGDCPPC 252

RESULT 45
US-10-953-349-22151
; Sequence 22151, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22151
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22151

Query Match 7.0%; Score 58.5; DB 6; Length 492;
Best Local Similarity 22.9%; Pred. No. 61;
Matches 22; Conservative 11; Mismatches 32; Indels 31; Gaps 5;
Qy 45 PAFRDLCTIVYRDGNPVAVDKCLKFYKISEYHHY-C-YSVYGTTLLEQQYKKPLCDLLIRC 103
Db 208 FSCENLC-----GNPVCGN-----HYCTKTHALENQLQSGQPCEDCYLSC 249

QY 104 INXKPLCEPKORHLDKQRFNINRGRTGRCMSC 139
DB 250 QKEREPACPHHCPR-----RCH-----PDCPCPC 273

RESULT 46

US-11-170-482-16
; Sequence 16, Application US/11170482
; Publication No. US2006094037A1
; GENERAL INFORMATION:
; APPLICANT: St. George-Hyslop, Peter H.
; APPLICANT: Fraser, Paul E.
; APPLICANT: University of Toronto
; TITLE OF INVENTION: PROTEINS RELATED TO SCHIZOPHRENIA AND USES THEREOF
; FILE REFERENCE: 1034/1570
; CURRENT APPLICATION NUMBER: US/11/170,482
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: US/09/945,258
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,889
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 708
; TYPE: PRT
; ORGANISM: mouse
US-11-170-482-16

Query Match 7.0%; Score 58.5; DB 7; Length 708;

Best Local Similarity 21.2%; Pred. No. 91; Indels 33; Gaps 8;
Matches 35; Conservative 26; Mismatches 71;

QY 2 FQDPOE-----RPRKLPLQCTELQTTIHDI-----ILECVYCKQQLRREYVDFAFRD 49
DB 469 WQSPBEDLNFVTDTAKLANVATVLAALYELAGTFFSSSIQADPQTVTRLLYGFLVRA 528

QY 50 -----LCIYVRDGNPVAVKCKLKFYSKISEYRHYCSVGTILEQYNNKPLCDLIRCI 104
DB 529 NNSWFOISLKHGDIKRSY-LIDRPLQHYTAVS-----SPNTTYVVOY--ALANLTGKAT 578

QY 105 NXQKPLCEPKORHLDKQRFNINRGRTGRCMSC 143
DB 579 NLTRQCQDPSKVPNESKDIYYSWQSPMNSNTERLPOCVAST 623

RESULT 47

US-10-953-349-24130
; Sequence 24130, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24130
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24130

Query Match 7.0%; Score 58; DB 6; Length 152;

Best Local Similarity 26.8%; Pred. No. 20; Indels 8; Gaps 3;
Matches 19; Conservative 15; Mismatches 29;

QY 88 LEOQYNNKPLCDLIRICINXKPLCE---EKORHLDKQRFNINRGRTGRC---MSCC 140
DB 62 LNEEMNKGILLTMSEELNLOKIVANETMEHTKQIMARKTFSHYQ-KEAEKCNIGVETC 120

QY 141 RSRRTRETOL 151
DB 121 EEARERAEAL 131

RESULT 48

US-10-953-349-24129
; Sequence 24129, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24129
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24129

Query Match 7.0%; Score 58; DB 6; Length 177;

Best Local Similarity 26.8%; Pred. No. 23; Indels 8; Gaps 3;
Matches 19; Conservative 15; Mismatches 29;

QY 88 LEOQYNNKPLCDLIRICINXKPLCE---EKORHLDKQRFNINRGRTGRC---MSCC 140
DB 87 LNEEMNKGILLTMSEELNLOKIVANETMEHTKQIMARKTFSHYQ-KEAEKCNIGVETC 145

QY 141 RSRRTRETOL 151
DB 146 EEARERAEAL 156

RESULT 49

US-10-953-349-22948
; Sequence 22948, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22948
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22948

Query Match 6.9%; Score 57.5; DB 6; Length 264;

Best Local Similarity 26.7%; Pred. No. 40; Indels 29; Gaps 8;
Matches 32; Conservative 20; Mismatches 39;

QY 6 QERPKLPQCTELQTTIHDIILECVYCKQQL---LRREYVDFAFRDLCIYVRDGNPVAV 62
DB 39 QYNNKPLCDLIRICINXKPLCE---EKORHLDKQRFNINRGRTGRC---MSCC 83

QY 63 XDKCLKFYSKISEYRHYCSVGTILEQYNNKPLCDLIRICINXKPLCE---EKORHLDK 120
DB 84 --KITTLKRNIV-EMDEYDVNHWRSFEER-----EATFIDISCRALGLPLEEPGQYMD 134

RESULT 50

US-10-953-349-22948
; Sequence 22948, Application US/10953349

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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; CURRENT APPLICATION NUMBER: US/10/953.349
; FILE REFERENCE: 2750-1579PUS2
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; SOFTWARE: Patentin version 3.3
; NUMBER OF SEQ ID NOS: 40252
; CURRENT FILING DATE: 2004-09-30
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 22948
; LENGTH: 359
; TYPE: PR1
; ORGANISM: Glycine max
US-10-953-349-22948

Query Match      6.9%; Score 57.5; DB 6; Length 359;
Best Local Similarity 26.7%; Pred. No. 56;
Matches 32; Conservative 20; Mismatches 39; Indels 29; Gaps 8;

Qy      6 QERRKLPOLCTELQTHIHIIIECVYCKQOL---LRREYVDFAFRDLCTIVRDGNPYAV 62
Db      134 QYKNTTLPQ--TTLKTSVKELDLPAALAEHLVAKRKEAD-----RGEKY-- 178

Qy      63 XDKCLKFEYSKISEYRHYCVSVGTTLLEQYNNKPLCDLLIRICINXQKPL-CP-EKKORHLD 120
Db      179 --KITKLRRNV-EMDEVYMHMRRSPFER-----EALTRDISCKRKLGLPLEBGRYMD 229

RESULT 51
US-10-953-349-22312
; Sequence 22312, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 22312
; LENGTH: 390
; TYPE: PR1
; ORGANISM: Glycine max
US-10-953-349-22312

Query Match      6.9%; Score 57.5; DB 6; Length 390;
Best Local Similarity 23.1%; Pred. No. 61;
Matches 30; Conservative 19; Mismatches 60; Indels 21; Gaps 6;

Qy      17 TELQTHIHIIIECVYCKQOLLRREYVDFAFRDL--CTVYRDGNPYAVXDKCLKFSKIS 74
Db      13 TKMQAEIOKIDDE---VNMKTLKNEBEKLAIDLEMALIKRRK---AEKCRRLAEAS 65

Qy      75 EYRHYCVSVGTTLLEQ-----QYNNKPLCDLLIRICINXQKPL-PEEKORHLDKKOR- 124
Db      66 SYRTMLEKMRDSDHOSVITYKEOYRLNOASNALMARLEAOREICDAAEKDLHKYKORD 125

Qy      125 --FHNIRGRW 132
Db      126 DIEKQIRPEW 135

RESULT 52
US-10-953-349-22947
; Sequence 22947, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; SOFTWARE: Patentin version 3.3
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; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 22947
; LENGTH: 393
; TYPE: PR1
; ORGANISM: Glycine max
US-10-953-349-22947

Query Match      6.9%; Score 57.5; DB 6; Length 393;
Best Local Similarity 26.7%; Pred. No. 61;
Matches 32; Conservative 20; Mismatches 39; Indels 29; Gaps 8;

Qy      6 QERRKLPOLCTELQTHIHIIIECVYCKQOL---LRREYVDFAFRDLCTIVRDGNPYAV 62
Db      168 QYKNTTLPQ--TTLKTSVKELDLPAALAEHLVAKRKEAD-----RGEKY-- 212

Qy      63 XDKCLKFEYSKISEYRHYCVSVGTTLLEQYNNKPLCDLLIRICINXQKPL-CP-EKKORHLD 120
Db      213 --KITKLRRNV-EMDEVYMHMRRSPFER-----EALTRDISCKRKLGLPLEBGRYMD 263

RESULT 53
US-10-953-349-22311
; Sequence 22311, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 22311
; LENGTH: 423
; TYPE: PR1
; ORGANISM: Glycine max
US-10-953-349-22311

Query Match      6.9%; Score 57.5; DB 6; Length 423;
Best Local Similarity 23.1%; Pred. No. 66;
Matches 30; Conservative 19; Mismatches 60; Indels 21; Gaps 6;

Qy      17 TELQTHIHIIIECVYCKQOLLRREYVDFAFRDL--CTVYRDGNPYAVXDKCLKFSKIS 74
Db      46 TKMQAEIOKIDDE---VNMKTLKNEBEKLAIDLEMALIKRRK---AEKCRRLAEAS 98

Qy      75 EYRHYCVSVGTTLLEQ-----QYNNKPLCDLLIRICINXQKPL-PEEKORHLDKKOR- 124
Db      99 SYRTMLEKMRDSDHOSVITYKEOYRLNOASNALMARLEAOREICDAAEKDLHKYKORD 158

Qy      125 --FHNIRGRW 132
Db      159 DIEKQIRPEW 168

RESULT 54
US-10-953-349-21322
; Sequence 21322, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
```

SEQ ID NO 21322
LENGTH: 429
TYPE: PRT
ORGANISM: Glycine max
US-10-530-349-21322

Query Match 6.9%; Score 57.5; DB 6; Length 429;
Best Local Similarity 22.6%; Pred. No. 67;
Matches 31; Conservative 13; Mismatches 54; Indels 39; Gaps 4;

QY 24 HDIIIECVYCKQQLRREYVDFAFRDLCIYRDGNPYAVXDKCLKFYSKISEYRHGYSV 83
DB 116 HLIILTSRC---LIGREVDKLFDDVSALFHDLDNGMLPISVLPFLPIPAHKKR----- 167
QY 84 YGTTLEQYNNKPLCDLLIRICINXQKPLCPBEK---QRHLDKK----- 122
DB 168 ---RDQARKKLAEIFASIIITSRSKASKEEDMLQCFIDSKYKDGRTTEAVTGLLIA 222
QY 123 ---QRFNIRGRWTG 134
DB 223 ALFAGQHTSSITSTWTG 239

RESULT 55

US-10-953-349-21321
Sequence 21321, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21321
LENGTH: 487
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-21321

Query Match 6.9%; Score 57.5; DB 6; Length 487;
Best Local Similarity 22.6%; Pred. No. 77;
Matches 31; Conservative 13; Mismatches 54; Indels 39; Gaps 4;

QY 24 HDIIIECVYCKQQLRREYVDFAFRDLCIYRDGNPYAVXDKCLKFYSKISEYRHGYSV 83
DB 174 HLIILTSRC---LIGREVDKLFDDVSALFHDLDNGMLPISVLPFLPIPAHKKR----- 225
QY 84 YGTTLEQYNNKPLCDLLIRICINXQKPLCPBEK---QRHLDKK----- 122
DB 226 ---RDQARKKLAEIFASIIITSRSKASKEEDMLQCFIDSKYKDGRTTEAVTGLLIA 280
QY 123 ---QRFNIRGRWTG 134
DB 281 ALFAGQHTSSITSTWTG 297

RESULT 56

US-10-953-349-22310
Sequence 22310, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22310

LENGTH: 495
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-22310

Query Match 6.9%; Score 57.5; DB 6; Length 495;
Best Local Similarity 23.1%; Pred. No. 79;
Matches 30; Conservative 19; Mismatches 60; Indels 21; Gaps 6;

QY 17 TELQTTIHDIIECVYCKQQLRREYVDFAFRDL--CIYRDGNPYAVXDKCLKFYSKIS 74
DB 118 TKQQAELQKIDDE---VNEKTLKNEBEKLAIQDLEMALIRRRK---AEKCRRLAQAQS 170
QY 75 EYRHGYSVYGTLEQ-----QYNNKPLCDLLIRICINXQKPLC-PEKQRHLDKKQR- 124
DB 171 SYRTMLEKMRDMSHQSIVYKEQVRINQAASNALMRLLEAQRREICDAAEKDLHKRYQRD 230
QY 125 ---FHNIRGRW 132
DB 231 DIEKQIRPEW 240

RESULT 57

US-10-953-349-21320
Sequence 21320, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21320
LENGTH: 518
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-21320

Query Match 6.9%; Score 57.5; DB 6; Length 518;
Best Local Similarity 22.6%; Pred. No. 82;
Matches 31; Conservative 13; Mismatches 54; Indels 39; Gaps 4;

QY 24 HDIIIECVYCKQQLRREYVDFAFRDLCIYRDGNPYAVXDKCLKFYSKISEYRHGYSV 83
DB 205 HLIILTSRC---LIGREVDKLFDDVSALFHDLDNGMLPISVLPFLPIPAHKKR----- 256
QY 84 YGTTLEQYNNKPLCDLLIRICINXQKPLCPBEK---QRHLDKK----- 122
DB 257 ---RDQARKKLAEIFASIIITSRSKASKEEDMLQCFIDSKYKDGRTTEAVTGLLIA 311
QY 123 ---QRFNIRGRWTG 134
DB 312 ALFAGQHTSSITSTWTG 328

RESULT 58

US-10-953-349-12540
Sequence 12540, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 12540
LENGTH: 320

TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-12540

Query Match 6.8%; Score 57; DB 6; Length 320;
Best Local Similarity 35.8%; Pred. No. 55;
Matches 19; Conservative 5; Mismatches 13; Indels 16; Gaps 4;

QY 80 CV-SVYGTTEQYQNK-----PLCDLLIRICINXQKPLCEBEKQRLDKQR 124
DB 209 CYNLYGNTLEQIDIKKCGNDLESILMTVICID----CPE---KRPKAVR 253

RESULT 59

US-11-318-156-6
Sequence 6, Application US/11318156
Publication No. US20060101529A1
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: Von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
FILE REFERENCE: 44158/254623
CURRENT APPLICATION NUMBER: US/11/318, 156
PRIOR FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/10/293, 816
PRIOR FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 09/782, 857
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/290, 333
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 08/810, 572
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-11-318-156-6

Query Match 6.8%; Score 56.5; DB 7; Length 166;
Best Local Similarity 26.7%; Pred. No. 31;
Matches 16; Conservative 6; Mismatches 17; Indels 21; Gaps 2;
QY 89 EQQYNKPLCDLLIRICINXQKPLCEBEKQRLDKQRHINIRGRTGRCMCSRRPRR 148
DB 36 EBOYWDPLDGTCMSC---KTICNHQSOR-----TCAAFCRSLSCRKE 74

RESULT 60

US-11-293-697-3341
Sequence 3341, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293, 697
PRIOR FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108, 260
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3341
LENGTH: 185
TYPE: PRT
ORGANISM: Homo sapiens
US-11-293-697-3341

Query Match 6.8%; Score 56.5; DB 7; Length 185;
Best Local Similarity 23.8%; Pred. No. 35;
Matches 29; Conservative 17; Mismatches 51; Indels 25; Gaps 5;

QY 16 CTELQTTIHDIIECVCKQQLRREYVDPFAFRDLCIV--YRD-----GNPYAV 62
DB 46 CCGLOEKGYSILIKPT---NQLTR--VNKALKVLCIEIGAYRDFELOYVASFKNNTFFLY 100
QY 63 XDKCKEYKISIEYRHYC-----YSVGTTEQQYNKPLCDLLIRICINXQKPLCEEK 115
DB 101 LVAAIKSHTKLASSRANCHGLSLWSHSILRMWTNNSQINMKAAAFIPRPMLTITAPCEVE 160
QY 116 QR 117
DB 161 LR 162

RESULT 61

US-11-318-156-2
Sequence 2, Application US/11318156
Publication No. US20060101529A1
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: Von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
FILE REFERENCE: 44158/254623
CURRENT APPLICATION NUMBER: US/11/318, 156
PRIOR FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/10/293, 816
PRIOR FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 09/782, 857
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/290, 333
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 08/810, 572
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
US-11-318-156-2

Query Match 6.8%; Score 56.5; DB 7; Length 293;
Best Local Similarity 26.7%; Pred. No. 57;
Matches 16; Conservative 6; Mismatches 17; Indels 21; Gaps 2;
QY 89 EQQYNKPLCDLLIRICINXQKPLCEBEKQRLDKQRHINIRGRTGRCMCSRRPRR 148
DB 36 EBOYWDPLDGTCMSC---KTICNHQSOR-----TCAAFCRSLSCRKE 74

RESULT 62

US-10-953-349-3991
Sequence 3991, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953, 349
PRIOR FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3991
LENGTH: 516
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-3991

Query Match 6.8%; Score 56.5; DB 6; Length 516;
Best Local Similarity 27.5%; Pred. No. 1e+02;
Matches 19; Conservative 10; Mismatches 21; Indels 19; Gaps 4;

	QY	78 HCYSAVYGTTLEEQ--YNKPLCDLLIRCNXOKPLCPBEKKORHLDKOFNFINIGRWYGR	135
Dd	387 HYVNHNHGYSSSEETWYSALTAFA-----SRNYPRFP-----RKSEFFHER----VGR	429 	
	QY	136 CWSCCRCSR	144
Dd	430 SOSCVASSR	438 	

```

RESULT 63
US-10-953-349-3990
; Sequence 3990, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3990
; LENGTH: 528
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-3990

```

```

RESULT 64
US-10-953-349-3989
: Sequence 3989, Application US//10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: Patentin version 3.3
: SEQ ID NO 3989
: LENGTH: 547
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
: US-10-953-349-3989

```

```

RESULT 65
US-11-293-697-3121
: Sequence 3121, Application US/11293697
: Publication No. US20060105376A1
: GENERAL INFORMATION:
: APPLICANT: HELIX RESEARCH INSTITUTE
: TITLE OF INVENTION: Novel full length cDNA
: FILE REFERENCE: H1-A0106
: CURRENT APPLICATION NUMBER: US/11/293,697
: CURRENT FILING DATE: 2005-12-05
: PRIOR APPLICATION NUMBER: US/10/108,260
: PRIOR FILING DATE: 2002-03-28
: NUMBER OF SEQ ID NOS: 5458
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3121
: LENGTH: 840
: TYPE: PRT
: ORGANISM: Homo sapiens
US-11-293-697-3121

```

```

RESULT 66
US-11-293-697-3838
; Sequence 3838, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3838
; LENGTH: 968
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-293-697-3838

```

Query Match	6.8%; Score 56.5; DB 6; Length 547;
Best Local Similarity	Pred. No. 1.1e+02;
Matches 19; Conservative 10; Mismatches 21; Indels 19; Gaps 4;	
Qy	78 HYCSVYGTLEQO--YNNPLCDLLIRCIKXQKPLCEEKQRLDKKQRFHNRIGMTWR 135
Db	418 HYYNNHNGYSEEBERTYSAEFAE-----SRNYPTP-----RKSEFHHER---VQR 460
Qy	136 CMSCCRSSR 144
Db	461 SQSCVSSSR 469

RESULT 67
US-10-953-349-19251
; Sequence 19251, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349

;; CURRENT FILING DATE: 2004-09-30
;; NUMBER OF SEQ ID NOS: 40252
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 19251
;; LENGTH: 233
;; TYPE: PRT
;; ORGANISM: Glycine max
US-10-953-349-19251

Query Match 6.7%; Score 56; DB 6; Length 233;
Best Local Similarity 23.9%; Pred. No. 50;
Matches 37; Conservative 20; Mismatches 54; Indels 44; Gaps 9;

QY 11 KLPLQELCTTHDITLCEYCKQQLRREVDFADL-----FDL-----CLVY 54
DB 26 KLVLQGNLSEKTH--TLQFVVLQNGTRADALKRTYLAFFASLNGKPEPKLMGCLLY 83
QY 55 R--DGNPYAVXDKLKFYSKISEY-RHYCYSVYGTTLLEQYINKPL-----CDLL 100
DB 84 AGRLES8PYSELSPHIMEMTTELTROFC-----TLGQSYENPLSAVAAGVGLPTL 138
QY 101 IRCIN--XQKPLCPBEKOR---HLDKORFNHI 128
DB 139 LKLANVMAKKQEWEMKOLPVPVLGKEFOFHSI 173

RESULT 68

US-11-259-950-95
;; Sequence 95; Application US/11259950
;; Publication No. US20060088524A1
;; GENERAL INFORMATION:
;; APPLICANT: Morrissey, James
;; APPLICANT: Pureza, Vincent
;; TITLE OF INVENTION: Tissue Factor Compositions and Methods
;; FILE REFERENCE: 46-04
;; CURRENT APPLICATION NUMBER: US/11/259, 950
;; CURRENT FILING DATE: 2005-10-27
;; PRIOR APPLICATION NUMBER: US 60/622, 737
;; PRIOR FILING DATE: 2004-10-27
;; PRIOR APPLICATION NUMBER: US 60/536, 281
;; PRIOR FILING DATE: 2004-01-13
;; PRIOR APPLICATION NUMBER: US 10/465, 789
;; PRIOR FILING DATE: 2003-06-18
;; PRIOR APPLICATION NUMBER: US 09/990, 087
;; PRIOR FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: US 60/252, 233
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 11/033, 489
;; PRIOR FILING DATE: 2005-01-11
;; NUMBER OF SEQ ID NOS: 96
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 95
;; LENGTH: 279
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Recombinant Tissue Factor with truncated cytoplasmic domain
US-11-259-950-95

Query Match 6.7%; Score 56; DB 7; Length 279;
Best Local Similarity 18.1%; Pred. No. 61;
Matches 19; Conservative 21; Mismatches 47; Indels 18; Gaps 3;

QY 14 QLCLELQTHDITLCEYCKQQLRREVDFADLCTVY-----RDGNPYAVX 63
DB 153 QVGKRVAVYED-----ERTLVRRNMFSLRDVFGKDLITLYYWKSSSGKKTAK 204
QY 64 DKCLKFYSKISEYRHYCYSVYGTTLLEQYINKPLCDLLIRICINXOK 108
DB 205 TNNMEFLIDVDKGENYCFSGVAVIPSRVAKRSTDSPECKGQK 249

RESULT 69

US-10-953-349-19822
;; Sequence 19822; Application US/10953349
;; Publication No. US20060107345A1
;; GENERAL INFORMATION:
;; APPLICANT: ALEXANDROV, Nikolai et al.
;; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;; FILE REFERENCE: 2750-1579PUS2
;; CURRENT APPLICATION NUMBER: US/10/953, 349
;; CURRENT FILING DATE: 2004-09-30
;; NUMBER OF SEQ ID NOS: 40252
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 19822
;; LENGTH: 291
;; TYPE: PRT
;; ORGANISM: Glycine max
US-10-953-349-19822

Query Match 6.7%; Score 56; DB 6; Length 291;
Best Local Similarity 22.6%; Pred. No. 64;
Matches 28; Conservative 23; Mismatches 47; Indels 26; Gaps 8;

QY 35 QQLRREVDFADLCTVYRDGNPYAVXDKLKFYSKISEYRHYCYSVYGTTLLEQYINK 94
DB 2 KHTEKOVNMLNNEBHILGEES-OSNDK-----KINDLRERGYMKYGC---QHYR 51
QY 95 -----PLCDLLIRICINXOKPLCPBEKOR--HLDKORFNHNGRWTGRCMCCRSRTR 146
DB 52 RCRIRAPCCDEIFDCRH-----CHNEKKNINIDQKR-HDIRRHQKVYI--CSLCETE 103
QY 147 RETQ 150
DB 104 QEVQ 107

RESULT 70

US-10-953-349-19821
;; Sequence 19821; Application US/10953349
;; Publication No. US20060107345A1
;; GENERAL INFORMATION:
;; APPLICANT: ALEXANDROV, Nikolai et al.
;; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;; FILE REFERENCE: 2750-1579PUS2
;; CURRENT APPLICATION NUMBER: US/10/953, 349
;; CURRENT FILING DATE: 2004-09-30
;; NUMBER OF SEQ ID NOS: 40252
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 19821
;; LENGTH: 303
;; TYPE: PRT
;; ORGANISM: Glycine max
US-10-953-349-19821

Query Match 6.7%; Score 56; DB 6; Length 303;
Best Local Similarity 22.6%; Pred. No. 66;
Matches 28; Conservative 23; Mismatches 47; Indels 26; Gaps 8;

QY 35 QQLRREVDFADLCTVYRDGNPYAVXDKLKFYSKISEYRHYCYSVYGTTLLEQYINK 94
DB 14 KHTEKOVNMLNNEBHILGEES-OSNDK-----KINDLRERGYMKYGC---QHYR 63
QY 95 -----PLCDLLIRICINXOKPLCPBEKOR--HLDKORFNHNGRWTGRCMCCRSRTR 146
DB 64 RCRIRAPCCDEIFDCRH-----CHNEKKNINIDQKR-HDIRRHQKVYI--CSLCETE 115
QY 147 RETQ 150
DB 116 QEVQ 119

RESULT 71


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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8916
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8916

Query Match      6.7%; Score 55.5; DB 6; Length 179;
Best Local Similarity 19.7%; Pred. No. 43;
Matches 31; Conservative 23; Mismatches 40; Indels 63; Gaps 7;

Qy      1 MFODPQRPRRLPOLCT-----ELQTTIHILLEC----- 30
Db      24 LLOLPSCPKMPPYKTRVYPPGWEILIEPTLRELDKMRLEATDSHGKRCETLWPI 83
Qy      31 -----YYCKQQLRREYVDPAFRDLCTVYRDGNPYAVXDKCLKFYSKISEYR 77
Db      84 FKVSHQSRVYVDYDYYRREISKELYE-----CL-----DQGYA--DRSLAKWKKGQYE 132
Qy      78 HYCY-----SYGTTLEEQYKPLC-DLIRICIN 105
Db      133 RLCCRLCIQPRDHNYGTTTCVGRVFKHLREKVCVH 169

RESULT 76
US-10-953-349-34190
; Sequence 34190, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34190
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34190

Query Match      6.7%; Score 55.5; DB 6; Length 274;
Best Local Similarity 23.5%; Pred. No. 67;
Matches 16; Conservative 8; Mismatches 21; Indels 23; Gaps 2;

Qy      36 QLRREYVDPAFRDLCTVYRDGNPYAVXDKCLKFY-----SKISEYRHICYSV 83
Db      209 ELARRAIYGATFRD-----AASGGCVSYVHVGPDPGWTKLSDGDVGLHYHYPPV 257
Qy      84 YGTTLEEQ 91
Db      258 QKTPEOE 265

RESULT 77
US-10-953-349-34189
; Sequence 34189, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34189
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34189

Query Match      6.7%; Score 55.5; DB 6; Length 278;
Best Local Similarity 23.5%; Pred. No. 68;
Matches 16; Conservative 8; Mismatches 21; Indels 23; Gaps 2;

Qy      36 QLRREYVDPAFRDLCTVYRDGNPYAVXDKCLKFY-----SKISEYRHICYSV 83
Db      213 ELARRAIYGATFRD-----AASGGCVSYVHVGPDPGWTKLSDGDVGLHYHYPPV 261
Qy      84 YGTTLEEQ 91
Db      262 QKTPEOE 269

RESULT 78
US-10-953-349-34188
; Sequence 34188, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34188
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34188

Query Match      6.7%; Score 55.5; DB 6; Length 280;
Best Local Similarity 23.5%; Pred. No. 69;
Matches 16; Conservative 8; Mismatches 21; Indels 23; Gaps 2;

Qy      36 QLRREYVDPAFRDLCTVYRDGNPYAVXDKCLKFY-----SKISEYRHICYSV 83
Db      215 ELARRAIYGATFRD-----AASGGCVSYVHVGPDPGWTKLSDGDVGLHYHYPPV 263
Qy      84 YGTTLEEQ 91
Db      264 QKTPEOE 271

RESULT 79
US-10-953-349-938
; Sequence 938, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 938
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
```

US-10-953-349-938

Query Match 6.7%; Score 55.5; DB 6; Length 403;
Best Local Similarity 36.4%; Pred. No. 1e+02;
Matches 12; Conservative 3; Mismatches 15; Indels 3; Gaps 1;

Qy 30 CVYCKQQLLRREYVDFAFRDLCIYRD---GNP 59
Db 195 CTTCCRLLHSHSVYDKVLEQLLTSYKQVKIGNP 227

RESULT 80

US-10-953-349-937
; Sequence 937, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 937
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

US-10-953-349-937

Query Match 6.7%; Score 55.5; DB 6; Length 436;
Best Local Similarity 36.4%; Pred. No. 1.1e+02;
Matches 12; Conservative 3; Mismatches 15; Indels 3; Gaps 1;

Qy 30 CVYCKQQLLRREYVDFAFRDLCIYRD---GNP 59
Db 228 CTTCCRLLHSHSVYDKVLEQLLTSYKQVKIGNP 260

RESULT 81

US-10-953-349-9969
; Sequence 9969, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9969
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

US-10-953-349-9969

Query Match 6.7%; Score 55.5; DB 6; Length 436;
Best Local Similarity 36.4%; Pred. No. 1.1e+02;
Matches 12; Conservative 3; Mismatches 15; Indels 3; Gaps 1;

Qy 30 CVYCKQQLLRREYVDFAFRDLCIYRD---GNP 59
Db 228 CTTCCRLLHSHSVYDKVLEQLLTSYKQVKIGNP 260

RESULT 82

US-10-953-349-936
; Sequence 936, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 936
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

US-10-953-349-936

Query Match 6.7%; Score 55.5; DB 6; Length 508;
Best Local Similarity 36.4%; Pred. No. 1.3e+02;
Matches 12; Conservative 3; Mismatches 15; Indels 3; Gaps 1;

Qy 30 CVYCKQQLLRREYVDFAFRDLCIYRD---GNP 59
Db 300 CTTCCRLLHSHSVYDKVLEQLLTSYKQVKIGNP 332

RESULT 83

US-10-953-349-9968
; Sequence 9968, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9968
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

US-10-953-349-9968

Query Match 6.7%; Score 55.5; DB 6; Length 508;
Best Local Similarity 36.4%; Pred. No. 1.3e+02;
Matches 12; Conservative 3; Mismatches 15; Indels 3; Gaps 1;

Qy 30 CVYCKQQLLRREYVDFAFRDLCIYRD---GNP 59
Db 300 CTTCCRLLHSHSVYDKVLEQLLTSYKQVKIGNP 332

RESULT 84

US-10-953-349-9967
; Sequence 9967, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9967
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

US-10-953-349-9967

Query Match 6.7%; Score 55.5; DB 6; Length 538;
Best Local Similarity 36.4%; Pred. No. 1.4e+02;
Matches 12; Conservative 3; Mismatches 15; Indels 3; Gaps 1;

```
QY      30  CVYCKQQLLRREVVDPFARDLCLVYRD---GNP  59
      |||  |||  |||  |||
Db      330  CTTCRLLHESVYDKVLEQLLTSTYKOVKIGNP  362
```

RESULT 85

```

1 Sequence 4398, Application US/11293697
2
3 Publication No. US20060105376A1
4
5 GENERAL INFORMATION:
6
7 APPLICANT: HELIX RESEARCH INSTITUTE
8
9 TITLE OF INVENTION: Novel full length cDNA
10
11 FILE REFERENCE: H1-A0106
12
13 CURRENT APPLICATION NUMBER: US/11/293.697
14
15 CURRENT FILING DATE: 2005-12-05
16
17 PRIOR APPLICATION NUMBER: US/10/108,260
18
19 PRIOR FILING DATE: 2002-03-28
20
21 NUMBER OF SEQ ID NOS: 5458
22
23 SOFTWARE: PatentIn Ver. 2.1
24
25 SEQ ID NO 4398
26
27 LENGTH: 764
28
29 TYPE: PRT
30
31 ORGANISM: Homo sapiens
32
33 US-11-293-697-4398

```

Query Match	6.7%	Score 55.5;	DB 7;	Length 764;
Best Local Similarity	21.3%;	Pred. NO. 2e+02;		
Matches 23; Conservative	13;	Mismatches 29;	Indels 43;	Gaps 4;

QY 66 KFYSKISEYRH-----YCYSVGYTLEEOYNK-----PLCDLLIRCIYKQK 108

```
QY      109 PL-----CPBEKQRHLDKQRF-----HNIRGRW 132
      |:      |::|||::|||      |:      |
Db      695 PMESRNIWREVTYRLGLGIDAAEOKRHLBEKQVVEERKRENLRTFW 742
```

RESULT 86
US-10-505-928-94

```

? Sequence 94, Application US/10505928
? Publication NO. US20060088532A1
? GENERAL INFORMATION:
? APPLICANT: Ludwig Institute for Cancer Research et al.
? TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
? FILE REFERENCE: 28967/39178
? CURRENT APPLICATION NUMBER: US/10/505,928
? CURRENT FILING DATE: 2004-08-27
? PRIOR APPLICATION NUMBER: US 66/363,019
? PRIOR FILING DATE: 2002-03-07
? NUMBER OF SEQ ID NOS: 866
? SOFTWARE: PatentIn 3.2
? SEQ ID NO 94
? LENGTH: 966
? TYPE: FRT
? ORGANISM: Homo sapiens
? US-10-505-928--94

```

Query Match	6.7%	Score 55.5;	DB 6;	Length 965;
Best Local Similarity	25.4%	Pred. NO. 2.6e+02;		
Matches 33; Conservative	9;	Mismatches 45;	Indels 43;	Gaps 8;

QY 25 ECVCYKQOQLLRVYDPAFRDLCTIYVRDGNPAVADKCLKFKYSKISEYRHYCYSVYGTLL 88
 DB 813 KCTAVK-----EGFSLA-RSSCI--PDCEPTTFPDEL---IRGEGCHTGTCTVCGVR 860

```
OY      EQQYNKPLCDLLIRCI NKX-----PLCPB-----EKORHLDDKKÖFRFNIRGRWTG 134
89
DB      EE-----CICHCAKNFHDWKVPCRGEGEYYENBPGLP-----HKVCRCRDE 903
```

QY	135	RCMSCRRSSR	144
		:	
DB	904	NCLSCAGSSR	913

RESULT 87
US-10-953-349-9685

```

1  APPLICANT: ALEXANDROV, Nickolai et al
2  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
3  TITLE OF INVENTION: ENCODED THERM
4  FILE REFERENCE: 2750-1579PUS2
5  CURRENT APPLICATION NUMBER: US/10/953,349
6  CURRENT FILING DATE: 2004-09-30
7  NUMBER OF SEQ ID NOS: 40252
8  SOFTWARE: PatentIn version 3.3
9  SEQ ID NO 9685
10 LENGTH: 426
11 TYPE: PRT
12 ORGANISM: Arabidopsis thaliana
13 US-10-953-349-9685

```

Query Match	6.6%	Score 55;	DB 6;	Length 426;
Best Local Similarity	21.8%	Pred. No. 1.2e+02;		
Matches 34;	Conservative 16;	Mismatches 56;	Indels 50;	Gaps 9;

```

QY      2 FQDPOERPRKPIQLCTELQTTTHIDIIIECVYCKQL-LRREYVDFAF----RDLCIVYRD 56
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB     43 FKDPVIEDGNIIPRVLDLNVNHP-HSI---CDGCSAIEYGRSVHALGVNMHPPECFCRYCD 98

```

QY 57 GNPAAVXDKCLKFYISKISEYRHYCVSGVTLLBQQYNKPLCDLLIFCINIXQKPLCPBEKO 116
Db : : : : :
99 -KPTAMHE-----FSNTKGRC-- --TTCYERHPNCHVCK- 130

```
OY      117 RHLDDKQR-----FHNIRGRWTCRMSCCR   141
          :    | : | : | : | : | : | : | : |
Db      131 KFPGRKYKEHPFWKEKYCPFEHVDG--TPKCCSCER   164
```

RESULT 88
US-10-953-349-9684

```

: sequence 9684, application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERAPY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 9684
: LENGTH: 433
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
US-10-953-349-9684

```

Query Match	6.6%;	Score 55;	DB 6;	Length 433;
Best Local Similarity	21.8%;	Pred. No. 1.2e+02;		
Matches 34;	Conservative 16;	Mismatches 56;	Indels 50;	Gaps 9;

QY 2 FQDQGERPRKLPOLCTELQTTIHIIILECYCKQOL-LRREVDPAF----RDLCIVYRD 56
| | | | |
Db 50 FKDPVEEDGNLPRVDNLVNHPR-HSL---CDGCKSAIEYGSSVHLGVNMHPECFRCRYCD 105
| | | | |

QY 57 GNPVAVXDKDLKFKYSISEYRHHYCSVGTTLBQQINKPLCDLLHICINXQKPLCPBEKK 116
| | | | |
DB 106 -KPIIMHE-----FSNTRGRCH- -ITCYERSHPHCVCCK 137

QY	117	RHLDKQR-----	FHNIRGRWTCRMSCCR	141
	:	:	:	:
Db	138	KFPGRKYKEHPFWKEK	YCPFEVDG--TPKCCS	CER 171

RESULT 89
US-11-293-3101
; Sequence 3101, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3101
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3101

Query Match 6.6%; Score 55; DB 7; Length 541;
Best Local Similarity 22.9%; Pred. No. 1.6e+02;
Matches 33; Conservative 16; Mismatches 53; Indels 42; Gaps 10;

QY 13 POLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDGNPYAVXDKCLKFYSK 72
DB 398 FYECKECCGKT---FIESAY---LIRHQ-----RHTGKPKYGC-NOCCKLFRN 438
QY 73 ISE-YRHYCVSVGTTLEGOYNKPLCDLLIR---CINXQKPL-----CPE-----EK 115
DB 439 IAGLIRHO---RHTGKPKYECNOCGAFRDSCLTGHQRIHYKETPYQCPECKSKFKQ 494
QY 116 QRHLDKQRFNIRGRWTCRCMSC 139
DB 495 NSHLAVHQRLHSRSG--PSRCPCQ 516

RESULT 90
US-11-293-3790
; Sequence 3790, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3790
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3790

Query Match 6.6%; Score 55; DB 7; Length 541;
Best Local Similarity 22.9%; Pred. No. 1.6e+02;
Matches 33; Conservative 16; Mismatches 53; Indels 42; Gaps 10;

QY 13 POLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDGNPYAVXDKCLKFYSK 72
DB 398 FYECKECCGKT---FIESAY---LIRHQ-----RHTGKPKYGC-NOCCKLFRN 438
QY 73 ISE-YRHYCVSVGTTLEGOYNKPLCDLLIR---CINXQKPL-----CPE-----EK 115
DB 439 IAGLIRHO---RHTGKPKYECNOCGAFRDSCLTGHQRIHYKETPYQCPECKSKFKQ 494
QY 116 QRHLDKQRFNIRGRWTCRCMSC 139
DB 495 NSHLAVHQRLHSRSG--PSRCPCQ 516

RESULT 91
US-10-953-349-9683
; Sequence 9683, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9683
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9683

Query Match 6.6%; Score 55; DB 6; Length 560;
Best Local Similarity 21.8%; Pred. No. 1.6e+02;
Matches 34; Conservative 16; Mismatches 56; Indels 50; Gaps 9;

QY 2 FQDQERPKLPOLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRD 56
DB 177 FKDVEEDGNLPRVDLWVNH-PSI---CDGCKSAIEYGSVHALGVNMHPECFCRCRYCD 232
QY 57 GNPYAVXDKCLKFYSKISEYRHYCVSVGTTLEGOYNKPLCDLLIRGINXQKPLCPEBKQ 116
DB 233 KPIAMHE-----FSNTRKGRCH-----ITCYERSHPNCHYCK 264
QY 117 RHLDKQR-----FHNIRGRWTCRCMSCR 141
DB 265 KFGKRYKEHPFWKEKYCPHEVDG--TPKCCSCER 298

RESULT 92
US-10-953-349-21080
; Sequence 21080, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21080
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21080

Query Match 6.6%; Score 54.5; DB 6; Length 167;
Best Local Similarity 20.2%; Pred. No. 50;
Matches 24; Conservative 24; Mismatches 44; Indels 27; Gaps 5;

QY 14 QCTELQTTIHDIILECVYCKQQLR-----REYVDFAFRDLCTIYRDGNPYAVXDK 65
DB 47 QLC-----H--LMISVYRNNMLQDLVLFKGLFAFDRKPRDKSIQKVAAYEVLG- 96
QY 66 CLKFYSKISEYRHYCVSVGTTLEGOYNKPLCDLLIRGINXQKPLCPEBKORHLDKQR 124
DB 97 LVKEKEVLEKYNHLFTETGPTKRNKNS-----FAKKGVHFTYKKGKQKQSKR 146

RESULT 93
US-11-293-697-3380
; Sequence 3380, Application US/11293697

```

; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3380
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3380

```

Query Match	6.6%	Score 54.5;	DB 7;	Length 281;
Best Local Similarity	21.2%	Pred. No. 88;		
Matches	18;	Conservative	15;	Mismatches 31;
			Indels	21;
			Gaps	4

QY 59 PYAVYDKLKFYSKISIEYRHYCYSVVGTLLBEQYNNKCLDLLRINCINQKPLCE--EKQ 116
Db 80 PFSTHTGCSGSEFNRRPDKLKAHLISHSGMKL-----KC-----ALCSKFSRR 122

Oy 117 RHLDKQRFHNIRGRWTGRCMSCCR 141
 123 : : : : :
 Db 123 AHLAEHQRAHT--GNYKFCAGCAK 145

RESULT 94
US-10-953-349-21079
; Sequence 21079, Application US/10953349
; Publication No. US20060107345A1

```
?
? APPLICANT: ALEXANDROV, Nickolai et al.
? TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
? TITLE OF INVENTION: ENCODED THERBY
? FILE REFERENCE: 2750-1579PU2
? CURRENT APPLICATION NUMBER: US/10/953,349
? CURRENT FILING DATE: 2004-09-30
? NUMBER OF SEQ ID NOS: 40252
? SOFTWARE: PatentIn version 3.3
```

```

; LENGTH: 300
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21079

```

Query Match	6.6%;	Score 54.5;	DB 6;	Length 300;
Best Local Similarity	20.2%;	Pred. No. 94;		
Matches 24;	Conservative 24;	Mismatches 44;	Indels 27;	Gaps 5

QY 14 QLTCLQTTHIDILECVCCKQQLR-----REYVDFARDLCTVYRDGNPNYAYXDK 65
Db 180 QLC-----H-LMISVYYRNMTDLVKLFKGLSEFDRKRPRDKSIIQKVAAYEVLG- 229

```

Qy      66 CLKFKYSKISEYHHYCYSVYGTTEQQYNKRLCDLLIRCLNXXOKRPLCEEKORHLDDKKR 124
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      230 LVKEKEKENVLEKKNHLLFTETGPTGRHKRNS-----FEAKGNHPTKKEGRHQKRSK 279

```

RESULT 95
US-10-953-349-21078
; Sequence 21078, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

```

: APPLICANT: ALEXANDROV, Nikolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30

```

```

; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21078
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Glycine max
;
US-10-953-349-21078

```

Query Match	6.6%	Score 54.5;	DB 6;	Length 308;
Best Local Similarity	20.2%;	Pred. No. 97;		
Matches 24;	Conservative 24;	Mismatches 44;	Indels 27;	Gaps 5;

Qy 14 QLCLEQTTHIDIIIECVYKQQLLR-----REVYDPAFRDLCTIVRBDGNPIAYVXDK 65
|||::||:|:
Db 188 QLC-----H-LMISVYVRNNMLQDLYKLFGKLEAFDRKPRDKSIIQKVANAYEVLG- 237

```

Oy      66 CLKFSKISEYRHVCYSVGTTEEOQYNKPLCDLLIRCLINXQKPLCPREEQRHLDKQR 124
      :  ::  ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      238 LVKEKERVLLEKYNHLLFTETGPKRHKNS-----FEAKGVNPTTEKRNHQQSRK 287

```

RESULT 96
US-10-953-349-33223
; Sequence 33223, Application US/10953349
; Publication No. US20060107345A1

```

; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33223
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33223

```

Query Match	6.6%	Score 54.5;	DB 6;	Length 337;
Best Local Similarity	21.6%	Pred. No. 1.1e+02;		
Matches 19;	Conservative 15;	Mismatches 17;	Indels 37;	Gaps 4;

```
Oy      12 LPQLCTELQ-----TTIHDIILECYV-----CKOOLLREVVDF    45
          ||:::||::||::|
Db      179 LPTICSPLRKACTGMDSAVHILLKGYKDDEGAENELSFEWQTQQVEMLNTKKFGDI  23
```

QY 46 AFRDLCIVRRDGNPYAVXDKCLKFYSKI 73
||| :|||
Db 239 AFRD-----KDAIDYYSKL 255

RESULT 97
US-10-953-349-33222
; Sequence 33222, Application US/10953349
; Publication No. US20060107345A1

```

: APPLICANT: ALEXANDROV, Nickolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERAPY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 33222
: LENGTH: 358
: TYPE: PRT
: ORGANISM: Zea mays subsp. mays
: US-10-953-349-33222

```

Query Match 6.6%; Score 54.5; DB 6; Length 358;

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:10:28 ; Search time 18.8916 Seconds
(without alignments)
499.124 Million cell updates/sec

Title: US-10-530-253-14ED

Perfect score: 517
Sequence: 1 MAGDPTLHEWMLDLPETT.....LEDLMGTGIVXPTCSQXP 98

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : PIR 80.*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512	99.0	98	1	E7 protein - human
2	381.5	73.8	99	1	E7 protein - human
3	372	72.0	98	1	E7 protein - human
4	295	57.1	97	1	E7 protein - human
5	294	56.9	99	2	E7 protein - human
6	289.5	56.0	98	1	E7 protein - human
7	245	47.4	98	1	E7 protein - human
8	243	47.0	98	1	E7 protein - human
9	222.5	43.0	97	2	E7 protein - human
10	218.5	42.3	113	2	E7 protein - human
11	213	41.2	106	2	E7 protein - human
12	209.5	40.5	105	2	E7 protein - human
13	208.5	40.3	105	2	E7 protein - human
14	200.5	38.8	101	1	E7 protein - human
15	200.5	38.8	105	1	E7 protein - human
16	194	37.5	98	1	E7 protein - human
17	183.5	35.5	93	1	E7 protein - human
18	183.5	35.5	105	2	E7 protein - human
19	178.5	34.5	92	1	E7 protein - human
20	178.5	34.5	105	2	E7 protein - human
21	178.5	34.5	111	2	E7 protein - human
22	178	34.4	101	1	E7 protein - human
23	175.5	33.9	92	1	E7 protein - human
24	173.5	33.6	86	2	E7 protein - human
25	170	32.9	95	2	E7 protein - human
26	170	32.9	109	1	E7 protein - human
27	169	32.7	104	2	E7 protein - human
28	166.5	32.2	92	2	E7 protein - human
29	157.5	30.5	110	1	E7 protein - human

30	150.5	29.1	111	2	S36556	E7 protein - human
31	148	28.6	93	2	S36474	E7 protein - human
32	140.5	27.2	104	2	S36545	E7 protein - human
33	138	26.7	93	1	W7ML	E7 protein - human
34	122	23.6	93	2	S36591	E7 protein - human
35	120.5	23.3	102	2	S36492	E7 protein - human
36	119	23.0	103	2	S36539	E7 protein - human
37	116.5	22.5	102	2	S36486	E7 protein - human
38	113	21.9	103	1	W7ML47	E7 protein - human
39	112	21.7	103	1	W7ML5	E7 protein - human
40	109	21.1	103	1	W7MLB5	E7 protein - human
41	105	20.3	103	1	W7ML8	E7 protein - human
42	87	16.8	94	1	W7MLRB	E7 protein - human
43	83.5	16.2	98	2	B61399	early protein E7 -
44	80	15.5	55	2	S19907	early protein E7 -
45	79.5	15.4	98	2	A61399	E7 protein - deer
46	77.5	15.0	102	1	W7MLDP	E7 protein - human
47	76	14.7	114	1	W7ML41	E7 protein - human
48	75	14.5	103	2	S36568	E7 protein - cotto
49	73.5	14.2	102	1	W7MLRP	early protein E7 -
50	70.5	13.6	1273	2	C96767	unknown protein F2
51	68	13.2	622	2	I48733	protein kinase rck
52	68	13.2	3924	2	S37431	ankyrin 2, neurona
53	66	12.8	261	2	T38157	short-chain dehydr
54	65.5	12.7	455	2	AD0782	probable L-serine
55	65	12.6	99	1	W6MLB4	B6 protein - bovin
56	65	12.6	770	2	A90880	hypothetical prote
57	65	12.6	770	2	H85738	hypothetical prote
58	64.5	12.5	100	2	C61399	early protein E7 -
59	64.5	12.5	614	2	D86342	hypothetical prote
60	64	12.4	138	1	PSRSAT	phospholipase A2 h
61	63.5	12.3	391	1	T14580	STEPL protein pre
62	63	12.2	138	1	I51380	phospholipase A2 h
63	63	12.2	855	2	S56948	KAL5 protein - yea
64	63	12.2	1250	2	T40062	probable nuclear e
65	62.5	12.1	1490	2	T20513	hypothetical prote
66	62	12.0	675	2	T00198	VP80 protein - leu
67	61.5	11.9	433	2	T04509	hypothetical prote
68	61.5	11.9	508	2	F86458	unknown protein, 7
69	61.5	11.9	823	2	T21104	hypothetical prote
70	61.5	11.9	1964	2	A59282	nonmuscle myosin I
71	61	11.8	338	2	JC7867	endo-1,3(4)-beta-g
72	61	11.8	635	2	T09648	nucleolin homolog
73	61	11.8	815	2	T40524	hypothetical prote
74	60.5	11.7	222	2	AB0007	probable DNA repai
75	60.5	11.7	411	2	S40936	hypothetical prote
76	60.5	11.7	551	2	C89134	protein F256.6 (i
77	60.5	11.7	1269	2	T14476	p61A protein - sli
78	60.5	11.7	1287	2	A41685	SIL protein - huma
79	60.5	11.7	1389	2	I50090	carboxypeptidase g
80	60.5	11.7	1826	2	H86502	excinnuclease ABC s
81	60.5	11.7	1826	2	D72120	excinnuclease ABC,
82	60	11.6	172	2	T03396	invertase inhibit
83	60	11.6	370	1	E70341	conserved hypotet
84	60	11.6	465	2	H86352	protein P282.2 (im
85	60	11.6	562	2	S46281	P element - fruit
86	60	11.6	1175	2	T37192	nebulin-related pr
87	60	11.6	1634	1	JC5500	phosphoinositide 3
88	59.5	11.5	333	2	T39642	conserved hypotet
89	59.5	11.5	389	1	A48355	coat protein - pel
90	59.5	11.5	404	2	C96640	hypothetical prote
91	59.5	11.5	438	2	C69455	tungenen formylmet
92	59.5	11.5	512	2	E71474	probable hsp60 cha
93	59.5	11.5	596	2	A85438	hypothetical prote
94	59.5	11.5	617	2	T10102	diphosphate-fructo
95	59.5	11.5	617	2	E96793	hypothetical prote
96	59.5	11.5	822	2	T01622	probable salt-indu
97	59.5	11.5	1708	2	F69189	protoporphyryn IX
98	59.5	11.5	1959	1	A33977	myosin heavy chain
99	59.5	11.5	4572	2	S57908	hypothetical 527K
100	59	11.4	214	2	AF1164	hypothetical prote

ALIGNMENTS

RESULT 1

E7 protein - human papillomavirus type 16

C/Species: human papillomavirus type 16

C/Date: 28-May-1986 #sequence revision 28-May-1986 #text_change 09-Jul-2004

C/Accession: A03688; S12367; T10428

R/Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Roweckamp, W.G.

Virology 145, 181-185, 1985

A/Title: Human papillomavirus type 16 DNA sequence.

A/Reference number: A22355; MUID:85246220; PMID:2990099

A/Accession: A03688

A/Molecule type: DNA

A/Residues: 1-98 <SEB>

A/Cross-references: UNIPROT:P03129; UNIPARC:UPI000000034E; GB:K02718; NID:G333031; PIDN:

R/Barbosa, M.S.; Edmonde, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Youaden, K.H.

EMBO J. 9, 153-160, 1990

A/Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large

A/Reference number: S12367; MUID:90107938; PMID:2155075

A/Accession: S12367

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-98 <BAR>

A/Cross-references: UNIPARC:UPI000000034E

R/Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A/Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A/Reference number: Z17014; MUID:91162763; PMID:1848319

A/Accession: T10428

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-98 <KEN>

A/Cross-references: UNIPARC:UPI000000034E; EMBL:K02718; NID:G333031; PIDN:AAAA6940.1; PI

C/Genetics:

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match

Best Local Similarity 96.9%; Score 512; DB 1; Length 98;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query

Db

1 MHGPTPLHEYMDLQPEPTDLYXXQUNDSSEDEIDGPAQAEPDRAHYNIVTFCC 60

1 MHGPTPLHEYMDLQPEPTDLYXXQUNDSSEDEIDGPAQAEPDRAHYNIVTFCC 60

61 CDSTLRFCVQSTHVDIRTELDLMTGLGIVXPICSQK 98

61 CDSTLRFCVQSTHVDIRTELDLMTGLGIVXPICSQK 98

RESULT 2

E7 protein - human papillomavirus type 35

C/Species: human papillomavirus type 35

C/Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004

C/Accession: F40824; S36522

R/Marich, J.E.; Pontleier, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virology 186, 770-776, 1992

A/Title: The phylogenetic relationship and complete nucleotide sequence of human papillid

A/Reference number: A40824; MUID:92124753; PMID:1310198

A/Accession: F40824

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-99 <MAR>

A/Cross-references: UNIPROT:P27230; UNIPARC:UPI000000035E; GB:M74117; NID:G333050; PIDN:

R/Delius, H.; Hofmann, B.

Submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36522

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-99

A/Cross-references: UNIPARC:UPI000000035E; EMBL:X74477; NID:G396997; PIDN:CA52562.1; PI

A/Experimental source: strain 35H

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:59-95/Region: zinc finger CCCC motif

Query Match

Best Local Similarity 73.8%; Score 381.5; DB 1; Length 99;

Matches 72; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

Query

Db

1 MHGPTPLHEYMDLQPEPTDLYXXQUNDSSEDEIDGPAQAEPDRAHYNIVTFCC 59

1 MHGPTPLHEYMDLQPEPTDLYXXQUNDSSEDEIDGPAQAEPDRAHYNIVTFCC 59

60 KCDSTLRFCVQSTHVDIRTELDLMTGLGIVXPICSQK 97

60 KCDSTLRFCVQSTHVDIRTELDLMTGLGIVXPICSQK 97

RESULT 3

E7 protein - human papillomavirus type 31

C/Species: human papillomavirus type 31

C/Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 09-Jul-2004

C/Accession: B32444

R/Goldborough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.

Virology 171, 306-311, 1989

A/Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ

A/Reference number: A94398; MUID:89299478; PMID:2545036

A/Accession: B32444

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-98 <GOL>

A/Cross-references: UNIPROT:P17387; UNIPARC:UPI000013840A; GB:J04353; NID:G333048; PIDN:

C/Comment: This protein may be involved in the oncogenic potential of this virus.

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match

Best Local Similarity 72.0%; Score 372; DB 1; Length 98;

Matches 69; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Query

Db

1 MHGPTPLHEYMDLQPEPTDLYXXQUNDSSEDEIDGPAQAEPDRAHYNIVTFCC 60

1 MHGPTPLHEYMDLQPEPTDLYXXQUNDSSEDEIDGPAQAEPDRAHYNIVTFCC 60

61 CDSTLRFCVQSTHVDIRTELDLMTGLGIVXPICSQK 97

61 CDSTLRFCVQSTHVDIRTELDLMTGLGIVXPICSQK 97

RESULT 4

E7 protein - human papillomavirus type 33

C/Species: human papillomavirus type 33

C/Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 09-Jul-2004

C/Accession: A03689; S23831; S23827

R/Cole, S.T.; Strebeck, R.E.

J. Virol. 58, 991-995, 1986

A/Title: Genome organization and nucleotide sequence of human papillomavirus type 33, whi

A/Reference number: A93020; MUID:86200464; PMID:3009902

A/Accession: A03689

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-97 <COL>

A/Cross-references: UNIPROT:P06429; UNIPARC:UPI000013840C; GB:M12732; NID:G333049; PIDN:

R/Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Meij

submitted to the EMBL Data Library, January 1992

A/Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via c

A/Reference number: S19906

A/Accession: S23831

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 197 <SN1>

A/Cross-references: UNIPARC:UPI000013840C; EMBL:X64085; NID:g60278; PIDN:CAA5434.1; PII

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation; zinc finger

F/58-94/Region: zinc finger CCCC motif

Query Match 57.1%; Score 295; DB 1; Length 97;

Best Local Similarity 57.7%; Pred. No. 9.4e-26; Mismatches 25; Indels 0; Gaps 0;

Matches 56; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPEPTDLYXXYQNDSEED--IDGPAGQAEPPRAHNYITFCCK 60

Db 1 MRGHKPTLKEYVDLYPEPTDLYCYEQLSDEDELDPRDGAQAPATADYIVTCCHT 60

Qy 61 CDSTLRVCVOSTHVDIRLTEDLMGTGIVXPICSQK 97

Db 61 CMTTVRLCVNSTASDTRITQQLMGTVNIVCPFCACQ 97

RESULT 5

S36574 E7 protein - human papillomavirus type 52

C/Species: human papillomavirus type 52

C/Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C/Accession: S36574

R/DeJans, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus E7eas.

A/Reference number: S36469

A/Accession: S36574

A/Molecule type: DNA

A/Residues: 1-99

A/Cross-references: UNIPROT:P36831; UNIPARC:UPI000013841C; EMBL:X74481; NID:g397038; PID

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation

Query Match 56.9%; Score 294; DB 2; Length 99;

Best Local Similarity 57.1%; Pred. No. 1.2e-25; Mismatches 23; Indels 2; Gaps 1;

Matches 56; Conservative 17; Mismatches 23; Indels 2; Gaps 1;

Qy 1 MHGDTPLHEYMDLQPEPTDLYXXYQNDSEED--IDGPAGQAEPPRAHNYITFC 58

Db 1 MRGHKPTLKEYVDLYPEPTDLYCYEQLSDEDELDPRDGAQAPATADYIVTCC 60

Qy 59 CKCDSTLRVCVOSTHVDIRLTEDLMGTGIVXPICSQ 96

Db 61 HSCDSTLRICHSATDRLTQGLTGLVVCGRAR 98

RESULT 6

W7ML58 E7 protein - human papillomavirus type 58

C/Species: human papillomavirus type 58

A/Note: host Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C/Accession: F36779

R/Kirill, Y.; Iwamoto, S.; Matsukura, T.

Virology 185, 424-427, 1991

A/Title: Human papillomavirus type 58 DNA sequence.

A/Reference number: A36779; MUID:92024102; PMID:1656594

A/Accession: F36779

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-98 <KIR>

A/Cross-references: UNIPROT:P26557; UNIPARC:UPI000000348B; GB:D90400; NID:g222386; PIDN:

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation; zinc finger

F/59-95/Region: zinc finger CCCC motif

Query Match 56.0%; Score 289.5; DB 1; Length 98;

Best Local Similarity 57.1%; Pred. No. 3.9e-25; Mismatches 25; Indels 1; Gaps 1;

Matches 56; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MHGDTPLHEYMDLQPEPTDLYXXYQNDSEED--EIDGPAGQAEPPRAHNYITFCCK 59

Db 1 MRGNPTLRKYVDLYPEPTDLYCYEQLSDEDELDGDPGQAQAPATADYIVTCCY 60

Qy 60 KCDSTLRVCVOSTHVDIRLTEDLMGTGIVXPICSQK 97

Db 61 TCGTVRLCVNSTASDTRITQQLMGTVNIVCPFCACQ 98

RESULT 7

W7ML11 E7 protein - human papillomavirus type 11

C/Species: human papillomavirus type 11

C/Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004

C/Accession: A03690

R/Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.

Virology 151, 124-130, 1986

A/Title: The nucleotide sequence and genome organization of human papilloma virus type 1

A/Reference number: A94338; MUID:86181601; PMID:3008427

A/Accession: A03690

A/Molecule type: DNA

A/Residues: 1-98 <DAR>

A/Cross-references: UNIPROT:P04020; UNIPARC:UPI00001383F7; GB:M14119; NID:g333026; PIDN:

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation; zinc finger

F/58-94/Region: zinc finger CCCC motif

Query Match 47.4%; Score 245; DB 1; Length 98;

Best Local Similarity 53.0%; Pred. No. 3.5e-20; Mismatches 29; Indels 4; Gaps 3;

Matches 53; Conservative 14; Mismatches 29; Indels 4; Gaps 3;

Qy 1 MHGDTPLHEYMDLQPEPTDLYXXYQNDSEED--DEIDGPAGQAEPPRAHNYITFC 58

Db 1 MRGHVTLKQIVDLQPPDPVGLHCYEQLSDEDEVDKQ--KQDAQPLTQHYQILVCC 58

Qy 59 CKCDSTLRVCVOSTHVDIRLTEDLMGTGIVXPICSQK 98

Db 59 CGCDSTLRVLCVOSTHVDIRLTEDLMGTGIVXPICSQK 98

RESULT 8

W7ML6 E7 protein - human papillomavirus type 6b

C/Species: human papillomavirus type 6b

C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004

C/Accession: D20558

R/Schwarz, E.; Dürst, M.; Demankowski, C.; Laternmann, O.; Zech, R.; Wolfesberger, E.; Su

EMBO J. 2, 2341-2348, 1983

A/Title: DNA sequence and genome organization of genital human papillomavirus type 6b.

A/Reference number: A90975; MUID:84131949; PMID:6321162

A/Accession: D20558

A/Molecule type: DNA

A/Residues: 1-98 <SCH>

A/Cross-references: UNIPROT:P06464; UNIPARC:UPI0000138429; GB:X00203; NID:g60955; PIDN:C

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation; zinc finger

F/58-94/Region: zinc finger CCCC motif

Query Match 47.0%; Score 243; DB 1; Length 98;

Best Local Similarity 52.5%; Pred. No. 5.9e-20; Mismatches 28; Indels 4; Gaps 3;

Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGDTPLHEYMDLQPEPTDLYXXYQNDSEED--DEIDGPAGQAEPPRAHNYITFC 58

Db 1 MRGHVTLKQIVDLQPPDPVGLHCYEQLSDEDEVDKQ--DSQPLKQHFQIVTCC 58

Qy 59 CKCDSTLRVCVOSTHVDIRLTEDLMGTGIVXPICSQK 97

Db 59 CGCDSNRLVVOCTETDIRVQQLLTGLTINVCPICAK 97

RESULT 9

S36516 E7 protein - human papillomavirus type 34

C:Species: human papillomavirus type 34
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36516

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36516

A:Molecule type: DNA

A:Residues: 1-97

A:Cross-references: UNIPROT:P36828; UNIPARC:UPI000013840D; EMBL:X74476; NID:g396989; PID

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 43.0%; Score 222.5; DB 2; Length 97;

Best Local Similarity 49.0%; Pred. No. 1.1e-17;

Matches 48; Conservative 18; Mismatches 29; Indels 3; Gaps 3;

Qy 1 MHGDPRLHEMYLLOPET--TDLYXXYQXQNDSSSEEDIDGPAQAEPDRAHNYTFCC 59

Db 1 MHGKPSYQDVLVLPKPTETDLCYESTL-DNSEBEDTSDHL-BRQAEQMYRLVTDCS 58

Qy 60 KCDSTLRKCVOSTHVDIRTLDELMLGTLGIYXPICSOK 97

Db 59 RCOSTVCLTETSTADLVLEDLMLGMLKIVCPNCSRR 96

RESULT 10

W7MLR1

E7 protein - rhesus papillomavirus (type 1)

C:Species: rhesus papillomavirus

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: B38503

R:Ostrow, R.S.; Labresh, K.V.; Paras, A.J.

Virology 181, 424-429, 1991

A:Title: Characterization of the complete Rbpv 1 genomic sequence and an integration loc

A:Reference number: A38503; MUID:91135018; PMID:1847267

A:Accession: B38503

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-113 <OST>

A:Cross-references: UNIPROT:P22161; UNIPARC:UPI000013842F; EMBL:M37717

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 42.3%; Score 218.5; DB 1; Length 113;

Best Local Similarity 43.8%; Pred. No. 3.7e-17;

Matches 49; Conservative 13; Mismatches 35; Indels 15; Gaps 2;

Qy 1 MHGDPRLHEMYLMLL---OPEITDLYXXQXNDSSSEEDIDGPAQAEPDRAH----- 51

Db 1 MIGKPTLEDVLVLPQPPQPVVLMCYEQLSSSEDEDDVHHNNQQQHHQHARPEV 60

Qy 52 -----YNIYTFCKCDSTLRKCVOSTHVDIRTLDELMLGTLGIYXPICSOK 97

Db 61 PEDDDCRIVSDCYSCGKRLVYVSSSHELRVLEDLMLGTLDIYCPSCASR 112

RESULT 11

S36562

E7 protein - human papillomavirus type 45

C:Species: human papillomavirus type 45

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36562

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36562

A:Molecule type: DNA

A:Residues: 1-106

A:Cross-references: UNIPROT:P21736; UNIPARC:UPI0000138416; EMBL:X74479; NID:g397022; PIDR

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 41.2%; Score 213; DB 2; Length 106;

Best Local Similarity 43.8%; Pred. No. 1.4e-16;

Matches 46; Conservative 15; Mismatches 32; Indels 12; Gaps 3;

Qy 1 MHGDPRLHEMYLLOPET--TDLYXXYQXQNDSSSEEDIDG-----PAGAEPDRA 50

Db 1 MHGPRETLQETVLHLEQONELDPVLDLCYEQLSSSEEDNDADVSQAQLPARAEFOR- 59

Qy 51 HNYIVTFCKCDSTLRKCVOSTHVDIRTLDELMLGTLGIYXPICS 95

Db 60 -HKLVCCKCDGRILTVSSAEDLRTIQQLFLSTISFVCPMCA 103

RESULT 12

S36504

E7 protein - human papillomavirus type 30

C:Species: human papillomavirus type 30

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36504

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36504

A:Molecule type: DNA

A:Residues: 1-105

A:Cross-references: UNIPROT:P36826; UNIPARC:UPI0000138409; EMBL:X74474; NID:g396973; PIDR

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 40.5%; Score 209.5; DB 2; Length 105;

Best Local Similarity 45.2%; Pred. No. 3.5e-16;

Matches 47; Conservative 17; Mismatches 33; Indels 7; Gaps 4;

Qy 1 MHGDPRLHEMYLLOPET--TDLYXXYQXQNDSSSEEDIDG---PAGAEPDRAH--YN 53

Db 1 MHGKVTIIPYIIDLVPQTEIDHLCYEQLSSSEEDDEVDNLOKQOQARQEHQHCYL 60

Qy 54 IVTFCKCDSTLRKCVOSTHVDIRTLDELMLGTLGIYXPICSOK 97

Db 61 INTGCRCAVQVLAVQSPVKELRALQMLGALVELVCPICATR 104

RESULT 13

S36528

E7 protein - human papillomavirus type 53

C:Species: human papillomavirus type 53

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36528

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36528

A:Molecule type: DNA

A:Residues: 1-105

A:Cross-references: UNIPROT:P36832; UNIPARC:UPI000013841D; EMBL:X74482; NID:g397046; PIDR

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 40.3%; Score 208.5; DB 2; Length 105;

Best Local Similarity 43.3%; Pred. No. 4.5e-16;

Matches 45; Conservative 23; Mismatches 29; Indels 7; Gaps 4;

Qy 1 MHGDTPTLHEHYMLDLOPFT-TDLYXXYXQLNDS-SEEBEDID---GRAGQAEPPRAH--YN 53
 Db 1 MGNVNTLPQYXIELLPQTEIDQLQCHQNLSSSEDEBDEVDHLQEQPQARDEQPCYL 60

Qy 54 IYTPCCCKDSTLRCLVOSTHVDIRTLBDMGLTGLIYXPCISQK 97
 Db 61 IETGCCRCESLVQANVQSTKEIRILQOMLGMSTVELVCPICATR 104

RESULT 14

W7ML13
 E7 protein - human papillomavirus type 13
 C/Species: human papillomavirus type 13
 A/Note: host Homo sapiens (man)
 C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C/Accession: B42955
 R:van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Odenakker, G.
 Virology 190, 587-596, 1992
 A/Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Comparison of the sequences of the early proteins and the DNA
 A/Reference number: A42955; PMID:92391075; PMID:1325697
 A/Accession: B42955
 A/Molecule type: DNA
 A/Residues: 1-101 <VAN>
 A/Cross-references: UNIPROT:Q02271; UNIPARC:UPI00001383F9; EMBL:X62843; NID:G60295; PIDN:C/Superfamily: papillomavirus E7 protein
 C/Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F/61-97/Region: zinc finger CCCC motif

Query Match 38.8%; Score 200.5; DB 1; Length 101;
 Best Local Similarity 44.7%; Pred. No. 3.3e-15;
 Matches 46; Conservative 13; Mismatches 35; Indels 9; Gaps 2;

Qy 1 MHGDTPTLHEHYMLDLOPFTTDLXXYXQLNDSSEEBEDIDGPAGQAEPPRAH-----YNT 54
 Db 1 MHGKTYTLKQIVLFDLPVGLHCNEQLDSS---EDEVDQAOATQATQSTLLQCYQI 57

Qy 55 VTFCCCKDSTLRCLVOSTHVDIRTLBDMGLTGLIYXPCISQK 97
 Db 58 LTSCSKCCSNVRLVWECTGPDHDLHDLGLTINIVCPICAPK 100

RESULT 15

W7ML18
 E7 protein - human papillomavirus type 18
 C/Species: human papillomavirus type 18
 C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
 C/Accession: B26165; H26251
 R:Seedorf, K.; Oltersdorf, T.; Kraemer, G.; Roewekamp, W.
 EMBO J. 6, 139-144, 1987
 A/Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16) and type 18 (HPV 18)
 A/Reference number: A91068; PMID:87218459; PMID:3034571
 A/Accession: B26165
 A/Molecule type: DNA
 A/Residues: 1-105 <SEB>
 A/Cross-references: UNIPROT:P06788; UNIPARC:UPI0000000DB5; GB:X04773; NID:G60876; PIDN:C/Superfamily: papillomavirus E7 protein

A/Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 16 (HPV 16) and type 18 (HPV 18) nucleotide sequences
 A/Reference number: A92937; PMID:87283882; PMID:3039146
 A/Accession: H26251
 A/Molecule type: DNA
 A/Residues: 1-105 <COL>
 A/Cross-references: UNIPARC:UPI0000000DB5; GB:X05015; NID:G60975; PIDN:CAA28665.1; PID:G60975
 C/Keywords: DNA binding; early protein; transcription regulation

Query Match 38.8%; Score 200.5; DB 1; Length 105;
 Best Local Similarity 39.6%; Pred. No. 3.5e-15;
 Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

Qy 1 MHGDTPTLHEHYMLDLOPFT-TDLYXXYXQLNDSSEEBEDIDG-----PAGQAEPPRAH 51
 Db 1 MHGKATLQIVLHLEPQNEIPVDLCHQQLSDSEENDEIDGYNHGLPARRAEPPR-- 58

Qy 52 YNIVTFCCCKDSTLRCLVOSTHVDIRTLBDMGLTGLIYXPCISQK 97
 Db 59 HTMLCMCKCEARIELVESSADDLRAFOQLFINTLSFVCPWCASQ 104

RESULT 16

W7MLC1
 E7 protein - pygmy chimpanzee papillomavirus (type 1)
 C/Species: pygmy chimpanzee papillomavirus
 C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jul-1999
 C/Accession: B36818
 R:van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Odenakker, G.
 Virology 190, 587-596, 1992
 A/Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Comparison of the sequences of the early proteins and the DNA
 A/Reference number: A42955; PMID:92391075; PMID:1325697
 A/Accession: B36818
 A/Molecule type: DNA
 A/Residues: 1-98 <VAN>
 A/Cross-references: UNIPARC:UPI000013842E; EMBL:X62844; NID:G61010; PIDN:CAA44656.1; PIDN:CAA44656.1
 C/Superfamily: papillomavirus E7 protein
 C/Keywords: DNA binding; early protein; transcription regulation; transforming protein; zinc finger
 F/58-94/Region: zinc finger CCCC motif

Query Match 37.5%; Score 194; DB 1; Length 98;
 Best Local Similarity 46.4%; Pred. No. 1.7e-14;
 Matches 45; Conservative 13; Mismatches 35; Indels 4; Gaps 2;

Qy 1 MHGDTPTLHEHYMLDLOPFTTDLXXYXQLNDSSEEBEDIDGPAGQAEPPRAH--RAHNYITFC 58
 Db 1 MHGKTYTLKQIVLFDLPVGLHCNEQLD--SSEBDEVDQAOATQATQSTLLQCYQI 58

Qy 59 CKCDSTLRCLVOSTHVDIRTLBDMGLTGLIYXPCISQK 95
 Db 59 GQCDSDNVRLVWECTGSDIDHRLHLLGLTINIVCPICLA 95

RESULT 17

W7ML42
 E7 protein - human papillomavirus type 42
 C/Species: human papillomavirus type 42
 A/Note: host Homo sapiens (man)
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C/Accession: F39451
 R:Phillips, W.; Honore, N.; Sapp, M.; Cole, S.T.; Strecek, R.E.
 Virology 186, 331-334, 1992
 A/Title: Human papillomavirus type 42: new sequence, conserved genome organization.
 A/Reference number: A39451; PMID:92087479; PMID:1309278
 A/Accession: F39451
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-93 <PHI>
 A/Cross-references: UNIPROT:P27231; UNIPARC:UPI0000138414; GB:M73236
 C/Superfamily: papillomavirus E7 protein
 C/Keywords: DNA binding; early protein; transcription regulation

Query Match 35.5%; Score 183.5; DB 1; Length 93;
 Best Local Similarity 44.4%; Pred. No. 2.4e-13;
 Matches 44; Conservative 17; Mismatches 27; Indels 11; Gaps 4;

Qy 1 MHGDTPTLHEHYMLDLOP-ET-TDLYXXYXQLNDSSEEBEDIDGPAGQAEPPRAHNYITFC 57
 Db 1 MHGKTYTLKQIVLFDLPVGLHCNEQLD--SSEBDEVDQAOATQATQSTLLQCYQI 52

Qy 58 CKCDSTLRCLVOSTHVDIRTLBDMGLTGLIYXPCISQK 96
 Db 53 CTQCYKSVKLWQCTEADIRNLQOMLGLTIDYCPICAR 91

RESULT 18

B44890
 E7 protein - human papillomavirus type 66
 C/Species: human papillomavirus type 66

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C/Accession: B44890
R/Taxweed, A.R.; Beaudenon, S.; Favre, M.; Orth, G.
J. Clin. Microbiol. 29, 2656-2660, 1991
A>Title: Characterization of human papillomavirus type 66 from an invasive carcinoma of
A/Reference number: A44890; MUID:92123556; PMID:1663515
A/Accession: B44890
A/Molecule type: DNA
A/Residues: 1-105 <TAM>
A/Cross-references: UNIPROT:Q80956; UNIPARC:UPI0000138426
A/Note: sequence extracted from NCBI backbone (NCBI:78637, NCBI:78639)
C/Superfamily: papillomavirus E7 protein
C/Keywords: DNA binding; early protein; transcription regulation

Query Match 35.5%; Score 183.5; DB 2; Length 105;
Best Local Similarity 42.7%; Pred. No. 2.7e-13;
Matches 44; Conservative 17; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MHGDTPTLHEWMLDQPT-TDLYXXYQJNDS-SEEDSID-----GPAGQAEPPRAHY 52
Db 1 MHGKVPPTQEVILEAPTEIDLDQCNEDSDSEDEDDHLLERPGQAQAQGHNC-Y 59
Qy 53 NITPCKCKDSTLRLCVOSTHVDIRTEEDLLMGLTGIYPICS 95
Db 60 LIHPCCCKCELVQDIOSTKEELRVVQQLMGALTVCPLCA 102

RESULT 19
S15622
E7 protein - human papillomavirus type 57
C/Species: human papillomavirus type 57
A/Note: host Homo sapiens (man)
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
A/Accession: S15622
R/Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A>Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and
A/Reference number: S15614; MUID:91188699; PMID:1964523
A/Accession: S15622
A/Molecule type: DNA
A/Residues: 1-92 <HIR>
A/Cross-references: UNIPROT:P2160; UNIPARC:UPI0000138421; EMBL:X55965; NID:g60882; PIDN
C/Superfamily: papillomavirus E7 protein
C/Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:55-91/Region: zinc finger CCCC motif

Query Match 34.5%; Score 178.5; DB 1; Length 92;
Best Local Similarity 43.3%; Pred. No. 8.6e-13;
Matches 42; Conservative 15; Mismatches 31; Indels 9; Gaps 3;

Qy 1 MHGDTPTLHEWMLDQ-PEFTDLYXXYQJNDSSEED-EIDGPAQAEPPRAHYNTVF 57
Db 1 MHGKVPPTQEVILEAPTEIDLDQCNEDSDSEDEDDHLLERPGQAQAQGHNC-Y 59
Qy 58 CCKCDSTLRLCVOSTHVDIRTEEDLLMGLTGIYPICS 94
Db 55 CCKCHSTRLVYECGADIRHLEQLFLNTLTIVCPRC 91

RESULT 20
S36580
E7 protein - human papillomavirus type 56
C/Species: human papillomavirus type 56
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
A/Accession: S36580
R/Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36580
A/Molecule type: DNA
A/Residues: 1-105
A/Cross-references: UNIPROT:P36633; UNIPARC:UPI0000138420; EMBL:X74483; NID:g397053; PMID:

```

C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation
Query Match 34.5%; Score 178.5; DB 2; Length 105;
Best Local Similarity 40.8%; Pred. No. 9, 9e-13;
Matches 42; Conservative 17; Mismatches 35; Indels 9; Gaps 3;

Qy 1 MHGDPPTLHEWMLDQPER-TDLVYXXQLNDSEEDDEIDGPAQAPBRDH-----Y 52
Db 1 MHGKPTLDVVLLELPQETIDLCNEQL-DSSEDEDEVDHLQERPDQARQAKHTCY 59
53 NIVTFCKCKDSTLRKCVGOSTHVDIRTLBMLMGLGIVPICS 95
60 LIHVPCKECKFVQDLIDQSTKEDLRVQQLMGALVTTCPLCA 102

RESULT 21
S36585
E7 protein - human papillomavirus type 7
C:Species: human papillomavirus type 7
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36585
Ridelius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36585
A:Molecule type: DNA
A:Residues: 1-111 <DEL>
A:Cross-References: UNIPROT:P36816; UNIPARC:UPI00001383F3; EMBL:X74463; NID:g397060; PIDD
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 34.5%; Score 178.5; DB 2; Length 111;
Best Local Similarity 39.8%; Pred. No. 1e-12;
Matches 45; Conservative 12; Mismatches 33; Indels 23; Gaps 3;

Qy 1 MHGDPPTLHEWMLDQPERTTDLVYXXQLNDSEEDDEIDGPAQAPBRDH----- 51
Db 1 MHGEPPTLGDIVLDLPQEPVSLSCNEQL-DSSEEDDHE-----QDOLDSHNRQEQPTQ 55
52 -----YNIVTFCKCKDSTLRKCVGOSTHVDIRTLBMLMGLGIVPICS 95
56 ODLYVNLQSFKIVTHCVFCHCLRVLVHACTADIRQVHQLMGLTINVCNCA 108

RESULT 22
W7ML51
E7 protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A>Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: F40415
R:lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type
A:Reference number: A40415; MUID:91303675; PMID:1649326
A:Accession: F40415
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-101 <LUN>
A:Cross-References: UNIPROT:P26558; UNIPARC:UPI000013841B; GB:M62877
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 34.4%; Score 178; DB 1; Length 101;
Best Local Similarity 41.0%; Pred. No. 1.1e-12;
Matches 41; Conservative 16; Mismatches 37; Indels 6; Gaps 3;

Qy 1 MHGDPPTLHEWMLDQPER-TDLVYXXQLNDSEEDDEIDGPAQAPBRDH-----YNI 55
Db 1 MHGVPQLKDVVLHLTPQETIDLCNEQF-DSSEDEVDNMKQDLPEPPAQATCYRIE 59

```

QY 56 TPCKCDSTLRKLCVOSTHVDIRTLBLLMGLTGLIYXPCIS 95
 DB 60 APCRCSSVAVQLAVASSSGDTLRVQOMLWGLSLVCPCCA 99

RESULT 23

S15615
 E7 protein - human papillomavirus type 2a
 C:Species: human papillomavirus type 2a
 A:Note: host Homo sapiens (man)
 C>Date: 17-Feb-1994 #sequence_rev: 17-Feb-1994 #text_change 09-Jul-2004
 C:Accession: S15615
 R:Ritzsch-Behnam, A.; Delius, H.; de Villiers, E.M.
 Virus Res. 18, 81-98, 1990
 A>Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and
 A:Reference number: S15614, PMID:91186699; PMID:1964523
 A:Accession: S15615
 A:Molecule type: DNA
 A:Residues: 192 <HR>
 A:Cross-references: UNIPROT:P25485; UNIPARC:UPI0000138408; EMBL:X55964
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F:55-91/Region: zinc finger CCCC motif

Query Match 33.9%; Score 175.5; DB 1; Length 92;
 Best Local Similarity 43.3%; Pred. No. 1.8e-12;
 Matches 42; Conservative 13; Mismatches 35; Indels 7; Gaps 3;

QY 1 MHGDTPLHEH--YMLDLPETDLYXXQLNDSSEEDIDGPAQAEPDRAHYNIYVFC 58
 DB 1 MGNRRSLKNDITLIDELIPVILHCHDEQ--DSSEENHNG---LTFPVOAYGVVTTTC 55

QY 59 CKCDSTLRKLCVOSTHVDIRTLBLLMGLTGLIYXPCIS 95
 DB 56 CKCGRTVRLVVECGQADRLRELQFLFKTLTVCPHCA 92

RESULT 24

S36533
 E7 protein - human papillomavirus type 10
 C:Species: human papillomavirus type 10
 C>Date: 20-Feb-1995 #sequence_rev: 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S36533
 R:Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469
 A:Accession: S36533
 A:Molecule type: DNA
 A:Residues: 1-86
 A:Cross-references: UNIPROT:P36818; UNIPARC:UPI00001383F6; EMBL:X74465; NID:G396901; PID
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 33.6%; Score 173.5; DB 2; Length 86;
 Best Local Similarity 42.6%; Pred. No. 2.9e-12;
 Matches 40; Conservative 10; Mismatches 35; Indels 9; Gaps 2;

QY 1 MHGDTPLHEHMDLP--ETTDLYXXQLNDSSEEDIDGPAQAEPDRAHYNIYVFC 60
 DB 1 MGNRRSLKNDITLIDELIPVILHCHDEQ--DSSEENHNG---LTFPVOAYGVVTTTC 51

QY 61 CDSTLRKLCVOSTHVDIRTLBLLMGLTGLIYXPCIS 94
 DB 52 CSLPLRLVVECSHADIRALQOLLGLTGLVCPHCA 85

RESULT 25

S36480
 E7 protein - human papillomavirus type 17
 C:Species: human papillomavirus type 17
 C>Date: 20-Feb-1995 #sequence_rev: 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S36480

R:Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469
 A:Accession: S36480
 A:Molecule type: DNA
 A:Residues: 1-95
 A:Cross-references: UNIPROT:P36821; UNIPARC:UPI00001383F8; EMBL:X74469; NID:G396932; PID

C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 32.9%; Score 170; DB 2; Length 95;
 Best Local Similarity 42.4%; Pred. No. 7.8e-12;
 Matches 42; Conservative 15; Mismatches 32; Indels 10; Gaps 3;

QY 1 MHGDTPLHEHMDLP--ETTDLYXXQLNDSSEEDIDGPAQAEPDRAHYNIYVFC 58
 DB 1 MGNRRSLKNDITLIDELIPVILHCHDEQ--DSSEENHNG---LTFPVOAYGVVTTTC 52

QY 59 CKCDSTLRKLCVOSTHVDIRTLBLLMGLTGLIYXPCIS 97
 DB 53 CFCSSKRLRLVAVTAGIRSQEBLLGEVQLVCPNCREK 91

RESULT 26

W7MLJ3
 E7 protein - human papillomavirus type 39
 C:Species: human papillomavirus type 39
 A:Note: host Homo sapiens (man)
 C>Date: 31-Dec-1991 #sequence_rev: 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: B38502
 R:Volpert, C.; Screcek, R.E.
 Virology 181, 419-423, 1991
 A>Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
 A:Reference number: A38502; PMID:1847266
 A:Accession: B38502
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-109 <VOL>
 A:Cross-references: UNIPROT:P24837; UNIPARC:UPI0000138411; GB:M62849; EMBL:M8185; NID:G

C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 32.9%; Score 170; DB 1; Length 109;
 Best Local Similarity 39.1%; Pred. No. 9.1e-12;
 Matches 43; Conservative 16; Mismatches 31; Indels 20; Gaps 4;

QY 1 MHGDTPLHEHMDLP--ETTDLYXXQLNDSSEEDIDGPAQAEPDRAHYNIYVFC 45
 DB 1 MGNRRSLKNDITLIDELIPVILHCHDEQ--DSSEENHNG---LTFPVOAYGVVTTTC 57

QY 46 EPDRAHYNIYVFCCKCDSTLRKLCVOSTHVDIRTLBLLMGLTGLIYXPCIS 95
 DB 58 EPQR--HTICSCCKCNTLQLVVEASRDTRLQQLFMDSLGFCVPCWCA 105

RESULT 27

S36510
 E7 protein - human papillomavirus type 32
 C:Species: human papillomavirus type 32
 C>Date: 20-Feb-1995 #sequence_rev: 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S36510
 R:Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469
 A:Accession: S36510
 A:Molecule type: DNA
 A:Residues: 1-104
 A:Cross-references: UNIPROT:P36827; UNIPARC:UPI0000138408; EMBL:X74475; NID:G396981; PID

C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation

E7 protein - human papillomavirus type 19
C:Species: human papillomavirus type 19
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: G36486
R:DeJure, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36486
A:Molecule type: DNA
A:Residues: 1-102
A:Cross-references: UNIPROT:P36822; UNIPARC:UPI00001383FC; EMBL:X74470; NID:G396940; PIDD:G396940
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 22.5%; Score 116.5; DB 2; Length 102;
Best Local Similarity 32.7%; Pred. No. 7.8e-06;
Matches 33; Conservative 18; Mismatches 35; Indels 15; Gaps 4;

Qy 1 MHGDPPTLHEHYMLD---QPEPT--TDLYXXYQLNDSSEEDDEIDGPAQAQEP--DRAHYN 53
Db 1 MIGKEVILQDVLVELSELQPEVQPVDFLCEBELPFEQGETE-----EPALERSAYK 52
54 IVTFCKKCDSTLRLCVOSTHVDIRTELDLNGTGLIYXPIC 94
53 VVVLGGCKVKLRIFVKATQFGIRTLQDILIEELQLLCPCC 93

RESULT 38

W7ML47
E7 protein - human papillomavirus type 47
C:Species: human papillomavirus type 47
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: B35324
R:Kiyono, T.; Adachi, A.; Ishibashi, M.
Virology 177, 401-405, 1990
A:Title: Genome organization and taxonomic position of human papillomavirus type 47 infect
A:Reference number: A35324; MUID:90281611; PMID:2162112
A:Accession: B35324
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-103 <KIT>
A:Cross-references: UNIPROT:P22423; UNIPARC:UPI0000138417; GB:M32305; NID:G333062; PIDD:
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 21.9%; Score 113; DB 1; Length 103;
Best Local Similarity 31.7%; Pred. No. 1.9e-05;
Matches 32; Conservative 21; Mismatches 34; Indels 14; Gaps 5;

Qy 1 MHGDPPTLHEHYMLD---QPEPT--TDLYXXYQLNDSSEEDDEIDGPAQAQEPDRAHYNIV 55
Db 1 MIGKEVITRDIVLELSEVQPEVLPVDFLFCDEBELPNEGQAEBELD-----IDRVVFKVI 53
56 TFC-QK-CDSTLRLCVOSTHVDIRTELDLNGTGLIYXPIC 94
54 APCGSCCEVKLRIFVNATNRGIRTFDELLTGDLQLLCPCC 94

RESULT 39

W7WLS
E7 protein - human papillomavirus type 5
C:Species: human papillomavirus type 5
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: G26277
R:Zachow, K.R.; Ostrow, R.S.; Farae, A.J.
Virology 158, 251-254, 1987
A:Title: Nucleotide sequence and genome organization of human papillomavirus type 5.
A:Reference number: A94360; MUID:87207670; PMID:3033892
A:Accession: G26277
A:Molecule type: DNA
A:Residues: 1-103 <ZAC>

```

C1:Cross-references: UNIPROT:P06932; UNIPARC:UPI000000130G; GB:M17463; NID:G333071; PIDN:
C1:Superfamily: papillomavirus E7 protein
C1:Keywords: DNA binding; early protein; transcription regulation

Query Match      21.7%; Score 112; DB 1; Length 103;
Best Local Similarity 31.7%; Pred. No. 2,5e-05;
Matches 32; Conservative 18; Mismatches 37; Indels 14; Gaps 5;

OY
1 MHGDPPTLHEWLDL---OPET--TDLYXXYLNDSSSEEDDIDGPAQAEPRAHYNIV 55
1 M1GKEVTVQDIIILESEVQPEVLPVDFCEEELPNEQETEEBBDN-----ERISYKVI 53
Db
56 TFC-CK-CDSTLRCLCVQSTHVDIRTLIEDLLMGTLGIVXPIC 94
54 APCGGRNCEVKKIRIFVHATFEGIRAFQQLLTGDLQLCCDC 94

RESULT 40
WTMLB
E7 protein - human papillomavirus type 5b
C1:Species: human papillomavirus type 5b
A1:Note: host Homo sapiens (man)
C1:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #ext_change 09-Jul-2004
C1:Accession: P40480
R1:Yabe, Y.; Sakai, A.; Hitsunoto, T.; Kato, H.; Ogura, H.
V1:ology 183, 793-798, 1991
A1>Title: A subtype of human papillomavirus 5 (HPV-5b) and its subgenomic segment amplified
A1:Reference number: A40480; MUID:913106467; PMID:1649510
A1:Accession: P40480
A1>Status: translation not shown
A1:Molecule type: DNA
A1:Residues: 1-103 <YAB>
A1:Cross-references: UNIPROT:P26559; UNIPARC:UPI00000006C7; GB:D90252; NID:G222395; PIDN:
C1:Superfamily: papillomavirus E7 protein
C1:Keywords: DNA binding; early protein; transcription regulation

Query Match      21.1%; Score 109; DB 1; Length 103;
Best Local Similarity 31.7%; Pred. No. 5,4e-05;
Matches 32; Conservative 18; Mismatches 37; Indels 14; Gaps 5;

OY
1 MHGDPPTLHEWLDL---OPET--TDLYXXYLNDSSSEEDDIDGPAQAEPRAHYNIV 55
1 M1GKEVTVQDIIILESEVQPEVLPVDFCEEELPNEQETEEBBDN-----TERISYKVI 53
Db
56 TFC-CK-CDSTLRCLCVQSTHVDIRTLIEDLLMGTLGIVXPIC 94
54 APCGGRNCEVKKIRIFVHATFEGIRAFQQLLTGDLQLCCDC 94

RESULT 41
WTMLB
E7 protein - human papillomavirus type 8
C1:Species: human papillomavirus type 8
C1:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #ext_change 09-Jul-2004
C1:Accession: A03691
R1:Fuchs, P.G.; Iftner, T.; Wenzinger, J.; Pfister, H.
V1:Virol. 58, 626-634, 1986
A1>Title: Epidermodysplasia verruciformis-associated human papillomavirus 8: genomic sequ
A1:Reference number: A93019; MUID:86200410; PMID:3009874
A1:Accession: A03691
A1:Molecule type: DNA
A1:Residues: 1-103 <FUC>
A1:Cross-references: UNIPROT:P06430; UNIPARC:UPI00001383F4; GB:M12737; NID:G333074
A1:Note: This ORF is not annotated in GenBank entry PPH8C3
C1:Superfamily: papillomavirus E7 protein
C1:Keywords: DNA binding; early protein; transcription regulation

Query Match      20.3%; Score 105; DB 1; Length 103;
Best Local Similarity 32.7%; Pred. No. 0.00015;
Matches 33; Conservative 17; Mismatches 37; Indels 14; Gaps 5;

OY
1 MHGDPPTLHEWLDL---DIQPER--TDLYXXYLNDSSSEEDDIDGPAQAEPRAHYNIV 55

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Db 1 MICKETVADPVLKLSIPEVLPVLDLCEBELFNEQTEBELD-----IERTVKIV 53
Qy 56 TFC-CK-CDSTLRLCVOSTHVDIRTELDLMGTGIVXPIC 94
Db 54 APCGCCCCQVKLRIFVATDSGIRTFQELLFRDLQLCPFC 94

RESULT 42
W7WLRB
E7 protein - cottontail rabbit papillomavirus
C:Species: cottontail rabbit papillomavirus
C>Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 16-Feb-1997
C:Accession: A03692
R:Giri, I.; Danos, O.; Yaniv, M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985
A:Title: Genomic structure of the cottontail rabbit (Shope) papillomavirus.
A:Reference number: A94027; PMID:85166175; PMID:2984661
A:Accession: A03692
A:Molecule type: DNA
A:Residues: 1-94 <GIR>
A:Cross-references: UNIPARC:UPI0000000954
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 16.8%; Score 87; DB 1; Length 94;
Best Local Similarity 32.6%; Pred. No. 0.014;
Matches 31; Conservative 15; Mismatches 45; Indels 4; Gaps 4;

Qy 1 MHGDTPLHEVMDLOPETTDLYXXYXQUNDSEEEDEIDGPAQAPDRAHNYITFCCK 60
Db 1 MGRPTPLSELVGETMELSLHCDLELNESDDDEE-DHDDQVFIERR-YANVSVCCK 58

Qy 61 CDSTLR-LCVOSTHVDIRTELDLMGTGIVXPIC 94
Db 59 CROTFSEVCAPFA-IRTLNRLSASLSIVCPFC 92

RESULT 43
B61399
early protein E7 - bovine papillomavirus type 4
C:Species: bovine papillomavirus type 4
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: B61399
R:Jackson, M.E.; Pennie, W.D.; McCaffery, R.E.; Smith, K.T.; Grindley, G.J.; Campo, M.S.
Mol. Cell. Biol. 14, 382-387, 1994
A:Title: The B subgroup bovine papillomaviruses lack an identifiable E6 open reading frame
A:Reference number: A61399; PMID:9200191; PMID:1654923
A:Accession: B61399
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <JAC>
A:Cross-references: UNIPROT:Q7LZV7; UNIPARC:UPI000002F8BF; GB:X59063
C:Superfamily: bovine papillomavirus type 4 E6 protein

Query Match 16.2%; Score 83.5; DB 2; Length 98;
Best Local Similarity 27.0%; Pred. No. 0.036;
Matches 27; Conservative 16; Mismatches 40; Indels 17; Gaps 4;

Qy 1 MHGDTPLHEVMDLOPETTDLYXXYXQUNDSEEE--DEIDGPAQAPDRAHNYITFC 57
Db 1 MKGQNTLQDAILED-----TISPINLHCEIEIEBVDTP-----NPFATAT 46

Qy 58 CCKCDSTLRLCVOSTHVDIRTELDLMGTGIVXPIC 97
Db 47 CYACEQVRLALVSTEGIHQLQLLFDNLFLCAACSKQ 86

RESULT 44
S19907
E7-C protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S19907

R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me
submitted to the EMBL Data Library, January 1992
A:Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via tr
A:Reference number: S19906
A:Accession: S19907
A:Molecule type: mRNA
A:Residues: 1-55 <SNI>
A:Cross-references: UNIPROT:Q81866; UNIPARC:UPI00000F593F; EMBL:X64086; NID:g60282; PIDN
C:Superfamily: papillomavirus E7 protein
C:Keywords: early protein

Query Match 15.5%; Score 80; DB 2; Length 55;
Best Local Similarity 55.6%; Pred. No. 0.047;
Matches 15; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 71 STHVDIRTELDLMGTGIVXPIC 97
Db 29 STASDLRTIQQLMGVTVIVCPFC 55

RESULT 45
A61399
early protein E7 - bovine papillomavirus type 3
C:Species: bovine papillomavirus type 3
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A61399
R:Jackson, M.E.; Pennie, W.D.; McCaffery, R.E.; Smith, K.T.; Grindley, G.J.; Campo, M.S.
Mol. Cell. Biol. 14, 382-387, 1994
A:Title: The B subgroup bovine papillomaviruses lack an identifiable E6 open reading fra
A:Reference number: A61399; PMID:9200191; PMID:1654923
A:Accession: A61399
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <JAC>
A:Cross-references: UNIPROT:Q8BD8; UNIPARC:UPI00000FA386; GB:X59062
C:Superfamily: bovine papillomavirus type 4 E6 protein

Query Match 15.4%; Score 79.5; DB 2; Length 98;
Best Local Similarity 25.3%; Pred. No. 0.099;
Matches 25; Conservative 19; Mismatches 40; Indels 15; Gaps 3;

Qy 1 MHGDTPLHEVMDLOPETTDLYXXYXQUNDSE--EEDIDGPAQAPDRAHNYITFC 58
Db 1 MKGQDTLKNVAVLEIVSPF-----ILDCIEIEBVDTP-----APFAVEAVC 47

Qy 59 CCKCDSTLRLCVOSTHVDIRTELDLMGTGIVXPIC 97
Db 48 YVCENPLRLALVSPDGIHQHLQQLDLCISILCANCSRE 86

RESULT 46
W7WLRB
E7 protein - deer papillomavirus
C:Species: deer papillomavirus
C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 16-Feb-1997
C:Accession: A03693
R:Groff, D.B.; Lancaster, W.D.
J. Virol. 56, 85-91, 1985
A:Title: Molecular cloning and nucleotide sequence of deer papillomavirus.
A:Reference number: A93013; PMID:85293253; PMID:2993669
A:Accession: A03693
A:Molecule type: DNA
A:Residues: 1-102 <GRO>
A:Cross-references: UNIPARC:UPI00001749SD
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 15.0%; Score 77.5; DB 1; Length 102;
Best Local Similarity 32.3%; Pred. No. 0.17; 31; Indels 3; Gaps 2;
Matches 20; Conservative 8; Mismatches 31; Indels 3; Gaps 2;

Qy 38 IDGPAQAPDRAHNYITFCCKCDSTLRLCVOSTHVDIRTELDLMGTGIVXPIC 95

Db 119 TANLINCKPKMDL-----SEQLDSTLTEN 144

RESULT 51
148733
protein kinase rck (EC 2.7.1.-) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C:Accession: I48733; S24241
R:Blatt, P.; Birnmeier, C.
D:Differentiation 53, 115-122, 1993
A:Title: Characterization and expression analysis of the murine rck gene: a protein kinase
A:Reference number: I48733; PMID:9336030; PMID:8359591
A:Accession: I48733
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-622 <RES>
A:Cross-references: UNIPROT:Q04859; UNIPARC:UPI000002747F; EMBL:X66983; NID:G53913; PIDD:R.Blatt, P.; Birnmeier, C.
Submitted to the EMBL Data Library, June 1992
A:Description: The murine rck gene encodes a protein kinase with a potential function in
A:Reference number: S24241
A:Accession: S24241
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-622 <BLA>
A:Cross-references: UNIPARC:UPI000002747F; EMBL:X66983; NID:G53913; PIDD:CAA47392.1; PIDD:Genetics:
A:Gene: rck
A:Keywords: ATP; phosphotransferase
F:2-260/Domain: protein kinase homology <KIN>
F:10-18/Region: protein kinase ATP-binding motif

Query Match 13.2%; Score 68; DB 2; Length 622;
Best Local Similarity 32.3%; Pred. No. 14;
Matches 20; Conservative 8; Mismatches 16; Indels 18; Gaps 3;

QY 2 HGCT-PTLHEVMDLPETTDLYXKQINDSBEDE-----IDGAGQAEPPRAHYNI 54
Db 296 HLDTKQTLHKQLPPLRPK-----PSSSRDPKPLPNTLDPAQGPQPKQGIQL 344

QY 55 VT 56
Db 345 QT 346

RESULT 52
S37431
ankyrin 2, neuronal long splice form - human
N:Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid
N:Contains: ankyrin 2, short form
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
R:Chan, W.
Submitted to the EMBL Data Library, September 1993
A:Reference number: S37431
A:Accession: S37431
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-3924 <CHA>
A:Cross-references: UNIPROT:Q01484; UNIPARC:UPI0000125B19; EMBL:Z26634; NID:G406287; PIDD:R:Chan, W.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
J. Cell Biol. 114, 241-253, 1991
A:Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a
A:Reference number: A39643; MUID:91302466; PMID:1830053
A:Accession: A39643
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2077 <OTI>
A:Cross-references: UNIPARC:UPI0000177547; GB:X56957
A:Accession: B39643
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-1443, 3585-3924 <OTT>
A:Cross-references: UNIPARC:UPI0000177548; EMBL:X56958
R:Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward, G.
Genomics 10, 858-866, 1991
A:Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
A:Reference number: A40334; MUID:92009921; PMID:1833308
A:Accession: A40334
A:Molecule type: DNA
A:Residues: 463-474, 'PE', 477-495 <TSE>
A:Cross-references: UNIPARC:UPI000016A5B5; GB:M37123; NID:G178647; PIDD:AAA62828.1; PIDD:R:Chan, W.; Kordeli, E.; Bennett, V.
J. Cell Biol. 123, 1463-1473, 1993
A:Title: 440-kD ankyrin: structure of the major developmentally regulated domain and seq
A:Reference number: A49462; MUID:94075409; PMID:8253844
A:Accession: A49462
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-3924 <RES>
A:Cross-references: UNIPARC:UPI0000125B19; EMBL:Z26634; NID:G406287; PIDD:CAA81387.1; PIDD:Genetics:
A:Gene: GDB:ANK2
A:Map position: 4q25-4q27
A:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:2-3924/Product: ankyrin 2, long form #status predicted <MAT>
F:2-1443, 3585-3924/Product: ankyrin 2, short form #status predicted <MA2>
F:63-95/Domain: ankyrin repeat homology <AN01>
F:96-128/Domain: ankyrin repeat homology <AN02>
F:129-161/Domain: ankyrin repeat homology <AN03>
F:162-190/Domain: ankyrin repeat homology <AN04>
F:191-223/Domain: ankyrin repeat homology <AN05>
F:232-264/Domain: ankyrin repeat homology <AN06>
F:265-297/Domain: ankyrin repeat homology <AN07>
F:298-330/Domain: ankyrin repeat homology <AN08>
F:331-363/Domain: ankyrin repeat homology <AN09>
F:364-396/Domain: ankyrin repeat homology <AN10>
F:397-429/Domain: ankyrin repeat homology <AN11>
F:430-462/Domain: ankyrin repeat homology <AN12>
F:463-495/Domain: ankyrin repeat homology <AN13>
F:496-528/Domain: ankyrin repeat homology <AN14>
F:529-561/Domain: ankyrin repeat homology <AN15>
F:562-594/Domain: ankyrin repeat homology <AN16>
F:595-627/Domain: ankyrin repeat homology <AN17>
F:628-660/Domain: ankyrin repeat homology <AN18>
F:661-693/Domain: ankyrin repeat homology <AN19>
F:694-726/Domain: ankyrin repeat homology <AN20>
F:727-759/Domain: ankyrin repeat homology <AN21>
F:760-792/Domain: ankyrin repeat homology <AN22>
F:793-825/Domain: ankyrin repeat homology <AN23>

Query Match 13.2%; Score 68; DB 2; Length 3924;
Best Local Similarity 27.3%; Pred. No. 1e+02;
Matches 15; Conservative 15; Mismatches 23; Indels 2; Gaps 1;

QY 4 DPTLHEVMDLPETTDLYX--YKQINDSBEDEIDGAGQAEPPRAHYNI 56
Db 2506 DTPSSEVSYEVPKTTDVTSTPRPAVHICAEEDSNGSKRFTPEEMFKWVT 2560

RESULT 53
T38157
short-chain dehydrogenase/reductase (EC 1.-.-.-) SPAC22A12.17c [similarity] - fission yeast
C:Species: Schizosaccharomyces pombe
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 05-Oct-2004
C:Accession: T38157
R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, September 1997
A:Reference number: Z21774
A:Accession: T38157
A:Molecule type: DNA
A:Residues: 1-261 <PEA>

Db 446 HGDLKMTPOESKXAVLYTKF-----ENDDLGALFLALPDNLQPNFKMEKSPAY 501
 QY 57 FCCCK 60
 |||:
 Db 502 FCCR 505

RESULT 58

C61399
 early protein E7 - bovine papillomavirus type 6
 C/Species: bovine papillomavirus type 6
 C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
 C/Accession: C61399
 R/Jackson, M.B.; Pennie, W.D.; McCafferty, R.E.; Smith, K.T.; Grindlay, G.J.; Campo, M.S.; Mol. Carcinog. 4, 382-387, 1991
 A/Title: The B subgroup bovine papillomaviruses lack an identifiable E6 open reading frame
 A/Reference number: A61399; MUID:92000191; PMID:1654923
 A/Accession: C61399
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-100 <JAC>
 A/Cross-references: UNIPROT:Q7LZV6; UNIPARC:UPI0000178418; GB:X59064
 C/Superfamily: bovine papillomavirus type 4 E6 protein

Query Match 12.5%; Score 64.5; DB 2; Length 100;
 Best Local Similarity 26.2%; Pred. No. 4.8;

Matches 28; Conservative 17; Mismatches 33; Indels 29; Gaps 6;

QY 1 MHGDTPLHEVMDLQPETTDLYXXQLNDSEEE--DEIDGPAQAEPDRAHYNIVTF 57
 |||:
 Db 1 MKQSMILKRLAELEEVVS-----PINDCHEEINAEVDCP-----VTF 41

QY 58 C-----CK-CDSTLRCLCVGSTHVDIRTELDLM-GLGIVXPICSQK 97
 |||:
 Db 42 CLVEAVCHVCEQVRLAVVASPDGIIQLQQLLTDSLSFLCTSCSRK 88

RESULT 59

DB6342
 hypothetical protein F9H16.6 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
 C/Accession: DB6342
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chiu, C.W.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huzar, L. Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: DB6342
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-614 <STO>
 A/Cross-references: UNIPARC:UPI000004829A; GB:AE005172; NID:94836893; PIDN:AMD30596.1; C/Genetics:
 A/Map position: 1
 C/Superfamily: pyrophosphate-dependent phosphofructokinase, PfFB type, 6-phosphofructoki

Query Match 12.5%; Score 64.5; DB 2; Length 614;
 Best Local Similarity 25.0%; Pred. No. 34;
 Matches 26; Conservative 15; Mismatches 28; Indels 35; Gaps 5;

QY 6 PTLHEVMDLQPETTDLYXXQLNDSEEE--ED-----EIDGPAQAEPDRAHYNIT 54
 |||:
 Db 507 PALHPAVVDDKGAAYD-----LRQNAQKFLMEDLYNNPGLQYDGGADAK----- 553

QY 55 VTFCKCDSTLRCLCVGSTHV--DIRTELDLMGLTGLVXPICSQ 96

Db 554 -----AVSLCVEDQDPMGRITKQLQEVLDQVRIIVKGCSSQ 588

RESULT 60

PSRSAT
 phospholipase A2 homolog crotoxin acidic subunit precursor - tropical rattlesnake
 C/Species: Crotalus durissus terrificus (tropical rattlesnake, cascade)
 C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
 C/Accession: S01392; A23861; S11382; B23861; C23861
 R/Bouchier, C.; Ducancel, F.; Guignery-Frelat, G.; Bon, C.; Boulain, J.C.; Menez, A.
 Nucleic Acids Res. 16, 9050, 1988
 A/Title: Cloning and sequencing of cDNAs encoding the two subunits of crotoxin.
 A/Reference number: S01392; MUID:89016587; PMID:3174444
 A/Accession: S01392
 A/Molecule type: mRNA
 A/Residues: 1-138 <BDU>
 A/Cross-references: UNIPROT:P08878; UNIPARC:UPI0000311108; EMBL:X12606; NID:952685; PIDN
 R/Aird, S.D.; Kaiser, I.I.; Lewis, R.V.; Kruggel, W.G.
 Biochemistry 24, 7054-7058, 1985
 A/Title: Rattlesnake presynaptic neurotoxins: primary structure and evolutionary origin
 A/Reference number: A90500; MUID:86104201; PMID:4084559
 A/Accession: A23861

A/Molecule type: protein
 A/Residues: 39-73,'N',75-76;'XXXXXXX',95-102,'G',104-118;125-138 <AIR1>
 A/Cross-references: UNIPARC:UPI0000172777; UNIPARC:UPI0000172778; UNIPARC:UPI0000172779
 R/Aird, S.D.; Yates III, J.R.; Martino, P.A.; Shabnovaltz, J.; Hunt, D.F.; Kaiser, I.I.
 Biochim. Biophys. Acta 1040, 217-224, 1990
 A/Title: The amino acid sequence of the acidic subunit B-chain of crotoxin.
 A/Reference number: S11382; MUID:90381276; PMID:2400773
 A/Accession: S11382
 A/Molecule type: protein
 A/Residues: 'Z',85-118 <AIR2>
 A/Cross-references: UNIPARC:UPI000017277A
 C/Comment: This subunit has no enzymatic or toxin activity. It helps target crotoxin base
 C/Complex: heterodimer of acidic and basic subunits; mature acidic subunit has 3 chains,
 C/Superfamily: Phospholipase A2
 C/Keywords: calcium; heterodimer; metalloprotein; pyroglutamic acid; venom
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-38/Domain: propeptide #status predicted <PRO>
 F:39-76,84-118,125-138/Product: crotoxin acidic subunit #status experimental <MTR>
 F:39-76/Domain: crotoxin acidic subunit chain A #status experimental <CHA>
 F:84-118/Domain: crotoxin acidic subunit chain B #status experimental <CHB>
 F:125-138/Domain: crotoxin acidic subunit chain C #status experimental <CHC>
 F:42-131,44-60,59-111,65-138,66-104,73-97,91-102/Dsulfide bonds: #status predicted
 F:43,45,47,64/Binding site: calcium (Tyr, Gly, Asp) #status predicted
 F:84/Modified site: pyroglutamic acid (Gln) (in mature form) #status experimental
 F:125/Modified site: pyroglutamic acid (Gln) (in mature form) #status experimental

Query Match 12.4%; Score 64; DB 1; Length 138;
 Best Local Similarity 29.3%; Pred. No. 7.7;
 Matches 17; Conservative 7; Mismatches 12; Indels 22; Gaps 3;
 QY 19 TTDLYXXQLNDSEEDF-----DGPAGQAEPDRAHYNIVTFCKCDSTLRCLCVGST 72
 |||:
 Db 76 TTDVYTRKQ-----EDGEIVCGEDPCG-----TQCECDKAAATCFRNS 115

RESULT 61

T14580
 SIEP1L protein precursor - bee
 C/Species: Beta vulgaris (beet)
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
 C/Accession: T14580
 R/Alexandrova, R.; Barkla, B.; Blumwald, E.
 submitted to the EMBL Data Library, June 1995
 A/Reference number: Z18149
 A/Accession: T14580
 A/Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-391 <ALE>
 A/Cross-references: UNIPROT:Q39436; UNIPARC:UPI00000AD016; EMBL:X87931; NID:G1107525
 A/Experimental source: storage tissue

C:Genetics:
A:Gene: *slepi1*
C:Superfamily: S-locus glycoprotein; S-locus-specific glycoprotein homology
F:1-26/Domain: signal sequence #status predicted <Stg>
F:27-391/Product: SLEP1 protein #status predicted <Mat>

Query Match	12.3%;	Score 63.5;	DB 2;	Length 391;
Best Local Similarity	31.8%;	Pred. No. 27;		
Matches 27; Conservative	4;	Mismatches 35;	Indels 19;	Gaps 4;

```

QY      6 PTLHEMLDL-----QPETDLYXXYQLNDSSEEDLEIDGP-AGQAEPRRAY 52
      |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     221 PLLYSMLDLSKSLKEVTFSCSPENDNNYAY----DITFAYQSIDGSIIGNAEIARPKY 277

```

RESULT 62
151380

Query Match	Score	DB	Length	#status
84/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form)	12.28	1	138	experiment

```
QY      19 TTDLXXHXQLNDSSBEDEI----DGPAGQAEPRRAHNYIVTFCCCKDSTLRJCVQST 72
```

Db 76 TTIDVYTYRQ-----EDGEIVCGGDDPCG-----TQICECDKAAICFRDS 115

RESULT 63
S56948
HALS protein - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein J03J1, protein YJL165c
C:Species: *Saccharomyces cerevisiae*
C:Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 05-Oct-2004

A;Map position: 10L
C;Keywords: ATP
F;501-835/Domain: protein kinase homology <KIN>
F;509-517/Region: protein kinase ATP-binding motif

```

Oy      29 NDSSEEEDEIDGPAQAEPRRAH-----YNIVTFCKCKDSTLRCAVQ 70
      :: |:::| | | | | | | | | | | | | | | | | | | | |
Db      473 SNQGEDSDDTTEGKAGTTNDTSHRPSQKYKSGIVGAGAYGVVKICARCTAKDVL PY 532

```

RESULT 64

Probable nuclear envelope pore membrane protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999#sequence_revision 03-Dec-1999 #text_change 31-Dec-2004

Query Match	12.2%	Score 63;	DB 2;	Length 1250;
Best Local Similarity	22.8%	Pred. No. 1.1e+02;		
Matches 21;	Conservative 16;	Mismatches 33;	Indels 22;	Gaps 2;

```

Oy      1 MHGDTPTLHEWMLDQPETT---DLYXXQLNDSSEBEDEIDGPAQAEPRDAHNIYV 56
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      141 IHSSRLIGQYTLQVLPETGAKINPLHENYCLNSLRKDQ-----YVD 182

```


QY 57 FCCKDSTLRACVQSTHYDIRTLEDLMMGTLG 88
 DB 183 LAIQFNSTIPKTYQYSHVDLETKEITLVEVSG 214

RESULT 65

T20513

hypothetical protein F02E9.4 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T20513

R/Gray: 1.

submitted to the EMBL Data Library, November 1996

A/Reference number: Z19285

A/Accession: T20513

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1490 <WIL>

A/Cross-references: UNIPROT:O01319; UNIPARC:UPI000007CA61; EMBL:Z81494; PIDD: CAB04052.1;

A/Experimental source: clone F02E9

C/Genetics:

A/Map position: 1

A/Map position: 1

A/Intons: 225/3; 321/2; 373/3; 474/3; 619/3; 664/3; 697/3; 828/3; 868/3; 902/2; 965/2;

Query Match 12.1%; Score 62.5; DB 2; Length 1490;

Best Local Similarity 37.1%; Pred. No. 1.5e+02;

Matches 13; Conservative 5; Mismatches 8; Indels 9; Gaps 1;

QY 29 NDSSEDEIDDPAGQAEPRDRA-----HYNI 54

DB 1385 DDEDEDEDEDEDESGADEPESTSGCNVPMDLNI 1419

RESULT 66

T00198

vp80 protein - Leucania separata nuclear polyhedrosis virus

C/Species: Leucania separata nuclear polyhedrosis virus

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: T00198

R/John, T.; Qi, B.; Qi, Y.

submitted to the EMBL Data Library, December 1997

A/Description: Leucania separata multiple nuclear polyhedrosis virus genome DNA 5118bp

A/Reference number: Z14120

A/Accession: T00198

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-675 <JIN>

A/Cross-references: UNIPROT:O55574; UNIPARC:UPI00000FOF12; EMBL:AB009613; NID:d1177438;

C/Genetics:

A/Map position: 1

A/Map position: 1

Query Match 12.0%; Score 62; DB 2; Length 675;

Best Local Similarity 25.6%; Pred. No. 71;

Matches 22; Conservative 12; Mismatches 34; Indels 18; Gaps 3;

QY 1 MHGDTPLHMYLDLPETDTLXXYXQANDSSEEDIDGPAQAEPRDRAHYNIIVTFCK 60

DB 436 VEGNEPTLG-----RPMRSORYIDTQLIG-----DGSFEPRPDQAHVVEALLN 481

QY 61 -----CDSTLRACVQSTHYDIRTLEDL 82

DB 482 VIPAPSRMAFCELKQHDIKRPENTL 507

RESULT 67

T04509

hypothetical protein F8F16.240 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C/Accession: T04509

R/Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Schafte, M.; Schon, O.; Hohlisel, J.; Mewe

submitted to the Protein Sequence Database, April 1998

A/Reference number: Z15375

A/Accession: T04509

A/Molecule type: DNA

A/Residues: 1-433 <BEV>

A/Cross-references: UNIPROT:O49591; UNIPARC:UPI00000AB12F; EMBL:AL021633

A/Experimental source: cultivar Columbia; BAC clone F8F16

C/Genetics:

A/Map position: 4

A/Intons: 14/1; 57/3; 246/3; 303/2; 394/3

A/Note: F8F16.240

Query Match 11.9%; Score 61.5; DB 2; Length 433;

Best Local Similarity 30.7%; Pred. No. 50;

Matches 23; Conservative 7; Mismatches 28; Indels 17; Gaps 4;

QY 18 ETTDLXXYXQANDSSEED-IDGPAQAEPRDRAHYNIIVTFCKCD---STLRACVQSTH 73

DB 167 EASDSLKLVNVSNGSABMDDDGDADKYELD-----PTCLMCDKHKHTLSGMLHMH 220

QY 74 -----VDIRTLED 81

DB 221 KHHGFPIPIEYKLD 235

RESULT 68

F86458

unknown protein, 73879-71181 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: F86458

R/Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Greasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Accession number: AB6141; MUID:21016719; PMID:11130712

A/Accession: F86458

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-508 <STO>

A/Cross-references: UNIPROT:Q9C804; UNIPARC:UPI00000A876C; GB:AE005172; NID:g10645505; P1

C/Genetics:

A/Map position: 1

Query Match 11.9%; Score 61.5; DB 2; Length 508;

Best Local Similarity 22.7%; Pred. No. 59;

Matches 15; Conservative 15; Mismatches 31; Indels 5; Gaps 2;

QY 6 PTLHEMYLDLPETDTLXXYXQANDSSEED-IDGPAQAEPRDRAHYNIIVTFCKCDS 63

DB 204 PVVNHGVSQPSQPV---NHTDGHQCCDDVBFKEMEDERNVIGTSSACSCRT 260

QY 64 TLRACV 69

DB 261 VHYCCV 266

RESULT 69

T21104

hypothetical protein F19B2.6 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T21104

R/Mortimore, B.

submitted to the EMBL Data Library, January 1998

A/Reference number: Z19374

A/Accession: T21104

A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-823 <WLI>
A:Cross-references: UNIPROT:Q9YXS6; UNIPARC:UPI0000060FA9; EMBL:AL021447; NID:e1519050;
A:Experimental source: clone F19B2
C:Genetics:
A:Gene: CESP:F19B2.6
A:Map position: 5
A:Insertions: 176/3; 369/3; 449/3; 495/1; 528/1; 552/3; 751/3

Query Match 11.9%; Score 61.5; DB 2; Length 823;
Best Local Similarity 27.2%; Pred. No. 1e+02;
Matches 22; Conservative 11; Mismatches 33; Indels 15; Gaps 4;

Qy 6 PTHHEWMLDQPEPTDLYXXYXQLNDSSEDEIDGPAGQAEPPRAHYNIYTFCKCSTL 65
Db 127 PTHRSQYVDAAPQA---YGSQALVPENORPE-----SAPDRP-YQIMVGVGNPQS-- 173
Qy 66 RLCVQSTHVDIRTLDELDMGT 86
Db 174 --AQQHAQMEIPTWSHQLIGT 192

RESULT 70
A59282
nonmuscle myosin II heavy chain A - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59282
R:Bhatl. Dey, N.; Talra, M.; Conci, M.A.; Nooruddin, H.; Adelstein, R.S.
Mech. Dev. 78, 33-36, 1998
A:Title: Differential expression of non-muscle myosin heavy chain genes during Xenopus e
A:Reference number: A59282; MUID:99077683; PMID:985676
A:Accession: A59282
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1964 <BHA>
A:Cross-references: UNIPROT:O93522; UNIPARC:UPI00000F86F7; GB:AF055895; NID:g3660671; PI
A:Experimental source: cell line XTC
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:84-764/Domain: myosin motor domain homology <MMO>

Query Match 11.9%; Score 61.5; DB 2; Length 1964;
Best Local Similarity 27.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 15; Mismatches 19; Indels 5; Gaps 2;

Qy 1 MHGPTLHEWMLDQPEPTDLYXXYXQLNDSSEDEIDGPAGQAEPPRAHYNI 54
Db 1053 LEGDSTLDHDIQLAQIAEL--KLQL--AKKEELQALALAREEAAQKTL 1101

RESULT 71
JC7867
endo-1,3(4)-beta-glucanase (EC 3.2.1.6) 1, Ose1 - rice
N:Alternate names: endo-1,3(4)-beta-glucanase; endo-1,3-beta-glucanase; Ose1 protein
C:Species: Oryza sativa (rice)
C:Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 09-Jul-2004
C:Accession: JC7867
R:Yamaguchi, T.; Nakayama, K.; Hayashi, T.; Tanaka, Y.; Koike, S.
Biosci. Biotechnol. Biochem. 66, 1403-1406, 2002
A:Title: Molecular cloning and characterization of a novel beta-1,3-glucanase gene from
A:Reference number: JC7867; MUID:22152203; PMID:12162569
A:Accession: JC7867
A:Molecule type: DNA
A:Residues: 1-338 <YAM>
A:Cross-references: UNIPROT:Q8LP99; UNIPARC:UPI00000A0PDD; DDBJ:AB070742
C:Comment: This enzyme, a hydrolytic enzyme, which belongs to monooxygenous endo-beta
glucanase, synergistically acts with chitinase to inhibit fungal growth in vitro. It is a
C:Genetics:
A:Gene: ose1
A:Insertions: 26/1
C:Keywords: glycosidase, hydrolase

Query Match 11.8%; Score 61; DB 2; Length 338;
Best Local Similarity 28.6%; Pred. No. 43;
Matches 12; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 16 QPETDLYXXYXQLNDSSEDEIDGPAGQAEPPRAHYNIYTF 57
Db 296 RPVPITERYIFAMFNEMKGTDEIERNGLPEPDKSPVPIYTF 337

RESULT 72
T09648
nucleolin homolog num1 - alfalfa
N:Alternate names: num1 protein
C:Species: Medicago sativa (alfalfa)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09648
R:Boegre, U.; Jonak, C.; Mink, M.; Meskene, I.; Traas, J.; Ha, D.T.C.; Snoboda, I.; Plar
Plant Cell 8, 417-428, 1996
A:Title: Developmental and cell cycle regulation of alfalfa nuclear a plant homolog of the
A:Reference number: 216796; MUID:96361876; PMID:8721748
A:Accession: T09648
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-635 <BOE>
A:Cross-references: UNIPROT:Q40363; UNIPARC:UPI00000AA67F; EMBL:X88845; NID:g1279562; PI
C:Genetics:
A:Gene: num1
C:Superfamily: nucleolin; ribonucleoprotein repeat homology

Query Match 11.8%; Score 61; DB 2; Length 635;
Best Local Similarity 33.3%; Pred. No. 86;
Matches 15; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

Qy 5 TPPTLHEWMLDQPEPTDLYXXYXQLNDSSEDEIDGPAGQAEPPR 49
Db 89 TPAKGNVKKQAQPEITS--ESDSDDISDBEEVKKPAKAVPSK 131

RESULT 73
T40524
hypothetical protein SPBC530.08 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40524
R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, May 1998
A:Reference number: 221934
A:Accession: T40524
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-815 <LYN>
A:Cross-references: UNIPROT:O59744; UNIPARC:UPI000006B51D; EMBL:AL023634; PIDN:CAA19174.1
A:Experimental source: strain 972h-; cosmid c530
C:Genetics:
A:Gene: SPBC:SPBC530.08
A:Map position: 2
F:26-62/Domain: GAL4 zinc binuclear cluster homology <GLA>

Query Match 11.8%; Score 61; DB 2; Length 815;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 6; Mismatches 16; Indels 8; Gaps 4;

Qy 37 EIDGPAGQA--EPPRAHYNIYTFCKCDSYRLCVQS--TRTLE 80
Db 510 EADSPAMQALKVPDR--QTAFILACKCVDSAYICVQNLSHLSGKIKRTLD 557

RESULT 74
AB0007
probable DNA repair protein radc [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB0007

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
 Nature 413, 523-527, 2001

A>Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AB0007

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-222 <KUR>

A/Cross-references: UNIPROT:Q8ZJP3; UNIPARC:UPI00001330CB; GB:AL590842; P1DN:CAC88916.1;

C/Genetics:

A/Gene: radC

C/Superfamily: DNA repair protein radC

Query Match 11.7%; Score 60.5; DB 2; Length 222;
 Best Local Similarity 37.8%; Pred. No. 31;
 Matches 17; Conservative 6; Mismatches 13; Indels 9; Gaps 1;

QY 41 PQAQEPDRAHNVITVFCCKDSTLRVCVOSTHVDITLEDL 85
 174 PSQAEPDRAHNVITVFCCKDSTLRVCVOSTHVDITLEDL 209

RESULT 75

S40936 hypothetical protein ZK632.4 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C/Accession: S40936

R/Berks, M.

Submitted to the EMBL Data Library, February 1993

A/Reference number: S40933

A/Accession: S40936

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-411 <BER>

A/Cross-references: UNIPROT:P34650; UNIPARC:UPI0000128B77; EMBL:Z22181

C/Genetics:

A/Intons: 44/3; 81/1; 147/1; 207/1

C/Superfamily: yeast mannose-6-phosphate isomerase

Query Match 11.7%; Score 60.5; DB 2; Length 411;
 Best Local Similarity 23.6%; Pred. No. 61;
 Matches 21; Conservative 17; Mismatches 40; Indels 11; Gaps 3;

QY 2 HGDPTLHE--YMLDQPTTDLXXYXQLNDSSEEDIDGPAQAEPDRAHNVITFC 58
 206 HEKTALEDEIVLFTYFGDVGAFAPILNFKLQ----PGEATFLEPNPHAYLKGDC 261

QY 59 CKC---DSTLRVCVOSTHVDITLEDL 83
 262 VECMAQSDNTIRAGLTPKYIDVSLVEML 290

RESULT 76

C89134 protein F25G6.6 [imported] - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: C89134

R/anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A>Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology

A/Reference number: A75000; MUID:99069613; PMID:9851916

A/Note: see webistes genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A/Accession: C89134

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-551 <STO>

A/Cross-references: UNIPROT:O16924; UNIPARC:UPI0000080118; GB:chr_V; P1DN:AAC5799.1; PT

A/Note: Similar to asparagine synthetase; F25G6.6

C/Genetics:
 A/Gene: F25G6.6
 A/Map position: 5
 C/Superfamily: asparagine synthase (glutamine-hydrolyzing)

Query Match 11.7%; Score 60.5; DB 2; Length 551;
 Best Local Similarity 27.6%; Pred. No. 84;
 Matches 24; Conservative 9; Mismatches 31; Indels 23; Gaps 3;

QY 14 DLQPTTDLXXYXQLNDSSEED-----EIDGPAQAEPD--RAHNVITFCCKD 62
 476 DRPETTEBYWYRQIFEDFVYDKMGLVTKYRTAAMRPPDEKSMLETLVDKTD 535

QY 63 STLRVCVOSTHVDITLEDL 89
 536 DLRLRRST-----GSLGV 550

RESULT 77

T14476 psIA protein - slime mold (*Dictyostelium discoideum*)

C/Species: *Dictyostelium discoideum*

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T14476

R/Yasukawa, H.; Mohanty, S.; Firtel, R.A.

Submitted to the EMBL Data Library, December 1997

A/Reference number: Z18117

A/Accession: T14476

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1269 <YAS>

A/Cross-references: UNIPROT:O43993; UNIPARC:UPI000007CA46; EMBL:AF038919; NID:q2766695; I

A/Experimental source: strain Kax3

C/Genetics:

A/Gene: psIA

Query Match 11.7%; Score 60.5; DB 2; Length 1269;
 Best Local Similarity 24.4%; Pred. No. 21e+02;
 Matches 21; Conservative 17; Mismatches 33; Indels 15; Gaps 4;

QY 6 PTLHEVYMLDQPTTDLXXYXQLNDSSEED-----EIDGPAQAEPDRA-----HYNI 54
 349 PSIHKF--TKKHNTNLFMSSTINDGEEDDDDDNDVDGDDNNKEXYDDTSNKKDSI 406

QY 55 VFECCKDSTLRVCVOSTHVDITLEDL 80
 407 VKF--KDDITIVLVNRQRFQFSNFE 430

RESULT 78

A41685 SIL protein - human

N/Contains: SIL protein, short form

C/Species: Homo sapiens (man)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C/Accession: A41685

R/Aplan, P.D.; Lombardi, D.P.; Kirsch, I.R.

Mol. Cell. Biol. 11, 5462-5469, 1991

A>Title: Structural characterization of SIL, a gene frequently disrupted in T-cell acute

A/Reference number: A41685; MUID:92017825; PMID:1992059

A/Accession: A41685

A/Molecule type: mRNA

A/Residues: 1-1287 <APL>

A/Cross-references: UNIPROT:Q15468; UNIPARC:UPI000072CA6; GB:M74558; NID:G338087; P1DN:J

A/Note: exon/intron borders were determined by genomic DNA sequencing

C/Genetics:

A/Intons: 15/2; 51/2; 89/1; 151/3; 166/1; 213/1; 262/2; 291/2; 341/3; 378/2; 416/3; 739/

C/Superfamily: human SIL protein

C/Keywords: alternative splicing

F/1-1287/Product: SIL protein #status predicted <MAT>

F/1-165,213-1287/Product: SIL protein, short form #status predicted <ALT>

Query Match 11.7%; Score 60.5; DB 2; Length 1287;

Best Local Similarity 23.8%; Pred. No. 2.1e+02;
Matches 19; Conservative 11; Mismatches 23; Indels 27; Gaps 3;
QY 23 YXXYQLNDSSEEPEDIDPA-----GQAEPPRAHYNIIVFCKCD 62
Db 1126 YGLIQQSDNSDEEPPNADSKSEYLLNQLRSLPEQLGQKPSKNDHILN-CSNCE 1184
QY 63 STURLCVQSTHVDIRTEDL 82
Db 1185 SV-----GTNADTPVLRLNI 1198

RESULT 79
150090
carboxypeptidase gp180 - Anas sp.
C/Species: Anas sp.
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C/Accession: 150090
R./Kuraki, K.; Eng, F.; Ishikawa, T.; Turck, C.; Harada, F.; Ganem, D.
J. Biol. Chem. 270, 15022-15028, 1995
A./Title: gp180, a host cell glycoprotein that binds duck hepatitis B virus particles, is
A./Reference number: A57010; MUID:95318059; PMID:7797483
A/Accession: 150090
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1389 <KUR>
A/Cross-references: UNIPROT:Q90240; UNIPARC:UPI00000FC41C; EMBL:U25126; NID:G1008477; PI

Query Match 11.7%; Score 60.5; DB 2; Length 1389;
Best Local Similarity 31.9%; Pred. No. 2.3e+02;
Matches 23; Conservative 1; Mismatches 23; Indels 25; Gaps 3;
QY 1 MHGDTPTLHEYMIDLOPE-----TTDLYXXQJLN-DSSEEDID--- 39
Db 138 MHGDEPLARILLRLAGELVRCMAGDERLGRLLNTTDLVLPRLNPGFPRAREGGCGG 197
QY 40 ----GPAQAE 47
Db 198 GGGGGGEGGGE 209

RESULT 80
H86502
excinnuclease ABC subunit A [imported] - Chlamydia pneumoniae (strain J138)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: H86502
R./Shirai, M.; Hirakawa, H.; Kinoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A./Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A./Reference number: A86491; MUID:20330349; PMID:10871362
A/Accession: H86502
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1826 <STO>
A/Cross-references: UNIPROT:Q92985; UNIPARC:UPI000016569B; GB:BA000008; NID:98978469; PI
A/Experimental source: strain J138
C/Genetics:
A/Gene: uvrA
C/Superfamily: Chlamydia trachomatis probable excinnuclease ABC chain A; ATP-binding case

Query Match 11.7%; Score 60.5; DB 2; Length 1826;
Best Local Similarity 23.7%; Pred. No. 3e+02;
Matches 23; Conservative 17; Mismatches 32; Indels 25; Gaps 4;
QY 10 EYMLDLOPETTDLYX-----XQLNDSSE-----EDIDGPAQAEPPRAHYN 53
Db 877 DYVLELGPBGDGLGYLLASCTPKDLIQLNTPRAKALAPYIEGSLDIPVKSPPSPKS 936
QY 54 IVTFCKCKDSTLR/CVOST--HVDIRTEDLMTGLG 88
Db 937 -----CDILIKDAYQNNLKHIDLALPRNSLIAAG 966

RESULT 81
D72120
excinnuclease ABC, chain A CP0678 [imported] - Chlamydia pneumoniae (strain CWL029 at
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: D72120; E81550
R./Kaiman, S.; Mitchell, W.; Marathe, R.; Lammell, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A./Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A./Reference number: A72000; MUID:99206606; PMID:10192288
A/Accession: D72120
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1826 <ARN>
A/Cross-references: UNIPROT:Q92985; UNIPARC:UPI0000137E7B; GB:AE001595; GB:AE001363; NID
A/Experimental source: strain CWL029
R./Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.
Nucleic Acids Res. 28, 1397-1406, 2000
A./Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A./Reference number: A81500; MUID:20150255; PMID:10684935
A/Accession: E81550
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1826 <REA>
A/Cross-references: UNIPARC:UPI0000137E7B; GB:AE002226; GB:AE002161; NID:G7189592; PIDN:J
A/Experimental source: strain AR39, HU cells
C/Genetics:
A/Gene: uvrA; CP0678
C/Superfamily: Chlamydia trachomatis probable excinnuclease ABC chain A; ATP-binding case
F./609-885/Domain: ATP-binding cassette homology <ABC>

Query Match 11.7%; Score 60.5; DB 2; Length 1826;
Best Local Similarity 23.7%; Pred. No. 3e+02;
Matches 23; Conservative 17; Mismatches 32; Indels 25; Gaps 4;
QY 10 EYMLDLOPETTDLYX-----XQLNDSSE-----EDIDGPAQAEPPRAHYN 53
Db 877 DYVLELGPBGDGLGYLLASCTPKDLIQLNTPRAKALAPYIEGSLDIPVKSPPSPKS 936
QY 54 IVTFCKCKDSTLR/CVOST--HVDIRTEDLMTGLG 88
Db 937 -----CDILIKDAYQNNLKHIDLALPRNSLIAAG 966

RESULT 82
T03396
invertase inhibitor homolog - common tobacco
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C/Accession: T03396
R./Greiner, S.; Krausgrill, S.; Rausch, T.
submitted to the EMBL Data Library, April 1997
A./Reference number: Z14924
A/Accession: T03396
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-172 <GRE>
A/Cross-references: UNIPROT:O49909; UNIPARC:UPI00000AC71C; EMBL:Y12806
A/Experimental source: strain petit havana
C/Superfamily: Ripening-related protein-like, contains similarity to pectinesterase

Query Match 11.6%; Score 60; DB 2; Length 172;
Best Local Similarity 38.1%; Pred. No. 27;
Matches 16; Conservative 6; Mismatches 14; Indels 6; Gaps 2;
QY 53 NIVTFCKCKDSTLR/CVOSTHVDIRTE-----DLMTGLGIV 90
Db 24 NIINTTCRATTNYPICITLTHSDPRTSBAAGALDT--TLGLV 63
RESULT 83

E70341
 conserved hypothetical protein eq_454 - Aquifex aeolicus
 C/Species: Aquifex aeolicus
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: E70341
 R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
 Nature 392, 353-358, 1998
 A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A/Reference number: A70300; MUID:98196666; PMID:9537320
 A/Accession: E70341
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-370 <AQP>
 A/Cross-references: UNIPROT:O66761; UNIPARC:UPI0000056374; GB:AE000690; GB:AE000657; NID
 A/Experimental source: strain VFS
 C/Genetics:
 A/Genes: eq_454
 C/Superfamily: conserved hypothetical protein yodo

Query Match 11.6%; Score 60; DB 1; Length 370;
 Best Local Similarity 33.3%; Pred. No. 62;
 Matches 18; Conservative 8; Mismatches 26; Indels 2; Gaps 2;

Oy 30 DSSESEIDGPAQAPRAHYNIVTFCC-KCDSLRLCVSTHYVDIRLTEDL 82
 Db 94 DALKEEDIPG-LTHRYPRVLTNTTFCVAYCHCKKRIFSQGERARTKEE 146

RESULT 84
 protein P2E2.2 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: H86352
 R/Theologis, A.; Eckert, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 anen, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucero, J.S.; Mailli, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: H86352
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-465 <STO>
 A/Cross-references: UNIPROT:Q9LM64; UNIPARC:UPI000004126E; GB:AE005172; NID:93280695; PI
 C/Genetics:
 A/Genes: P2E2.2
 A/Map position: 1
 C/Superfamily: Arabidopsis thaliana hypothetical protein F17J16.30

Query Match 11.6%; Score 60; DB 2; Length 465;
 Best Local Similarity 25.0%; Pred. No. 79;
 Matches 27; Conservative 17; Mismatches 36; Indels 28; Gaps 5;

Oy 4 DTPPL-----HEY---MLDLOPETDLYXXYXQLNSSSEDEIDGPAQAPRA 50
 Db 233 DTSLSLVLDYSGHVARRYTLMGSLERARLNLFWEOGLISDEDDDDPDGYPWPKRSK 292

Oy 51 HYNIVTFCCKCDSTLRLCVSTHYVDIRLTEDLMTGLGIYVPCSQRP 98
 Db 293 -----DANGIAMIS---NVKTLHLSSDSLBVHSLCKWMP 325

RESULT 85
 S46281
 P element - fruit fly (Drosophila ananassae)
 C/Species: Drosophila bifasciata

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S46281
 R/Hagemann, S.; Miller, W.J.; Pinker, W.
 Mol. Gen. Genet. 244, 168-175, 1994
 A/Title: Two distinct P element subfamilies in the genome of Drosophila bifasciata.
 A/Reference number: S46281; MUID:94329069; PMID:8052236
 A/Accession: S46281
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-562 <HAG>
 A/Cross-references: UNIPROT:Q9TX47; UNIPARC:UPI000017BE6B

Query Match 11.6%; Score 60; DB 2; Length 562;
 Best Local Similarity 22.2%; Pred. No. 97;
 Matches 26; Conservative 14; Mismatches 35; Indels 42; Gaps 5;

Oy 4 DPTLHERYMDLOPE-----TTDL-----YXXYXQLNSSSE-----EDE-----I 38
 Db 280 DVPTLVELIKGLHRRGVFVVSIVDWAGNQRLMRELIGISEKTFGHPEDDLKIFVS 339

Oy 39 DGP-----AGQAPRAHYNIVTFCCKCDSTLRLCVSTHYVDIR 78
 Db 340 DAPHLIKLVNHYLATGALINGQTLTKSVETITRCKCTDVTILFKVNESHNVRS 396

RESULT 86
 T37192
 nebulin-related protein, skeletal muscle - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T37192
 R/Luo, G.; Zhang, J.O.; Nguyen, T.P.; Herrera, A.H.; Paterson, B.; Horowitz, R.
 Cell Motil. Cytoskeleton 38, 75-90, 1997
 A/Title: Complete cDNA sequence and tissue localization of N-RAP, a novel nebulin-relate
 A/Reference number: Z21630; MUID:97439586; PMID:9295142
 A/Accession: T37192
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1175 <LHO>
 A/Cross-references: UNIPROT:Q35884; UNIPARC:UPI0000029C98; EMBL:U76618; NID:92351567; PI
 A/Function:
 A/Description: supposed to play a role in anchoring the terminal actin filaments in the
 A/Note: specifically expressed in skeletal and cardiac muscle
 C/Keywords: skeletal muscle; tandem repeat

Query Match 11.6%; Score 60; DB 2; Length 1175;
 Best Local Similarity 30.0%; Pred. No. 2.1e+02;
 Matches 21; Conservative 8; Mismatches 37; Indels 4; Gaps 2;

Oy 11 YMDLOPETDLYXXYXQLNSSSEDEIDGPAQ---QAEPRAHYNIVTFCCKCDSTLRL 67
 Db 405 YKADYKRDVVD-YNYLPLHSLIPNNDAGSPESCQLQAEDHMKFSSVTNPQIVQAKIN 463

Oy 68 CVQSTHYDIR 77
 Db 464 AQQLSHYNVR 473

RESULT 87
 JC5500
 phosphoinositide 3-kinase (EC 2.7.1.1) - human
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: JC5500
 R/Brown, R.A.; Ho, L.K.F.; Weber-Hall, S.J.; Shipley, J.M.; Fry, M.J.
 Biochem. Biophys. Res. Commun. 233, 537-544, 1997
 A/Title: Identification and cDNA cloning of a novel mammalian C2 domain-containing phosph
 A/Reference number: JC5500; MUID:97289668; PMID:9144573
 A/Accession: JC5500
 A/Molecule type: mRNA
 A/Residues: 1-1634 <BRO>
 A/Cross-references: UNIPROT:O00750; UNIPARC:UPI0000131B5A; GB:Y11312; NID:92808446; PIDN:
 A/Experimental source: breast cell

C;Comment: This enzyme is involved in receptor signal transduction, in a signalling comp
vival.
C;Genetics:
A;Gene: GDB:PIK3CB; C2-PI3K; PI3K-C2beta
A;Cross-references: GDB:9837703; OMIM:602838
A;Map position: 1q32-1q32
C;Superfamily: Hsc2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology
C;Keywords: phosphotransferase
F;156-162,169-174/Domain: SH3 #status predicted <SH3>
F;1037-1320/Domain: catalytic #status predicted <CAT>
F;1498-1612/Domain: protein kinase C C2 region homology <KC2A>

Query Match 11.6%; Score 60; DB 1; Length 1634;
Best Local Similarity 25.8%; Pred. No. 3.1e+02;
Matches 24; Conservative 17; Mismatches 36; Indels 16; Gaps 6;

Qy 11 YMLDLPETTL-----YXXQLNDSSSE-EDRIDPAQAEPRRAHYIVTFCKCD 62
Db 341 HMLDILSGSDIQYFLTGYVSAVTPSPHIGDEVMLKV-TVLCDRLO-BALTFTCNCS 398

Qy 63 STRLCVQS---THVDIRTL--DLMTGLGI 89
Db 399 STVDLLIYQTLCTYHDLRNVGDVYLKPGCL 431

RESULT 88
T39642
conserved hypothetical protein SPBC1709.14 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39642
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z21868
A;Accession: T39642
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-333 <LYN>
A;Cross-references: UNIPROT:O74739; UNIPARC:UPI000006C436; EMBL:AL031852; PIDD:CAA21253.
A;Experimental source: strain 972h-; cosmid c1709
C;Genetics:
A;Gene: SPDB:SPBC1709.14
A;Map position: 2
A;Intons: 109/3; 168/3; 222/1; 235/1
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YPL096w

Query Match 11.5%; Score 59.5; DB 2; Length 333;
Best Local Similarity 32.6%; Pred. No. 63;
Matches 14; Conservative 6; Mismatches 20; Indels 3; Gaps 1;

Qy 8 LHEYMLDLPETTLVYXXQLNDSSSEDEIDG---PAGQNEP 47
Db 267 LHEINIEFRRLTDSERKALEEERKREKDELDTGMRVPSQATP 309

RESULT 89
A48355
coat protein - pelargonium leaf curl virus
C;Species: pelargonium leaf curl virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A48355
R;Li, Y.; Bachmann, S.; Maiss, E.; Commandeur, U.; Breyel, E.; Timpe, U.; Koenig, R.
Arch. Virol. 129, 349-356, 1993
A;Title: Nucleotide sequence of the coat protein gene of pelargonium leaf curl virus and
A;Reference number: A48355; MUID:93228459; PMID:8470957
A;Accession: A48355
A;Molecule type: genomic RNA
A;Residues: 1-389 <LI1>
A;Cross-references: UNIPROT:Q86586; UNIPARC:UPI00000F7BB9; GB:SS8174; NID:9299096; PIDD:
A;Note: sequence extracted from NCBI backbone (NCBIN:129117, NCBIPI:129118)
C;Superfamily: carnation mottle virus coat protein
C;Keywords: coat protein, glycoprotein
F;8,9,117,118,139,353/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.5%; Score 59.5; DB 1; Length 389;
Best Local Similarity 26.8%; Pred. No. 74;
Matches 26; Conservative 13; Mismatches 39; Indels 19; Gaps 5;

Qy 4 DTPLHEYMLDLP--ETTLVYXXQLNDSSSEDEIDGPAQAEPRRAHYIV----- 55
Db 154 DQYFNNVVLYVPLCATTEVGAVMYFDDXSEIVE---PADRYE--LANYGVLEKETA PW 208

Qy 56 ---TFCKCDSTRLCVQSTHVDIRTEDELMGTGLI 89
Db 209 AEATLNIPICDRIKRYCDSATVDKLLD---LQQLGI 242

RESULT 90
C96640
hypothetical protein T25B24.14 (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C96640
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C96640
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <STO>
A;Cross-references: UNIPROT:Q9S199; UNIPARC:UPI00000A6CC0; GB:AE005173; NID:94585884; PII
A;Gene: T25B24.14
A;Map position: 1

Query Match 11.5%; Score 59.5; DB 2; Length 404;
Best Local Similarity 32.7%; Pred. No. 77;
Matches 18; Conservative 5; Mismatches 23; Indels 9; Gaps 2;

Qy 5 TPTLHEYMLDLPETTLVYXXQLNDSSSEDEIDG---PAGQAEPRRAHYNI 54
Db 338 TMLAHNVIRSQGSDSFRHMEIVSEYEGDNDGHRVPLPG---DVMENI 388

RESULT 91
C69455
tungsten formylmethanofuran dehydrogenase, subunit F (fwdf) homolog - Archaeoglobus fulgi
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C;Accession: C69455
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kitzness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uitterlinden, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.;
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69455
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-438 <KLE>
A;Cross-references: UNIPROT:Q28629; UNIPARC:UPI0000056C46; GB:AE000989; GB:AE000782; NID
C;Superfamily: formylmethanofuran dehydrogenase, subunit F; ferredoxin 2 [Fe-4S] homolog
F;28-94/Domain: ferredoxin 2 [Fe-4S] homolog <FER3>

Query Match 11.5%; Score 59.5; DB 2; Length 438;
Best Local Similarity 21.3%; Pred. No. 84;

Matches 19; Conservative 16; Mismatches 45; Indels 9; Gaps 2;

Qy 5 PTLHEVMDLQPETTDLYXXQLNDSSE-----EDIDGPAQAEPRRAHNIYT 56
 Db 106 SPWVYTKVETCECTCYKCPFNIAKREVKITRQOIEENKEGIEGKVEIDRDKNLG 165

Qy 57 FCCCKDSTLRVCVSTH-VDIRTLEDLLM 84
 Db 166 ICABFCEVFKEKPEHPEDVMPSDIL 194

RESULT 92
 B71474
 probable hep6 chaperonin, mitochondrial - Chlamydia trachomatis (serotype D, strain UM3
 C/Species: Chlamydia trachomatis
 C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
 C/Accession: B71474
 R:Stephens, R.S.; Kaiman, S.; Lamell, C.J.; Fan, J.; Marache, R.; Aravind, L.; Mitchell,
 Science 282, 754-759, 1998
 A>Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
 A/Reference number: A71570; MUID:9900809; PMID:9784136
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-512 <ARN>
 A/Cross-references: UNIPROT:O84760; UNIPARC:UPI00000D339E; GB:AE001348; GB:AE001273; NIH
 A/Experimental source: serotype D, strain UM-3/Cx
 C/Genetics:
 A/Gene: CT755
 C/Superfamily: chaperonin groEL
 C/Keywords: mitochondrion

Query Match 11.5%; Score 59.5; DB 2; Length 512;
 Best Local Similarity 24.3%; Pred. No. 1e+02;
 Matches 26; Conservative 15; Mismatches 41; Indels 25; Gaps 4;

Qy 4 DTPPLHEVMDLQETTD-----LYXXYQLNDSSEEDIDGPAQAEPRRAHNI 52
 Db 370 DTPPLHEVMDLQETTD-----LYXXYQLNDSSEEDIDGPAQAEPRRAHNI 52

Qy 53 NIVFCCCKDSTLRVCVSTHVDIRTLEDLL-MGTIGIVXPICSOX 97
 Db 420 QIIQOTAR--TLLEQLNVSVYMDCKLVADKLCSTGTSIGENVISQ 464

RESULT 93
 A85438
 hypothetical protein A7437080 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
 C/Accession: A85438
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
 Nature 402, 769-777, 1999
 A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A/Reference number: A85001; MUID:20083488; PMID:10617138
 A/Accession: A85438
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-596 <STO>
 A/Cross-references: UNIPROT:O23178; UNIPARC:UPI000009E6AC; GB:NC_001268; NID:97270657; F
 C/Genetics:
 A/Gene: A7437080
 A/Map position: 4
 C/Superfamily: Putative ternary complex factor MIP1

Query Match 11.5%; Score 59.5; DB 2; Length 596;
 Best Local Similarity 26.1%; Pred. No. 1.2e+02;
 Matches 23; Conservative 11; Mismatches 33; Indels 21; Gaps 2;

Qy 10 EYMLDLPETTDLYXXQLNDSSEEDIDGPAQAEPRRAHNIYTFCKCKDSTLRVCV 69
 Db 262 EAADKSESTKQLDRLADQDKAQSVSQSSSE-----DKTL----- 300

Qy 70 QSTHVDIRTLEDLLMGTIGIVXPICSOX 97
 Db 301 QSGVNAVRSDDLKCLVITILNISSK 328

RESULT 94
 T10102
 diphosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) alpha chain - castor
 N/Alternate names: 6-phosphofructokinase (pyrophosphate)
 C/Species: Ricinus communis (castor bean)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C/Accession: T10102
 R:Todd, J.P.; Blakeley, S.D.; Dennis, D.T.
 Gene 152, 181-186, 1995
 A>Title: Structure of the genes encoding the alpha- and beta-subunits of castor pyrophos
 A/Reference number: Z16949; MUID:95137384; PMID:7835697
 A/Accession: T10102
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-617 <TOD>
 A/Cross-references: UNIPROT:Q41140; UNIPARC:UPI000013175D; EMBL:Z32849; NID:9483546; PID
 C/Genetics:
 A/Intons: 30/3; 88/2; 126/1; 151/1; 189/1; 211/3; 239/3; 257/3; 284/3; 316/1; 340/3; 37
 C/Superfamily: pyrophosphate-dependent phosphofructokinase, PFB type; 6-phosphofructoki
 C/Keywords: phosphotransferase

Query Match 11.5%; Score 59.5; DB 2; Length 617;
 Best Local Similarity 23.3%; Pred. No. 1.2e+02;
 Matches 24; Conservative 15; Mismatches 33; Indels 31; Gaps 4;

Qy 6 PTLHEVMDLQPETTDLYXXQLNDSSEEDIDGPAQAEPRRAHNIYT 56
 Db 505 PAIHPAVVDLKGK--YELLRLNAVKFLMDLRYNCPLOFSGPADAKP----- 552

Qy 57 FCCCKDSTLRVCVSTH--DIRTLEDLLMGTIGIVXPICSOX 97
 Db 553 -----ITLCVEDDQYMRIRKLTGEYLDKVRIVFGSGQE 587

RESULT 95
 E96793
 hypothetical protein F14G6.15 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
 C/Accession: E96793
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maitl, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: E96793
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-617 <STO>
 A/Cross-references: UNIPARC:UPI0000048495; GB:AE005173; NID:96642673; PID:AAF20253.1; G
 C/Genetics:
 A/Gene: F14G6.15
 A/Map position: 1
 C/Superfamily: pyrophosphate-dependent phosphofructokinase, PFB type; 6-phosphofructoki

Query Match 11.5%; Score 59.5; DB 2; Length 617;
 Best Local Similarity 24.0%; Pred. No. 1.2e+02;
 Matches 25; Conservative 15; Mismatches 29; Indels 35; Gaps 5;

Qy 6 PTLHEVMDLQPETTDLYXXQLNDSSE-----EDIDGPAQAEPRRAHNI 54
 Db 505 PVIHPASVVDLKGKAYD-----LRQNAQKFLMEDMYNPPGVQYDVGADAK----- 551

Qy 55 VTFCCKCDSTRLCQVSTHV--DIRTLEDLMGTGLGVPCISQ 96
Db 552 -----AVSLCEVDODYKGIKKIQEYLDQVRTIVKPCSQ 586

RESULT 96
T01622
probable salt-inducible protein At2g18940 (imported) - Arabidopsis thaliana
N/Alternate names: hypothetical protein F19F24.14
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C/Accession: T01622; E84570
R/Rounaley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, April 1998
A/Description: Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence.
A/Reference number: Z14153
A/Accession: T01622
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-822 <ROU>
A/Cross-references: UNIPROT:O64624; UNIPARC:UPI00000A9EDA; EMBL:AC003673; NID:G3004543;
A/Experimental source: cultivar Columbia
R/Lin, X.; Kaul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Unayam, L.; Tallon, L.
euser, D.; Niemann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617157
A/Accession: E84570
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-822 <STO>
A/Cross-references: UNIPARC:UPI00000A9EDA; GB:A8002093; NID:G3004555; PIDN:AAC09028.1; C
C/Genetics:
A/Gene: At2g18940; F19F24.14
A/Map position: 2

Query Match 11.5%; Score 59.5; DB 2; Length 822;
Best Local Similarity 30.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 10; Mismatches 17; Indels 15; Gaps 3;

Qy 4 DTPTLHEVMDLQPTDTLXXYXQANDSSEDEID-----GPAGQAEPPRAHYNYV 55
Db 199 DKPIPLQGYLDDVRAVYITLHAYSR---TGKYEKAIDLEFRMKEMGPS---PTLVTVYVNI 251

RESULT 97
F69189
protophyrin IX magnesium chelatase (EC 4.99.1.-) - Methanobacterium thermoautotrophic
C/Species: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: F69189
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Viscarte, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Neolling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A/Reference number: A69000; MUID:98037514; PMID:9371463
A/Accession: F69189
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1708 <MTH>
A/Cross-references: UNIPROT:O26769; UNIPARC:UPI0000066625; GB:A8000847; GB:A8000666; NID
A/Experimental source: strain Delta H
C/Genetics:
A/Gene: MTH73
C/Superfamily: Methanobacterium thermoautotrophicum cobalamin biosynthesis protein N
C/Keywords: lyase

Query Match 11.5%; Score 59.5; DB 2; Length 1708;
Best Local Similarity 23.9%; Pred. No. 3.7e+02;
Matches 28; Conservative 12; Mismatches 46; Indels 31; Gaps 4;

Qy 3 GDPTLHEVMD-----LQPTDTLXXYXQAND-----SSEDEID 38
Db 853 GDTPSLYIYIMDVGESGLQAKRGLAYIIDHLTPPLRTKGLDGLQGLAGVSSYEAT-- 910

Qy 39 DGPAGQAEPPRAHYNYVTFCCKCDSTRLCQVSTHV--DIRTLEDLMGTGLGVPC 92
Db 911 --PTGNPMRDEYAKQIRETIIKLDLARDLGINATNTMTDDIDRVHVDLITSTLMP 965

RESULT 98
A33977
myosin heavy chain, nonmuscle - chicken
N/Contains: myosin ATPase (EC 3.6.4.1)
C/Species: Gallus gallus (chicken)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A33977; S06116; A43422
R/Shohet, R.V.; Conti, M.A.; Kawamoto, S.; Preston, Y.A.; Brill, D.A.; Adelstein, R.S.
Proc. Natl. Acad. Sci. U.S.A. 86, 7726-7730, 1989
A/Title: Cloning of the cDNA encoding the myosin heavy chain of a vertebrate cellular my
A/Reference number: A33977; MUID:90046668; PMID:2813355
A/Accession: A33977
A/Molecule type: mRNA
A/Residues: 1-1959 <SHO>
A/Cross-references: UNIPROT:P14105; UNIPARC:UPI000012PB7F; GB:M26510; NID:G212382; PIDN:
R/Katsuragawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.
Eur. J. Biochem. 184, 611-616, 1989
A/Title: Two distinct nonmuscle myosin-heavy-chain mRNAs are differentially expressed in
B.
A/Reference number: S06116; MUID:90032648; PMID:2806244
A/Accession: S06116
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 716-1008 <KAT>
A/Cross-references: UNIPARC:UPI0000173E31; GB:X17589
A/Note: this translation is not annotated in GenBank entry GCMCFMTH, release 114
R/Hodge, T.P.; Cross, R.; Kendrick-Jones, J.
J. Cell Biol. 118, 1085-1095, 1992
A/Title: Role of the COOH-terminal nonhelical tailpiece in the assembly of a vertebrate r
A/Reference number: A43422; MUID:92381096; PMID:1512291
A/Accession: A43422
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1900-1959 <HOD>
A/Cross-references: UNIPARC:UPI000008A46C
A/Experimental source: brush border
A/Note: sequence extracted from NCBI backbone (NCBI:P111947)
C/Superfamily: myosin heavy chain; myosin motor domain homology
C/Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide
F/84-764/Domain: myosin motor domain homology <MMOT>
F/174-181/Region: nucleotide-binding motif A (P-loop)
F/552-565/Region: actin binding #status predicted
F/636-640/Region: actin binding #status predicted
F/837-1936/Domain: coiled coil #status predicted <COI>
F/837-1277/Region: S2
F/1278-1959/Region: light meromyosin
F/1937-1959/Domain: carboxyl-terminal <CBT>
F/125/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F/180/Binding site: ATP (Lys) #status predicted
F/694/704/Active site: Cys #status predicted

Query Match 11.5%; Score 59.5; DB 1; Length 1959;
Best Local Similarity 27.8%; Pred. No. 4.2e+02;
Matches 15; Conservative 11; Mismatches 20; Indels 5; Gaps 2;

Qy 1 MEGDPTLHEVMDLQPTDTLXXYXQANDSSEDEIDGPAGQAEPPRAHYNYV 54
Db 1053 IEGDSSDIHQIAELQQAIEL--KIQL--SKKEELQAALARVEEAAQKMN 1101

RESULT 99
S57908
hypothetical 527k polypeptide - rice

C:Species: Oryza sativa (rice)

C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C/Accession: S57908; S33529

R/Moriyama, H.; Nitta, T.; Fukuhara, T.

Mol. Gen. Genet. 248, 364-369, 1995

A>Title: Double-stranded RNA in rice: a novel RNA replicon in plants.

A/Reference number: S57908; MUID:96004703; PMID:7565598

A/Accession: S57908

A/Status: preliminary; nucleic acid sequence not shown

A/Residues: 1-4572 <MOR>

A/Molecule type: DNA

A/Cross-references: UNIPROT:Q40712; UNIPARC:UPI00001101CF; EMBL:D32136; NID:9511666; PIR

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994

A/Note: only a part of the coding sequence is given

R/Fukuhara, T.; Moriyama, H.; Pak, J.Y.; Hyakutake, H.; Nitta, T.

Plant Mol. Biol. 21, 1121-1130, 1993

A>Title: Enigmatic double-stranded RNA in Japonica rice.

A/Reference number: S33529; MUID:93257627; PMID:8490131

A/Accession: S33529

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 3854-4370 <PUK>

A/Cross-references: UNIPARC:UPI0000179215; EMBL:D12639

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992

C:Keywords: polyprotein

Query Match 11.5%; Score 59.5; DB 2; Length 4572;

Best Local Similarity 23.6%; Pred. No. 1.1e+03;

Matches 26; Conservative 14; Mismatches 49; Indels 21; Gaps 4;

QY 7 TLHEVMDLPETTDLYXXQVNDSSSE--EDRIDCPAGAEPPRAHNIIVTFCK-CD 62

DB 2664 TTHBES-DLENTQEKSETDGLDENSEALGLDDEVGDNQSSSENVVYVVEKDMTKETD 2722

QY 63 STRLCTGVSTHVDIRTL-----DLMGTLGIYXPICSQ 96

DB 2723 ATEKPSANDHKSVPTSDTEIKLPSDGTQISFTEIKPTITLPTPICVQ 2772

RESULT 100

AP1164

hypothetical protein lmo0718 [imported] - Listeria monocytogenes (strain EGD-e)

C/Species: Listeria monocytogenes

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: AP1164

R/Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A/authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluteter, T.; Simeos, N.; Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A>Title: Comparative genomics of Listeria species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AP1164

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-214 <GIA>

A/Cross-references: UNIPROT:Q8Y924; UNIPARC:UPI0000556BC; GB:NC_003210; PIDN:CAC98796.1

A/Experimental source: strain EGD-e

C/Genetic:

A/Gene: lmo0718

Query Match 11.4%; Score 59; DB 2; Length 214;

Best Local Similarity 21.4%; Pred. No. 44;

Matches 15; Conservative 12; Mismatches 25; Indels 18; Gaps 1;

QY 11 YMDLDPETTDLYXXQVNDSSSEEDRIDCPAGAEPPRAHNIIVTFCKCDSTLRICVQ 70

DB 137 YMDIFNEESEEYHYANLD-----EKQYKNIGPICQNDAAEIAITK 178

QY 71 STHVDIRTL 80

DB 179 LTNEMLETTLE 188

Search completed: May 27, 2006, 05:17:20
Job time : 22.8916 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2006, 05:00:16 ; Search time 151.133 Seconds
(Without alignments)
599.815 Million cell updates/sec

Title: US-10-530-253-14ED
Perfect score: 517
Sequence: 1 MGDITLTHERYMLDLPETT.....LEDLMGTGIVYPCISQKP 98

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	512	99.0	98	1	VE7_HPV16
2	512	99.0	98	2	Q547B8_HPV16
3	512	99.0	98	2	Q778G4_HPV16
4	512	99.0	98	2	Q778G6_HPV16
5	512	99.0	98	2	Q778G8_HPV16
6	512	99.0	98	2	Q778G9_HPV16
7	512	99.0	98	2	Q778H1_HPV16
8	512	99.0	98	2	Q778H2_HPV16
9	512	99.0	98	2	Q778H7_HPV16
10	512	99.0	98	2	Q778H9_HPV16
11	512	99.0	98	2	Q778I0_HPV16
12	512	99.0	98	2	Q778I1_HPV16
13	512	99.0	98	2	Q778I3_HPV16
14	512	99.0	98	2	Q778I5_HPV16
15	512	99.0	98	2	Q778I7_HPV16
16	512	99.0	98	2	Q778I9_HPV16
17	508	98.3	98	2	Q12337_HPV16
18	507	98.1	98	2	Q11650_HPV16
19	507	98.1	98	2	Q778H3_HPV16
20	507	98.1	98	2	Q778H5_HPV16
21	507	98.1	98	2	Q8QRD3_HPV16
22	507	98.1	98	2	Q8QRD3_HPV16
23	507	98.1	98	2	Q2MJT4_HPV16
24	504	97.5	98	2	Q12338_HPV16
25	500	96.7	98	2	Q8V10_HPV16
26	499	96.5	98	2	Q8QRD4_HPV16
27	486	94.0	94	2	Q8B5P6_HPV16
28	478	92.5	93	2	Q9QDH6_HPV16
29	477	92.3	93	2	Q9QDH2_HPV16
30	477	92.3	93	2	Q9QDH4_HPV16
31	477	92.3	93	2	Q9QDH8_HPV16

32	406	78.5	77	2	Q8B5P5_9PAPI	Q8B5P5 human papil
33	381.5	73.8	99	1	VE7_HPV15	VE7_HPV15 human papil
34	381.5	73.8	99	2	Q76FP2_9PAPI	Q76FP2 human papil
35	372	72.0	98	1	VE7_HPV31	VE7_HPV31 human papil
36	367	71.0	98	2	Q6T377_HPV11	Q6T377 human papil
37	343	66.3	65	2	Q8B5G3_9PAPI	Q8B5G3 human papil
38	316	61.1	99	2	Q90724_HPV67	Q90724 human papil
39	295	57.1	97	1	VE7_HPV73	VE7_HPV73 human papil
40	294	56.9	99	1	VE7_HPV52	VE7_HPV52 human papil
41	289.5	56.0	98	1	VE7_HPV58	VE7_HPV58 human papil
42	289.5	56.0	98	2	Q547M4_HPV58	Q547M4 human papil
43	288.5	55.8	98	2	Q9QCZ1_HPV58	Q9QCZ1 human papil
44	286.5	55.4	98	2	Q8QSF0_HPV58	Q8QSF0 human papil
45	285.5	55.2	98	2	Q8QHN7_HPV58	Q8QHN7 human papil
46	285.5	55.2	98	2	Q8QHO2_HPV58	Q8QHO2 human papil
47	284.5	55.0	98	2	Q9QCZ2_HPV58	Q9QCZ2 human papil
48	283.5	54.8	98	2	Q8QSE8_HPV58	Q8QSE8 human papil
49	281.5	54.4	98	2	Q8QSE8_HPV58	Q8QSE8 human papil
50	247	47.8	98	2	Q9QLP4_9PAPI	Q9QLP4 human papil
51	245	47.4	98	1	VE7_HPV11	VE7_HPV11 human papil
52	243	47.0	98	1	VE7_HPV6B	VE7_HPV6B human papil
53	242	46.8	98	1	VE7_HPV6A	VE7_HPV6A human papil
54	222.5	43.0	97	1	VE7_HPV34	VE7_HPV34 human papil
55	221.5	42.8	98	2	Q8JNA0_9PAPI	Q8JNA0 human papil
56	221	42.7	43	2	Q91194_HPV16	Q91194 human papil
57	218.5	42.3	113	1	VE7_RHPV1	VE7_RHPV1 human papil
58	216	41.8	108	2	Q9WHG1_9PAPI	Q9WHG1 human papil
59	213	41.2	106	1	VE7_HPV45	VE7_HPV45 human papil
60	212	41.0	106	2	Q9Y4Y3_HUMAN	Q9Y4Y3 homo sapien
61	212	41.0	106	2	Q10609_HPV45	Q10609 human papil
62	211.5	40.9	95	2	Q8B5W9_9PAPI	Q8B5W9 human papil
63	209.5	40.5	105	1	VE7_HPV30	VE7_HPV30 human papil
64	208.5	40.3	105	1	VE7_HPV53	VE7_HPV53 human papil
65	207.5	40.1	90	2	Q56947_9PAPI	Q56947 human papil
66	207.5	40.1	97	2	Q82006_HPV73	Q82006 human papil
67	206.5	39.9	94	2	Q6EGG8_9PAPI	Q6EGG8 human papil
68	206	39.8	95	2	Q2VJC6_9PAPI	Q2VJC6 human papil
69	204.5	39.6	90	1	VE7_HPV29	VE7_HPV29 human papil
70	202.5	39.2	105	1	VE7_HPV18	VE7_HPV18 human papil
71	202.5	39.2	101	1	VE7_HPV13	VE7_HPV13 human papil
72	200.5	38.8	105	2	Q76Z96_HPV18	Q76Z96 human papil
73	200.5	38.6	94	2	Q6RGQ1_9PAPI	Q6RGQ1 human papil
74	199.5	38.4	105	2	Q9QNP7_HPV18	Q9QNP7 human papil
75	198.5	38.3	99	2	Q705H9_HPV43	Q705H9 human papil
76	198	38.0	105	2	Q9QNP6_HPV18	Q9QNP6 human papil
77	195.5	37.8	107	2	Q81965_HPV59	Q81965 human papil
78	195.5	37.8	98	1	VE7_PCPIV1	VE7_PCPIV1 human papil
79	194	37.5	98	1	Q8V5K9_HPV18	Q8V5K9 human papil
80	192.5	37.2	105	2	Q8B5X6_HPV54	Q8B5X6 human papil
81	191.5	37.0	95	2	Q9QNP5_HPV18	Q9QNP5 human papil
82	191.5	36.9	105	2	Q8UTG7_9PAPI	Q8UTG7 human papil
83	191	36.9	98	2	Q21263_HPV13	Q21263 human papil
84	190	36.8	98	2	Q98005_9PAPI	Q98005 human papil
85	189	36.6	96	2	VE7_HPV28	VE7_HPV28 human papil
86	186	36.0	87	1	VE7_HPV42	VE7_HPV42 human papil
87	183.5	35.5	93	1	VE7_HPV46	VE7_HPV46 human papil
88	183.5	35.5	105	1	Q37386_CCPIV1	Q37386 common chim
89	180.5	34.9	99	2	VE7_HPV54	VE7_HPV54 human papil
90	179.5	34.7	95	1	VE7_HPV70	VE7_HPV70 human papil
91	179	34.6	109	1	VE7_HPV57	VE7_HPV57 human papil
92	178.5	34.5	92	1	VE7_HPV56	VE7_HPV56 human papil
93	178.5	34.5	105	1	VE7_HPV07	VE7_HPV07 human papil
94	178.5	34.5	111	1	VE7_HPV51	VE7_HPV51 human papil
95	178	34.4	101	1	VE7_HPV25	VE7_HPV25 human papil
96	176.5	34.1	97	1	VE7_HPV2A	VE7_HPV2A human papil
97	175.5	33.9	92	1	Q91R58_HPV82	Q91R58 human papil
98	175.5	33.9	96	2	Q2VUB9_9PAPI	Q2VUB9 human papil
99	174.5	33.8	96	2	VE7_HPV10	VE7_HPV10 human papil
100	173.5	33.6	86	1	VE7_HPV10	VE7_HPV10 human papil

ALIGNMENTS

RESULT 1
 VEE7 HPV16 STANDARD; PRT; 98 AA.
 AC POS129;
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 21-JUL-1986, sequence version 1.
 DT 07-FEB-2006, entry version 43.
 DE Protein E7.
 GN Name=E7;
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxID=333760;
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RP MEDLINE=85246220; PubMed=2390099;
 RA Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
 RT "Human papillomavirus type 16 DNA sequence."; Virol
 RL Virol. 145:181-185 (1985).
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RP MEDLINE=90218027; PubMed=2157796;
 RA Schneider-Maunoury S., Penau-Arnaudet G., Breitburd F., Orth G.;
 RT "Expression of the human papillomavirus type 16 genome in SK-V cells, a line derived from a vulvar intraepithelial neoplasia."; J. Gen. Virol. 71:809-817 (1990).
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
 RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RA Tonesello M.L., Buonaguro F.M., Meglio A., Buonaguro L., Beth-Giraldo E., Giraldo G.;
 RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RC STRAIN=Isolate African 1, and Isolate European German 131;
 RA Terat M., Fu L., Ma Z., Burk R.D.;
 RT "Cloning and sequencing of non-European human papillomavirus (HPV) variant complete genomes from cervicovaginal cells by an overlapping PCR method."; Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 RN FUNCTION.
 RP MEDLINE=88223347; PubMed=2836062;
 RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
 RT "The human papillomavirus type 16 E7 gene encodes transactivation and transformation functions similar to those of adenovirus E1A."; Cell 53:539-547 (1988).
 RL Cell 53:539-547 (1988).
 CC -!- FUNCTION: E7 protein has both transforming and trans-activating activities.
 CC -!- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more often associated with malignant genital cancers in humans.
 CC -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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DR Interpro; IPR000148; Papv1_E7.
 DR Pfam; PF00527; E7; 1.
 KW DNA-binding; Early protein; Oncogene; Transcription;
 KW Transcription regulation.
 FT CHAIN 1
 FT 1
 FT MOTIF 58 61 /FTID=PRO_0000133414.
 FT MOTIF 91 94 C-XX-C motif-1.
 FT MOTIF 91 94 C-XX-C motif-2.
 SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
 Query Match 99.0%; Score 512; DB 1; Length 98;
 Best Local Similarity 96.9%; Pred. No. 4.5e-52;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MHGDTPLTHEYMDLQGETTDLYXXYXQUNDSSSEDEDIDGPAQAEPDRAHYNTVTECK 60
 DB 1 MHGDTPLTHEYMDLQGETTDLYCYEQUNDSSSEDEDIDGPAQAEPDRAHYNTVTECK 60
 QY 61 CDSTLRLCVOSTHYDITRLDLMGTIGIYXPCISQKP 98
 DB 61 CDSTLRLCVOSTHYDITRLDLMGTIGIYXPCISQKP 98
 RESULT 3
 Q78G4 HPV16 PRELIMINARY; PRT; 98 AA.
 AC Q78G4;
 DT 10-MAY-2005, integrated into UniProtKB/TREMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.

Query Match	99.0%	Score 512	DB 2	Length 98
OS	E7 protein (Fragment)			
OS	Human papillomavirus type 16.			
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;			
OC	Alphapapillomavirus.			
OX	NCBI_TaxID=333760;			
OX	[1]			
RN	NUCLEOTIDE SEQUENCE.			
RP	Medline=20112892; PubMed=10644829;			
RX	van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,			
RA	Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;			
RT	"Analysis of human papillomavirus type 16 E6 variants in relation to			
RT	p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";			
RL	J. Gen. Virol. 81:317-325(2000).			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NonDerivs License			
CC	EMBL; AJ388069; CAB45131.1; -; Genomic_DNA.			
DR	GO; GO:0005632; C:intracellular; IEA.			
DR	GO; GO:0003700; F:transcription factor activity; IEA.			
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.			
DR	InterPro; IPR000148; Papv1_E7.			
DR	Pfam; PF00527; E7; 1.			
DR	NON TER			
FT	SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;			
SO				
Query Match	99.0%	Score 512	DB 2	Length 98
Best Local Similarity	96.9%	Pred. No. 4.5e-52;		
Matches	95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
OY	1 MHGPTTHERWMLDQPTETDLYXXXXOLNDSEEDIEDPGAGAEPPRAHNYTPCK 60			
DB	1 MHGPTTHERWMLDQPTETDLYCYEQLNDSSEEDIEDPGAGAEPPRAHNYTPCK 60			
OY	61 CDSTLRLCVSTHVDIRLTEDLMTGLTGVXPCISQKP 98			
DB	61 CDSTLRLCVSTHVDIRLTEDLMTGLTGVPCISQKP 98			
RESULT 4				
O778G6_HPV16	PRELIMINARY; PRT; 98 AA.			
AC	O778G6_HPV16			
DT	10-MAY-2005, integrated into UniProtKB/TrEMBL.			
DT	10-MAY-2005, sequence version 1.			
DT	07-FEB-2006, entry version 3.			
DE	E7 protein (Fragment).			
OS	Human papillomavirus type 16.			
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;			
OC	Alphapapillomavirus.			
OX	NCBI_TaxID=333760;			
OX	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	Medline=20112892; PubMed=10644829;			
RA	van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,			
RA	Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;			
RT	"Analysis of human papillomavirus type 16 E6 variants in relation to			
RT	p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";			
RL	J. Gen. Virol. 81:317-325(2000).			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NonDerivs License			
CC	EMBL; AJ388068; CAB45129.1; -; Genomic_DNA.			
DR	GO; GO:0005623; C:intracellular; IEA.			
DR	GO; GO:0003700; F:transcription factor activity; IEA.			
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.			
DR	InterPro; IPR000148; Papv1_E7.			
DR	Pfam; PF00527; E7; 1.			
DR	NON TER			
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SO				

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      1. Best Local Similarity 96.9%; Pred. No. 4.5e-52;
      Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHERMLDLOPETTDLYXXQLNDSSSEEDSIDDPAGGAEPDRAHYNIVTFCK 60
Db 1 MHGDTPTLHERMLDLOPETTDLYCYEQLNDSSEEDSIDDPAGGAEPDRAHYNIVTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTDLEDLMGITGIYPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRTDLEDLMGITGIYPCISQKP 98

RESULT 5
0778G8_HPV16 PRELIMINARY; PRT; 98 AA.
ID Q778G8_HPV16
AC Q778G8;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
CX NCBI_TaxID=3333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorthorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC
CC EMBL: AJ388067; CAB45127.1; -: Genomic DNA.
DR GO:00005622; C:intracellular; IEA.
DR GO:00003760; F:transcription factor activity; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
DR NON TER
FT 98
SQ SEQUENCE 98 AA, 11022 MW, 9BD612534CD2C9B CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHERMLDLOPETTDLYXXQLNDSSSEEDSIDDPAGGAEPDRAHYNIVTFCK 60
Db 1 MHGDTPTLHERMLDLOPETTDLYCYEQLNDSSEEDSIDDPAGGAEPDRAHYNIVTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTDLEDLMGITGIYPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRTDLEDLMGITGIYPCISQKP 98

RESULT 6
0778G9_HPV16 PRELIMINARY; PRT; 98 AA.
ID Q778G9_HPV16
AC Q778G9;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
CX NCBI_TaxID=3333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;

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RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
DR EMBL; AJ388066; CAB45125.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHYMDLQPEPTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
DB 1 MHGDPPTLHEHYMDLQPEPTDLYCYEQINDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98

RESULT 7
Q778H1 HPV16 PRELIMINARY; PRT; 98 AA.
ID Q778H1;
AC Q778H1;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
DR EMBL; AJ388065; CAB45123.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHYMDLQPEPTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
DB 1 MHGDPPTLHEHYMDLQPEPTDLYCYEQINDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
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DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98

RESULT 8
Q778H2 HPV16 PRELIMINARY; PRT; 98 AA.
ID Q778H2;
AC Q778H2;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
DR EMBL; AJ388064; CAB45121.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHYMDLQPEPTDLYXXQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
DB 1 MHGDPPTLHEHYMDLQPEPTDLYCYEQINDSSEDEIDGPAGQAEPRAHYNIIVTFCK 60
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98

RESULT 9
Q778H7 HPV16 PRELIMINARY; PRT; 98 AA.
ID Q778H7;
AC Q778H7;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
DR EMBL: AJ388061; CAB45115.1; -: Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMDLQPEETDLYXXYQLNDSSEDEIDGPAGAEPRAHYNI VTFCK 60
Db 1 MGGDTPLHEHYMDLQPEETDLYXXYQLNDSSEDEIDGPAGAEPRAHYNI VTFCK 60
Cc 61 CDSTLRKCVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 98
Db 61 CDSTLRKCVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 98

RESULT 10
07789 HPV16 PRELIMINARY; PRT; 98 AA.
ID 07789 HPV16
AC 07789
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 B6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
CC -----
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Cc -----
DR EMBL: AJ388060; CAB45113.1; -: Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMDLQPEETDLYXXYQLNDSSEDEIDGPAGAEPRAHYNI VTFCK 60
Db 1 MGGDTPLHEHYMDLQPEETDLYXXYQLNDSSEDEIDGPAGAEPRAHYNI VTFCK 60
Cc 61 CDSTLRKCVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 98
Db 61 CDSTLRKCVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 98

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DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 B6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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Cc -----
DR EMBL: AJ388059; CAB45111.1; -: Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMDLQPEETDLYXXYQLNDSSEDEIDGPAGAEPRAHYNI VTFCK 60
Db 1 MGGDTPLHEHYMDLQPEETDLYXXYQLNDSSEDEIDGPAGAEPRAHYNI VTFCK 60
Cc 61 CDSTLRKCVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 98
Db 61 CDSTLRKCVOSTHVDIRTLIEDLMGTLGIYCPICSQKP 98

RESULT 12
077811 HPV16 PRELIMINARY; PRT; 98 AA.
ID 077811 HPV16
AC 077811
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 B6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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Cc -----
DR EMBL: AJ388058; CAB45109.1; -: Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

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SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
 Best Local Similarity 96.9%; Pred. No. 4.5e-52;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLTHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAQAEPDRAHYNIVTFCK 60
 DB 1 MHGDTPLTHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAQAEPDRAHYNIVTFCK 60

QY 61 CDSTRLCVOSTHVDIRLTEDLLMGTGIVXPCSQKP 98
 DB 61 CDSTRLCVOSTHVDIRLTEDLLMGTGIVXPCSQKP 98

RESULT 13
 Q77813 HPV16 PRELIMINARY; PRT; 98 AA.
 AC Q77813;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxID=3333760;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
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DR EMBL: AJ388057; CAB45107.1; -: Genomic_DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000148; Papv1_E7.
 DR Pfam: PF00527; E7; 1.
 DR NON TER 98
 FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

QY 99.0%; Score 512; DB 2; Length 98;
 Best Local Similarity 96.9%; Pred. No. 4.5e-52;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLTHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAQAEPDRAHYNIVTFCK 60
 DB 1 MHGDTPLTHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAQAEPDRAHYNIVTFCK 60

QY 61 CDSTRLCVOSTHVDIRLTEDLLMGTGIVXPCSQKP 98
 DB 61 CDSTRLCVOSTHVDIRLTEDLLMGTGIVXPCSQKP 98

RESULT 14
 Q77815 HPV16 PRELIMINARY; PRT; 98 AA.
 AC Q77815;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxID=3333760;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
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DR EMBL: AJ388056; CAB45105.1; -: Genomic_DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000148; Papv1_E7.
 DR Pfam: PF00527; E7; 1.
 DR NON TER 98
 FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

QY 99.0%; Score 512; DB 2; Length 98;
 Best Local Similarity 96.9%; Pred. No. 4.5e-52;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLTHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAQAEPDRAHYNIVTFCK 60
 DB 1 MHGDTPLTHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAQAEPDRAHYNIVTFCK 60

QY 61 CDSTRLCVOSTHVDIRLTEDLLMGTGIVXPCSQKP 98
 DB 61 CDSTRLCVOSTHVDIRLTEDLLMGTGIVXPCSQKP 98

RESULT 15
 Q77A11 HPV16 PRELIMINARY; PRT; 98 AA.
 ID Q77A11 HPV16
 AC Q77A11;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxID=3333760;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
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DR EMBL: AJ388057; CAB45107.1; -: Genomic_DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000148; Papv1_E7.
 DR Pfam: PF00527; E7; 1.
 DR NON TER 98
 FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

QY 99.0%; Score 512; DB 2; Length 98;
 Best Local Similarity 96.9%; Pred. No. 4.5e-52;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGDPTLHEHYMLDLPETTDLYXXQLNDSSEEDIDGPAQAEPRRAHYNIITFCCK 60
DB 1 MGDPTLHEHYMLDLPETTDLYCYEQLNDSSEEDIDGPAQAEPRRAHYNIITFCCK 60

QY 61 CDSTLRLCVOSTHVDIRTLTDLMLGTLGTYXPCISQKP 98
DB 61 CDSTLRLCVOSTHVDIRTLTDLMLGTLGTYXPCISQKP 98

RESULT 16
07GV7 HPV16
ID 07GV7 HPV16 PRELIMINARY; PRT; 98 AA.
AC 07GV7;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE E7 protein (Early transforming protein E7).
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Terai M., Burk R.D.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=QV16936E, QV15521E, QV15351AA, QV18158E, QV17722E, and
RC QV1531AA;
RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
RA Chen Z., Terai M., Fu L., Herrero R., Desalle R., Burk R.D.;
RT "Diversifying selection in human papillomavirus type 16 lineages based
RT on complete genome analyses.";
RL J. Virol. 79:7014-7023(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99434235; PubMed=10502513; DOI=10.1006/viro.1999.9868;
RA Flores E.R., Allen-Hoffmann B.L., Lee D., Sattler C.A., Lambert P.F.;
RT "Establishment of the human papillomavirus type 16 (HPV-16) life cycle
RT in an immortalized human foreskin keratinocyte cell line.";
RL Virology 262:344-354(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2242222; PubMed=12355266; DOI=10.1007/s00239-002-2344-Y;
RA DeFilippis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
RT but not E7 oncogenes.";
RL J. Mol. Evol. 55:491-499(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=QEH-2076, QEH-186, PWM-Q42, QEH-525, QEH-453, QEH-501, QEH-561,
RC QEH-1220, QEH-400, PWM-Q27, QEH-318, and PWM-Q39;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).

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CC EMBL; AF402678; AA085409.1; -; Genomic DNA.
CC EMBL; AY86580; AA091653.1; -; Genomic DNA.
CC EMBL; AY86581; AA091651.1; -; Genomic DNA.
CC EMBL; AY86582; AA091659.1; -; Genomic DNA.

DR EMBL; AY86583; AA091677.1; -; Genomic DNA.
DR EMBL; AY86584; AA091685.1; -; Genomic DNA.
DR EMBL; AF125673; AA033253.1; -; Genomic DNA.
DR EMBL; AF472508; AA015698.1; -; Genomic DNA.
DR EMBL; AY089951; AA011876.1; -; Genomic DNA.
DR EMBL; AY089952; AA011878.1; -; Genomic DNA.
DR EMBL; AY089953; AA011880.1; -; Genomic DNA.
DR EMBL; AY089954; AA011882.1; -; Genomic DNA.
DR EMBL; AY089955; AA011884.1; -; Genomic DNA.
DR EMBL; AF486328; AA096633.1; -; Genomic DNA.
DR EMBL; AF486335; AA096640.1; -; Genomic DNA.
DR EMBL; AF486337; AA096642.1; -; Genomic DNA.
DR EMBL; AF486339; AA096644.1; -; Genomic DNA.
DR EMBL; AF486340; AA096645.1; -; Genomic DNA.
DR EMBL; AF486341; AA096646.1; -; Genomic DNA.
DR EMBL; AF486342; AA096647.1; -; Genomic DNA.
DR EMBL; AF486343; AA096648.1; -; Genomic DNA.
DR EMBL; AF486347; AA096652.1; -; Genomic DNA.
DR EMBL; AF486348; AA096653.1; -; Genomic DNA.
DR EMBL; AF486349; AA096654.1; -; Genomic DNA.
DR EMBL; AF486352; AA096657.1; -; Genomic DNA.
DR EMBL; AY86579; AA091645.1; -; Genomic DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR InterPro; IPR000146; PapV_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4, 5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGDPTLHEHYMLDLPETTDLYXXQLNDSSEEDIDGPAQAEPRRAHYNIITFCCK 60
DB 1 MGDPTLHEHYMLDLPETTDLYCYEQLNDSSEEDIDGPAQAEPRRAHYNIITFCCK 60

QY 61 CDSTLRLCVOSTHVDIRTLTDLMLGTLGTYXPCISQKP 98
DB 61 CDSTLRLCVOSTHVDIRTLTDLMLGTLGTYXPCISQKP 98

RESULT 17
012337 HPV16
ID 012337 HPV16 PRELIMINARY; PRT; 98 AA.
AC 012337;
DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT 01-JUL-1997, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97437474; PubMed=9292007;
RA Torneelli M.L., Buongiorno F.M., Meglio A., Buongiorno L.,
RA Beth-Girardo E., Girardo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).

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CC EMBL; AF003021; AAB70738.1; -; Genomic DNA.
CC GO; GO:0005622; C:intracellular; IEA.
CC GO; GO:0003700; F:transcription factor activity; IEA.
CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC InterPro; IPR000146; PapV_E7.
CC Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11056 MW; 19DBB8F14CD2C705 CRC64;

Query Match 98.3%; Score 508; DB 2; Length 98;
 Best Local Similarity 95.9%; Pred. No. 1.3e-51;
 Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEBEIDDPAGQAEPRRAHYNIYTFCK 60
 Db 1 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSEBEIDDPAGQAEPRRAHYNIYTFCK 60

Qy 61 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSQKP 98
 Db 61 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSQKP 98

RESULT 18
 ID 01650 HPV16 PRELIMINARY; PRT; 98 AA.
 AC 011650;
 DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
 DT 01-JUL-1997, sequence version 1.
 DT 07-FEB-2006, entry version 24.
 DE Putative transforming protein E7.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 NCBI_TaxID=333760;
 RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
 RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
 Lee H.-P.;
 RT "Major sequence variants in E7 gene of human papillomavirus type 16
 from cervical cancerous and noncancerous lesions of Korean women.";
 RL Gynecol. Oncol. 66:275-281(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
 Lee H.-P.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Teraï M., Ma Z., Burk R.D.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
 RA Chan P.-K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Teraï M., Fu L., Ma Z., Burk R.D.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
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EMBL: U76404; AAC58243.1; -; Genomic DNA.
 EMBL: AF472509; AA015706.1; -; Genomic DNA.
 EMBL: AF486326; AAL96631.1; -; Genomic DNA.
 EMBL: AF486327; AAL96632.1; -; Genomic DNA.
 EMBL: AF486330; AAL96635.1; -; Genomic DNA.
 EMBL: AF486331; AAL96636.1; -; Genomic DNA.
 EMBL: AF486332; AAL96637.1; -; Genomic DNA.
 EMBL: AF486333; AAL96638.1; -; Genomic DNA.
 EMBL: AF486334; AAL96639.1; -; Genomic DNA.
 EMBL: AF486336; AAL96641.1; -; Genomic DNA.
 EMBL: AF486338; AAL96643.1; -; Genomic DNA.
 EMBL: AF486346; AAL96651.1; -; Genomic DNA.
 EMBL: AF486350; AAL96655.1; -; Genomic DNA.
 EMBL: AF486351; AAL96656.1; -; Genomic DNA.

DR EMBL: AF534061; AA010404.1; -; Genomic DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000149; Papv1_E7.
 DR Pfam: PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 98.1%; Score 507; DB 2; Length 98;
 Best Local Similarity 95.9%; Pred. No. 1.7e-51;
 Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEBEIDDPAGQAEPRRAHYNIYTFCK 60
 Db 1 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSEBEIDDPAGQAEPRRAHYNIYTFCK 60

Qy 61 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSQKP 98
 Db 61 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSQKP 98

RESULT 19
 ID 07783 HPV16 PRELIMINARY; PRT; 98 AA.
 AC 07783;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE E7 protein (fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 NCBI_TaxID=333760;
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorthorst F.,
 Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorthorst F.,
 Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Teraï M., Fu L., Ma Z., Burk R.D.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
 RA Chan P.-K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Teraï M., Fu L., Ma Z., Burk R.D.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
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EMBL: AJ388063; CAB45119.1; -; Genomic DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000148; Papv1_E7.
 DR Pfam: PF00527; E7; 1.
 FT NON TER 98
 SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 98.1%; Score 507; DB 2; Length 98;
 Best Local Similarity 95.9%; Pred. No. 1.7e-51;
 Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEBEIDDPAGQAEPRRAHYNIYTFCK 60
 Db 1 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSEBEIDDPAGQAEPRRAHYNIYTFCK 60

Qy 61 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSQKP 98
 Db 61 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSQKP 98

RESULT 20
 ID 07785 HPV16 PRELIMINARY; PRT; 98 AA.
 AC 07785;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.

07-FEB-2006, entry version 9.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Heijmerikx T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
DE EMBL: AJ389062; CAB45117.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
DR NON_TPR 98
FT SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;
SQ
Query Match 98.1%; Score 507; DB 2; Length 98;
Best Local Similarity 95.9%; Pred. No. 1.7e-51;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPLHEHYMDLQPETTDLYXXYQNDSSSEEDIDGPAGQAEPPDRAHYNI VTFCK 60
DB 1 MHGDTPLHEHYMDLQPETTDLYCYEQNDSSSEEDIDGPAGQAEPPDRAHYNI VTFCK 60
QY 61 CDSTLRLCVQSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVQSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
RESULT 21
ID O6ORD2_HPV16 PRELIMINARY; PRT; 98 AA.
AC O6ORD2;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DE EMBL: AF486345; AAL96650.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
DR SEQUENCE 98 AA; 11045 MW; 9CA4F8C534CD76C4B CRC64;
SQ
Query Match 98.1%; Score 507; DB 2; Length 98;
Best Local Similarity 95.9%; Pred. No. 1.7e-51;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Best Local Similarity 95.9%; Pred. No. 1.7e-51;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPLHEHYMDLQPETTDLYXXYQNDSSSEEDIDGPAGQAEPPDRAHYNI VTFCK 60
DB 1 MHGDTPLHEHYMDLQPETTDLYCYEQNDSSSEEDIDGPAGQAEPPDRAHYNI VTFCK 60
QY 61 CDSTLRLCVQSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVQSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
RESULT 22
ID O6ORD3_HPV16 PRELIMINARY; PRT; 98 AA.
AC O6ORD3;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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CC -----
DE EMBL: AF486344; AAL96649.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
DR SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;
SQ
Query Match 98.1%; Score 507; DB 2; Length 98;
Best Local Similarity 95.9%; Pred. No. 1.7e-51;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPLHEHYMDLQPETTDLYXXYQNDSSSEEDIDGPAGQAEPPDRAHYNI VTFCK 60
DB 1 MHGDTPLHEHYMDLQPETTDLYCYEQNDSSSEEDIDGPAGQAEPPDRAHYNI VTFCK 60
QY 61 CDSTLRLCVQSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
DB 61 CDSTLRLCVQSTHVDIRTLIEDLIMGTLGIYXPCISQKP 98
RESULT 23
ID Q2MJT4_HPV16 PRELIMINARY; PRT; 98 AA.
AC Q2MJT4;
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 1.
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Meshkat Z., Hasean Z.M., Soleimanjahi H., Mahmoudi M., Mirshahabi H.,

RA Ghafari S.R., Sabokbar T.;
 RT "Cloning and sequence analysis of Human papillomavirus type 16 E7 gene
 in Iran."
 RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: DQ333401; ABC54573.1; -; Genomic DNA.
 DR SEQUENCE 98 AA; 10992 MW; 9BD6125357D379EB CRC64;

Query Match 98.1%; Score 507; DB 2; Length 98;
 Best Local Similarity 95.9%; Pred. No. 1.7e-51;
 Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMLDQPEPTDLYXXQUNDSEEDIEDGPAQAEPDRAHYNIVTFCK 60
 DB 1 MHGDTPLHEHYMLDQPEPTDLYCYEQUNDSEEDIEDGPAQAEPDRAHYNIVTFCK 60
 QY 61 CDSTLRLCVOSTHVDIRTEIDLMGTGIVXPICSQKP 98
 DB 61 CDSTLRLCVOSTHVDIRTEIDLMGTGIVCPICQKP 98

RESULT 24
 ID 012338 HPV16 PRELIMINARY; PRT; 98 AA.
 AC 012338

DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.

DT 01-JUL-1997, sequence version 1.

DT 07-FEB-2006, entry version 20.

DE E7 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Alphapapillomavirus.

OX NCBI_TaxID=333760;

NP NUCLEOTIDE SEQUENCE.

RX MEDLINE=97437474; PubMed=9292007;

RA Tonesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

RA Beth-Giraldo E., Giraldo G.;

RT "Sequence variations and viral genomic state of human papillomavirus

RT type 16 in penile carcinomas from Ugandan patients.";

RL J. Gen. Virol. 78:2199-2208(1997).

RN [2]

NP NUCLEOTIDE SEQUENCE.

RA Jinhua X., Xinxing W., Yun T.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

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CC -----

CC EMBL: AF003022; AAB70739.1; -; Genomic DNA.

DR EMBL: AF477385; AAM03025.1; -; Genomic DNA.

DR GO: GO:0005622; C:intracellular; IEA.

DR GO: GO:0003700; F:transcription factor activity; IEA.

DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro: IPR000148; Papv1_E7.

DR Pfam: PF00527; E7; 1.

DR SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 97.5%; Score 504; DB 2; Length 98;
 Best Local Similarity 95.9%; Pred. No. 3.9e-51;
 Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMLDQPEPTDLYXXQUNDSEEDIEDGPAQAEPDRAHYNIVTFCK 60
 DB 1 MHGDTPLHEHYMLDQPEPTDLYCYEQUNDSEEDIEDGPAQAEPDRAHYNIVTFCK 60

QY 61 CDSTLRLCVOSTHVDIRTEIDLMGTGIVXPICSQKP 98
 DB 61 CDSTLRLCVOSTHVDIRTEIDLMGTGIVCPICQKP 98

RESULT 25
 ID 08V1J0 HPV16 PRELIMINARY; PRT; 98 AA.
 AC 08V1J0;

DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2002, sequence version 1.

DT 07-FEB-2006, entry version 11.

DE E7 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Alphapapillomavirus.

OX NCBI_TaxID=333760;

NP NUCLEOTIDE SEQUENCE.

RA Jinhua X., Xinxing W., Yun T.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

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CC -----

CC EMBL: AF461264; AAL66736.1; -; Genomic DNA.

DR GO: GO:0005622; C:intracellular; IEA.

DR GO: GO:0003700; F:transcription factor activity; IEA.

DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro: IPR000148; Papv1_E7.

DR Pfam: PF00527; E7; 1.

DR SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match 96.7%; Score 500; DB 2; Length 98;
 Best Local Similarity 94.9%; Pred. No. 1.2e-50;
 Matches 93; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMLDQPEPTDLYXXQUNDSEEDIEDGPAQAEPDRAHYNIVTFCK 60
 DB 1 MHGDTPLHEHYMLDQPEPTDLYCYEQUNDSEEDIEDGPAQAEPDRAHYNIVTFCK 60

QY 61 CDSTLRLCVOSTHVDIRTEIDLMGTGIVXPICSQKP 98
 DB 61 CDSTLRLCVOSTHVDIRTEIDLMGTGIVCPICQKP 98

RESULT 26
 ID 08ORD4 HPV16 PRELIMINARY; PRT; 98 AA.

AC 08ORD4;

DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.

DT 01-JUN-2002, sequence version 1.

DT 07-FEB-2006, entry version 10.

DE E7 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Alphapapillomavirus.

OX NCBI_TaxID=333760;

NP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;

RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,

RA Cheung J.L.K., Xu L.Y., Cheng A.F.;

RT "Human papillomavirus type 16 intracytic variant infection and risk

RT for cervical neoplasia in southern China.";

RL J. Infect. Dis. 186:696-700(2002).

RN [2]

NP NUCLEOTIDE SEQUENCE.

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CC -----

CC EMBL: AF486329; AAL96634.1; -; Genomic DNA.

DR GO: GO:0005622; C:intracellular; IEA.

DR GO: GO:0003700; F:transcription factor activity; IEA.

DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro: IPR000148; Papv1_E7.

DR Pfam: PF00527; E7; 1.

DR SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 96.5%; Score 499; DB 2; Length 98;
Best Local Similarity 94.3%; Pred. No. 1.5e-50;
Matches 93; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60
DB 1 MHGDTPLHRYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60

QY 61 CDSTLRACVSTHVDIRTTLEDLMGTGIVXPC 98
DB 61 CDSTLRACVSTHVDIRTTLEDLMGTGIVXPC 98

RESULT 27
Q98SP6_HPV16 PRELIMINARY; PRT; 94 AA.
AC Q98SP6;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ponglikitmongkol M., Vaeeseewoatcharn K.,
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
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EMBL: AF469197; AAO15692.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
FT NON TER 94 94
SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 94.0%; Score 486; DB 2; Length 94;
Best Local Similarity 95.7%; Pred. No. 4.9e-45;
Matches 90; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60
DB 1 MHGDTPLHRYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60

QY 61 CDSTLRACVSTHVDIRTTLEDLMGTGIVXPC 94
DB 61 CDSTLRACVSTHVDIRTTLEDLMGTGIVXPC 94

RESULT 28
Q9QDH6_HPV16 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee H.P., Song Y.S., Kim J.W., Park N.H., Kang S.B.,
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
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EMBL: AF187867; AAF13395.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
FT NON TER 93 93
SQ SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 92.5%; Score 478; DB 2; Length 93;
Best Local Similarity 95.7%; Pred. No. 4.2e-48;
Matches 89; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60
DB 1 MHGDTPLHRYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60

QY 61 CDSTLRACVSTHVDIRTTLEDLMGTGIVXPI 93
DB 61 CDSTLRACVSTHVDIRTTLEDLMGTGIVXPI 93

RESULT 29
Q9QDH2_HPV16 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee H.P., Song Y.S., Kim J.W., Park N.H., Kang S.B.,
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
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EMBL: AF187869; AAF13399.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
FT NON TER 93 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 92.3%; Score 477; DB 2; Length 93;
Best Local Similarity 95.7%; Pred. No. 5.6e-48;
Matches 89; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60
DB 1 MHGDTPLHRYMDLOPETTDLYXXYQOLNDSSEEDSIDDPAGQAEPRRAHYNIVTFCK 60

QY 61 CDSTLRACVSTHVDIRTTLEDLMGTGIVXPI 93
DB 61 CDSTLRACVSTHVDIRTTLEDLMGTGIVXPI 93

RESULT 30
Q9QDH4_HPV16 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.

DT 07-FEB-2006, entry version 14.
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 CC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 CC AlphaPapillomavirus.
 NCBI_TaxID=333760;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
 RL Submitted (SFP-1999) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AF187868; AAF13397.1; -; Genomic_DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000148; Papv1_E7.
 DR Pfam: PF00527; E7; 1.
 FT NON TER 93 93
 SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C6A1F CRC64;

Query Match 92.3%; Score 477; DB 2; Length 93;
 Best Local Similarity 95.7%; Pred. No. 5.6e-48;
 Matches 89; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPFLHEHYMLDLPETTDLYXXYXOLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
 Db 1 MHGDPFLHEHYMLDLPETTDLYCYEQSDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
 61 CDSTLRFCVOSTHVDIRTLIEDLTMGTGIVXPI 93
 61 CDSTLRFCVOSTHVDIRTLIEDLTMGTGIVCPI 93

RESULT 31
 ID Q9QDH8 HPV16 PRELIMINARY; PRT; 93 AA.
 AC Q9QDH8;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE E7 protein (Fragment).
 OS Human papillomavirus type 16.
 CC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 CC AlphaPapillomavirus.
 NCBI_TaxID=333760;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
 RL Submitted (SFP-1999) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AF187866; AAF13393.1; -; Genomic_DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000148; Papv1_E7.
 DR Pfam: PF00527; E7; 1.
 FT NON TER 93 93
 SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C6A1F CRC64;

Query Match 92.3%; Score 477; DB 2; Length 93;
 Best Local Similarity 95.7%; Pred. No. 5.6e-48;
 Matches 89; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPFLHEHYMLDLPETTDLYXXYXOLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
 Db 1 MHGDPFLHEHYMLDLPETTDLYCYEQSDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60

Qy 61 CDSTLRFCVOSTHVDIRTLIEDLTMGTGIVXPI 93
 Db 61 CDSTLRFCVOSTHVDIRTLIEDLTMGTGIVCPI 93

RESULT 32
 ID Q8B5P5 9PAPI PRELIMINARY; PRT; 77 AA.
 AC Q8B5P5;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 11.
 DE E7 protein (Fragment).
 OS Human Papillomavirus.
 CC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 CC AlphaPapillomavirus.
 NCBI_TaxID=10566;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ponglikitmongkol M., Vaeeteewoatcharn K.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AF469198; AAO15694.1; -; Genomic_DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000148; Papv1_E7.
 DR Pfam: PF00527; E7; 1.
 FT NON TER 77 77
 SQ SEQUENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;

Query Match 78.5%; Score 406; DB 2; Length 77;
 Best Local Similarity 96.1%; Pred. No. 1e-39;
 Matches 74; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MHGDPFLHEHYMLDLPETTDLYXXYXOLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
 Db 1 MHGDPFLHEHYMLDLPETTDLYCYEQSDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
 61 CDSTLRFCVOSTHVDIR 77
 61 CDSTLRFCVOSTHVDIR 77

RESULT 33
 ID VE7 HPV35 STANDARD; PRT; 99 AA.
 AC P27230;
 DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.
 DT 07-FEB-2006, entry version 32.
 DE Protein E7.
 GN Name=E7;
 OS Human papillomavirus type 35.
 CC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 CC AlphaPapillomavirus.
 NCBI_TaxID=10587;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=Isolate 35H;
 RX MEDLINE=94265501; PubMed=8205838;
 RA Delius H., Hofmann B.;
 RL Curr. Top. Microbiol. Immunol. 186:13-31 (1994).
 CC -----
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 CC -----
 DR EMBL: AF469198; AAO15694.1; -; Genomic_DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000148; Papv1_E7.
 DR Pfam: PF00527; E7; 1.
 FT NON TER 77 77
 SQ SEQUENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;

Query Match 78.5%; Score 406; DB 2; Length 77;
 Best Local Similarity 96.1%; Pred. No. 1e-39;
 Matches 74; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Virology 186:770-776(1992).
CC -FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC -----
DR EMBL: W74117; AAA46967.1; -; Genomic_DNA.
DR EMBL: X74477; CAAS2562.1; -; Genomic_DNA.
DR PIR: F40824; W7ML35.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1
FT PROTEIN 99
FT MOTIF 59 /FTID=PRO_0000133433.
FT MOTIF 92 C-XX-C motif-1.
FT MOTIF 95 C-XX-C motif-2.
SQ SEQUENCE 99 AA; 10954 MW; 8EBA8F248051E226 CRC64;

Query Match 73.8%; Score 381.5; DB 1; Length 99;
Best Local Similarity 73.5%; Pred. No. 1,1e-36;
Matches 72; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

QY 1 MHGDTPLHEHYMDLOPETTDLYXXQLNDS--EEBEIDGPAQAPDPRAHNYIVTFCC 59
DB 1 MHGEITTLQDYVLDLPEATDLYCYEQLCSSSEBEEDTIDGPAQAPDTSNINIVTSCC 60
DB 61 KCSTLRCLCVQSTHVDIRKEDLMGTFGIVCPGCSQR 98

RESULT 34
Q76WP2_9PAPI PRELIMINARY; PRT; 99 AA.
AC Q76WP2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE E7 protein.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_Taxid=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fujinaga K.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: D10597; BAA01448.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 99 AA; 10954 MW; 8EBA8F248051E226 CRC64;

Query Match 73.8%; Score 381.5; DB 2; Length 99;
Best Local Similarity 73.5%; Pred. No. 1,1e-36;
Matches 72; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

QY 1 MHGDTPLHEHYMDLOPETTDLYXXQLNDS--EEBEIDGPAQAPDPRAHNYIVTFCC 59
DB 1 MHGEITTLQDYVLDLPEATDLYCYEQLCSSSEBEEDTIDGPAQAPDTSNINIVTSCC 60
DB 61 KCSTLRCLCVQSTHVDIRKEDLMGTFGIVCPGCSQR 98

RESULT 35
VE7_HP31 STANDARD; PRT; 98 AA.
AC P17387;
DT 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1990, sequence version 1.
DT 07-FEB-2006, entry version 34.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 31.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=10585;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=89299478; PubMed=2545036;
RA Goldborough M.D., Diehlvestre D., Temple G.F., Lorincz A.T.;
RT "Nucleotide sequence of human papillomavirus type 31: a cervical
neoplasia-associated virus."
RL Virology 171:306-311(1989).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC -----
DR EMBL: J04353; AAA46951.1; -; Genomic_DNA.
DR PIR: B32444; W7ML31.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1
FT PROTEIN 98
FT MOTIF 58 /FTID=PRO_0000133429.
FT MOTIF 91 C-XX-C motif-1.
FT MOTIF 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 10918 MW; 793B7F5BC734E9B9 CRC64;

Query Match 72.0%; Score 372; DB 1; Length 98;
Best Local Similarity 71.1%; Pred. No. 1,4e-35;
Matches 69; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLOPETTDLYXXQLNDS--EEBEIDGPAQAPDPRAHNYIVTFCC 60
DB 1 MHGEITTLQDYVLDLPEATDLYCYEQLPDSSEBEEDVIDSPAQAPDTSNINIVTSCC 60
DB 61 KCSTLRCLCVQSTHVDIRKEDLMGTFGIVCPGCSQR 97

RESULT 36
Q6T377_HP31 PRELIMINARY; PRT; 98 AA.
AC Q6T377;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE E7 transforming protein variant.
OS Human papillomavirus type 31.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=10585;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fiedler M., Fitzky B., Durst M., Zwerschke W., Jansen-Durr P.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AY38621; AAR13015.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10917 MW; 9D31DF1CF9064B1 CRC64;

Query Match
Best Local Similarity 71.0%; Score 367; DB 2; Length 98;
Matches 67; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEXYMLDLOPETTDLYXXYXQLNDSSEDEIDGPAQAEPRRAHNYITVFCCK 60
Db 1 MRGEPFLQDVLLDQPKATDHCYEQPLDSSEEDVDSDAGQAKPDTSNIVITFCCK 60

Qy 61 CDSTLRLCVOSTHVDIRTLIEDLMTGLGIVXPICSK 97
Db 61 CESTLRLCVOSTQYDIRTLQELMLGMSFGIVCPNCSTR 97

RESULT 37
Q8B563_9PAPI PRELIMINARY; PRT; 65 AA.
AC Q8B563;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE E7 protein (fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Unclassified Papillomaviridae.
OX NCBI_Taxid=10566;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ponglikitmongkol M., Vaeeteewoottacharn K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL: AF548023; AAO16240.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
FT NON_TER
SQ SEQUENCE 65 AA; 7373 MW; E9D7AD7923700195 CRC64;

Query Match
Best Local Similarity 66.3%; Score 343; DB 2; Length 65;
Matches 62; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEXYMLDLOPETTDLYXXYXQLNDSSEDEIDGPAQAEPRRAHNYITVFCCK 60
Db 1 MHGEPFLHEXYMLDLOPETTDLYCYEQPLDSSEEDIDGPAQAEPRRAHNYITVFCCK 60

Qy 61 CDSTLR 65
Db 61 CDSTLR 65

RESULT 38
O90724_HPV67 PRELIMINARY; PRT; 99 AA.
AC O90724;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE ORF E7.
OS Human papillomavirus type 67.

```

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CC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
CC Alphapapillomavirus.
OX NCBI_Taxid=37120;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99073695; PubMed=9857984; DOI=10.1023/A:1008002905588;
RA Kiril Y., Matsukura T.;
RT "Nucleotide sequence and phylogenetic classification of human
RT papillomavirus type 67."
RL Virus Genes 17:117-121(1998).
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DR EMBL: D21208; BA28853.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 99 AA; 11157 MW; 81A4A636D7568C44 CRC64;

Query Match
Best Local Similarity 61.1%; Score 316; DB 2; Length 99;
Matches 59; Conservative 17; Mismatches 21; Indels 2; Gaps 1;

Qy 1 MHGDPPTLHEXYMLDLOPETTDLYXXYXQLNDSSEDEIDGPAQAEPRRAHNYITVFC 58
Db 1 MRGDKATLDYLLDKPETTDLYCYEQPLDSSEEDVGVGDRPDGAKPDTTNHIVTVC 60

Qy 59 CKDSTLRLCVOSTHVDIRTLIEDLMTGLGIVXPICSK 97
Db 61 NICECTRLCTHSTADVTRTQGLMTMTGLIVPTCAQQ 99

RESULT 39
VE7 HPV33 STANDARD; PRT; 97 AA.
AC P06429;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1988, sequence version 1.
DT 07-FEB-2006, entry version 40.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 33.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=10586;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=86200464; PubMed=3009902;
RA Cole S.T., Streeck R.E.;
RT "Genome organization and nucleotide sequence of human papillomavirus
RT type 33, which is associated with cervical cancer."
RL J. Virol. 58:991-995(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=92219410; PubMed=1313922;
RA Snijders P.J.F., van den Brule A.J.C., Schrijnemakers H.F.J.,
RA Raaphorst P.M.C., Meijer C.J.L.M., Walboomers J.M.M.;
RT "Human papillomavirus type 33 in a tonsillar carcinoma generates its
RT putative E7 mRNA via two 86* transcribed species which are terminated
RT at different early region poly(A) sites."
RL J. Virol. 66:3172-3178(1992).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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DR EMBL: M12732; AAA46959.1; -; Genomic_DNA.
DR EMBL: X64084; CAA45430.1; -; mRNA.

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DR EMBL: X64085; CAA45434.1; -, mRNA.
DR PIR: A03689; W7ML33.
DR InterPro: IPR00148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
DR DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1 97 Protein E7.
FT MOTIF 58 61 /FTid=PRO_0000133431.
FT MOTIF 91 94 C-XX-C motif-2.
SQ SEQUENCE 97 AA; 10837 MW; 639DCFF4343243C8 CRC64;

Query Match 57.1%; Score 295; DB 1; Length 97;
Best Local Similarity 57.7%; Pred. No. 1.6e-26;
Matches 56; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MGGDTPLHRYMDDLQPETTDLYXXYQINDSSEEDIDPGAGPDRAHYNIYTFCC 60
Db 1 MRGHKPTLKEVYIDLPEPTDLYCYEQLSDSDDEGLDRPDGAQAPATADYIIVICCHT 60
61 CDTSTRLCVOSTHVDIRTLIEDLMGTGLGVXPCISQK 97
61 CTTTTRLCVNSTASDLRTIQQLMGTIVIVCPICACQ 97

RESULT 40
VE7_HPV52 STANDARD; PRT; 99 AA.
AC P36831;
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1994, sequence version 1.
DT 07-FEB-2006, entry version 32.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 52.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10618;
RN RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP MEDLINE=94265501; PubMed=8205838;
RA Dellus H., Hofmann B.;
RT "Cloning and characterization of human papillomavirus type 52 from
RT cervical carcinoma in Indonesia.";
RL Int. J. Cancer 48:516-522(1991).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC -----
EMBL: X74481; CAA52586.1; -, Genomic_DNA.
DR PIR: S36574; S36574.
DR InterPro: IPR00148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
DR DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1 99 Protein E7.
FT MOTIF 60 63 /FTid=PRO_0000133448.
FT MOTIF 93 96 C-XX-C motif-1.
FT MOTIF 96 96 C-XX-C motif-2.
SQ SEQUENCE 99 AA; 11032 MW; 55CFA02EAD6F96F CRC64;

Query Match 56.9%; Score 294; DB 1; Length 99;
Best Local Similarity 57.1%; Pred. No. 2.2e-26;

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Matches 56; Conservative 17; Mismatches 23; Indels 2; Gaps 1;

Qy 1 MGGDTPLHRYMDDLQPETTDLYXXYQINDSSEED--IDGAGAGPDRAHYNIYTFCC 58
Db 1 MRGHKPTLKEVYIDLPEPTDLYCYEQLSDSDDEGLDRPDGAQAPATADYIIVICCHT 60
59 CKCDSTRLCVOSTHVDIRTLIEDLMGTGLGVXPCISQ 96
61 HSCDSTRLCVOSTHVDIRTLIEDLMGTGLGVXPCISQ 98

RESULT 41
VE7_HPV58 STANDARD; PRT; 98 AA.
AC P26557;
DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1992, sequence version 1.
DT 07-FEB-2006, entry version 32.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10598;
RN RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP MEDLINE=92024102; PubMed=1656594;
RA Kiril Y., Iwamoto S., Matsukura T.;
RT "Human papillomavirus type 58 DNA sequence.";
RL Virology 185:424-427(1991).
RN [2]
RP UBIQUITINATION SITE MET-1.
RX PubMed=15254040; DOI=10.1074/jbc.M407201200;
RA Ben-Saadon R., Fajerman I., Ziv T., Hellman U., Schwartz A.L.,
RA Clechanover A.;
RT "The tumor suppressor protein p16(INK4a) and the human papillomavirus
RT oncoprotein-58 E7 are naturally occurring lysine-less proteins that
RT are degraded by the ubiquitin system. Direct evidence for
RT ubiquitination at the N-terminal residue.";
RL J. Biol. Chem. 279:41414-41421(2004).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -!- PTM: Polyubiquitinated on the N-terminus; which leads to
CC proteasomal degradation (by host).
CC -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC -----
EMBL: D90400; BA33846.1; -, Genomic_DNA.
DR PIR: F36779; W7ML58.
DR InterPro: IPR00148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
DR DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation; Ub1 conjugation.
FT CHAIN 1 98 Protein E7.
FT MOTIF 59 62 /FTid=PRO_0000133454.
FT MOTIF 92 95 C-XX-C motif-1.
FT MOTIF 95 95 C-XX-C motif-2.
FT CROSSLINK 1 1 Peptide (Met-Gly) (interchain with G-Cter
in ubiquitin) (by host).
SQ SEQUENCE 98 AA; 10819 MW; D719984F3CF48D12 CRC64;

Query Match 56.0%; Score 289.5; DB 1; Length 98;
Best Local Similarity 57.1%; Pred. No. 7.2e-26;
Matches 56; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MGGDTPLHRYMDDLQPETTDLYXXYQINDSSEED-IDGAGAGPDRAHYNIYTFCC 59
Db 1 MRGHKPTLKEVYIDLPEPTDLYCYEQLSDSDDEGLDRPDGAQAPATADYIIVICCHT 60
60 KCDDSTRLCVOSTHVDIRTLIEDLMGTGLGVXPCISQK 97
60 KCDSTRLCVOSTHVDIRTLIEDLMGTGLGVXPCISQK 97

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Db      61 TCGTTRLCINSTTTDVRLTQQLMGTCCTIVCPSCAQ 98

RESULT 42
OS47M4 HPV58
ID   OS47M4_HPV58      PRELIMINARY;   PRT;       98 AA.
AC   OS47M4;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DE   07-FEB-2006, entry version 4.
DE   E7 protein.
GN   Name=E7;
OS   Human papillomavirus type 58.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Alphapapillomavirus.
OX   NCBI_TaxId=10598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=E6/E7-HK-7, E6/E7-HK-9, E6/E7-HK-12, and E6/E7-HK-5;
RX   MEDLINE=2216796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RA   Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA   Cheung J.L.K., Cheng A.F.;
RT   "Association of human papillomavirus type 58 variant with the risk of
RT   cervical cancer.";
RL   J. Natl. Cancer Inst. 94:1249-1253(2002).
CC   -----
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CC   -----
DR   EMBL; AF478138; ALA85383.1; -; Genomic_DNA.
DR   EMBL; AF478140; AAL85385.1; -; Genomic_DNA.
DR   EMBL; AF478143; AAL85388.1; -; Genomic_DNA.
DR   EMBL; AF478146; AAL85391.1; -; Genomic_DNA.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ   SEQUENCE   98 AA; 10819 MW; D71984f3cf48d12 CRC64;

Query Match      56.0%; Score 289.5; DB 2; Length 98;
Best Local Similarity 57.1%; Pred. No. 7.2e-26;
Matches 56; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

Qy      1 MHGDPPLHRYMDLQPEPTDLYXXQLNDSSSEED-EIDGPAGQAEPRAHYIVTFCC 59
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MRGNPFLREYIDLHPEPTDLFCYEQLCSDBDEGLRPPDQAPATANYIVTCY 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      60 KCDSTRLCVQSTHVDIRTEDLMLGTLGIVXPICSQK 97
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 TCGTTRLCINSTTTDVRLTQQLMGTCCTIVCPSCAQ 98
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 43
OSQC21 HPV58
ID   OSQC21_HPV58      PRELIMINARY;   PRT;       98 AA.
AC   OSQC21;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DE   07-FEB-2006, entry version 17.
DE   E7 protein.
OS   Human papillomavirus type 58.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Alphapapillomavirus.
OX   NCBI_TaxId=10598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=E7-HK-2;
RA   Chan P.K.S., Lam C.W., Chan M.Y.M., Li W.W.H., Cheung J.L.K.,
RA   Cheng A.F.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=E6/E7-HK-1, E6/E7-HK-11, E6/E7-HK-14, E6/E7-HK-15, and
RC   E6/E7-HK-16;

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RX   MEDLINE=2216796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RA   Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA   Cheung J.L.K., Cheng A.F.;
RT   "Association of human papillomavirus type 58 variant with the risk of
RT   cervical cancer.";
RL   J. Natl. Cancer Inst. 94:1249-1253(2002).
CC   -----
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CC   -----
DR   EMBL; AF192270; AAF15691.1; -; Genomic_DNA.
DR   EMBL; AF478132; AAL85377.1; -; Genomic_DNA.
DR   EMBL; AF478142; AAL85387.1; -; Genomic_DNA.
DR   EMBL; AF478146; AAL85391.1; -; Genomic_DNA.
DR   EMBL; AF478147; AAL85392.1; -; Genomic_DNA.
DR   EMBL; AF478145; AAL85390.1; -; Genomic_DNA.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro: IPR000148; Papv1_E7.
DR   Pfam: PF00527; E7_1.
SQ   SEQUENCE   98 AA; 10976 MW; D70C8D4DD4CE5D12 CRC64;

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Query Match      55.8%; Score 288.5; DB 2; Length 98;
Best Local Similarity 57.1%; Pred. No. 9.4e-26;
Matches 56; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

Qy      1 MHGDPPLHRYMDLQPEPTDLYXXQLNDSSSEED-EIDGPAGQAEPRAHYIVTFCC 59
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MRGNPFLREYIDLHPEPTDLFCYEQLCSDBDEGLRPPDQAPATANYIVTCY 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      60 KCDSTRLCVQSTHVDIRTEDLMLGTLGIVXPICSQK 97
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 TCGTTRLCINSTTTDVRLTQQLMGTCCTIVCPSCAQ 98
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 44
OSQSF0 HPV58
ID   OSQSF0_HPV58      PRELIMINARY;   PRT;       98 AA.
AC   OSQSF0;
DT   01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2002, sequence version 1.
DE   07-FEB-2006, entry version 11.
DE   E7 protein.
OS   Human papillomavirus type 58.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Alphapapillomavirus.
OX   NCBI_TaxId=10598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=E6/E7-HK-8;
RX   MEDLINE=2216796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RA   Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA   Cheung J.L.K., Cheng A.F.;
RT   "Association of human papillomavirus type 58 variant with the risk of
RT   cervical cancer.";
RL   J. Natl. Cancer Inst. 94:1249-1253(2002).
CC   -----
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CC   -----
DR   EMBL; AF478139; AAL85384.1; -; Genomic_DNA.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro: IPR000148; Papv1_E7.
DR   Pfam: PF00527; E7_1.
SQ   SEQUENCE   98 AA; 10833 MW; 8248DD5321354CC9 CRC64;

Query Match      55.4%; Score 286.5; DB 2; Length 98;
Best Local Similarity 56.1%; Pred. No. 1.6e-25;
Matches 55; Conservative 17; Mismatches 25; Indels 1; Gaps 1;

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Oy		1	MHGDPPTLHEXWMLDQPEPTTDLXXYXOLNDSSEED -SIDGPAQAEPDRAHYNIVTECC	59
Dd		1	MRGNPNPLIREIYLHDHPETPDLCYEQLCDSSDEBEIGIDPDDGAQPATANYIIVTCY	60
Oy		60	KCDSTLRCLVOSTHVDIRTEDLLMGTLGIYXPISQK	97
Dd		61	TCSITVRCLINSTSTATEVRTLQQLLMGTCIYCPSCAQ	98
RESULT 45				
OBOHN7 HPV58				
AC	OBOHN7 HPV58	PRELIMINARY;	PRT;	98 AA.
Dt	01-JUN-2002,	integrated into UniProtKB/TrEMBL.		
Dt	01-JUN-2002,	sequence version 1.		
Dt	07-FEB-2006,	entry version 12.		
Dt	E7 protein.			
Os	Human papillomavirus type 58.			
OC	Virusae; deDNA viruses, no RNA stage; Papillomaviridae;			
OC	Alphapapillomavirus.			
OK	NCBI_TaxID=10598;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=E6/E7-HK-3, and E6/E7-HK-4;			
Rx	MEDLINE=22116796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;			
RA	Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,			
RA	Cheung J.L.K., Cheng A.F.;			
RT	"Association of human papillomavirus type 58 variant with the risk of			
RL	cervical cancer";			
RL	J. Natl. Cancer Inst. 94:1249-1253(2002).			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
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CC	-----			
DR	EMBL; AF478134; AAL85379.1; -; Genomic DNA.			
DR	EMBL; AF478135; AAL85380.1; -; Genomic DNA.			
DR	GO; GO:0005622; C:intracellular; IEA.			
DR	GO; GO:0003700; F:transcription factor activity; IEA.			
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.			
DR	InterPro; IPR000148; Papyv_E7.			
DR	Pfam; PF00527; E7_1.			
SQ	SEQUENCE 98 AA, 10791 MW, D719984F3CEC3A42 CRC64;			
Query Match	55.2%; Score 285.5; DB 2; Length 98;			
Best Local Similarity	57.1%; Pred. No. 2.1e-25;			
Matches	56; Conservative 15; Mismatches 26; Indels 1; Gaps 1.			
Oy		1	MHGDPPTLHEXWMLDQPEPTTDLXXYXOLNDSSEED -RIDGNAQAEPDRAHYNIVTECC	59
Dd		1	MRGNPNPLIREIYLHDHPETPDLCYEQLCDSSDEBEIGIDPDDGAQPATANYIIVTCY	60
Oy		60	KCDSTLRCLVOSTHVDIRTEDLLMGTLGIYXPISQK	97
Dd		61	TCSITVRCLINSTTTDARTLQQLMGTCIYCPSCAQ	98
RESULT 46				
OBOHQ2 HPV58				
AC	OBOHQ2 HPV58	PRELIMINARY;	PRT;	98 AA.
Dt	01-JUN-2002,	integrated into UniProtKB/TrEMBL.		
Dt	01-JUN-2002,	sequence version 1.		
Dt	07-FEB-2006,	entry version 12.		
Dt	E7 protein.			
Os	Human papillomavirus type 58.			
OC	Virusae; deDNA viruses, no RNA stage; Papillomaviridae;			
OC	Alphapapillomavirus.			
OK	NCBI_TaxID=10598;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=E6/E7-HK-17, and E6/E7-HK-18;			
Rx	MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;			
RA	Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,			

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RA      Cheung J.L.K., Cheng A.F.;
RT      "Association of human papillomavirus type 58 variant with the risk of
RL      cervical cancer.";
RL      J. Natl. Cancer Inst. 94:1249-1253(2002).
CC      -----
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CC      -----
DR      EMBL; AF478148; ALA85393.1; -; Genomic DNA.
DR      EMBL; AF478149; ALA85394.1; -; Genomic DNA.
DR      GO; GO:0005622; C:intracellular; IEA.
DR      GO; GO:0003700; F:transcription factor activity; IEA.
DR      GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR      InterPro; IPR000148; Papv1_E7.
DR      Pfam; PF00527; E7; 1.
SQ      SEQUENCE 98 AA; 10803 MW; 8248DD4F3CF48CC9 CRC64;
Query Match 55.2%; Score 285.5; DB 2; Length 98;
Best Local Similarity 56.1%; Pred. No. 2,1e-25;
Matches 55; Conservative 17; Mismatches 25; Indels 1; Gaps 1;

Cy      1 MHGDTPLTLEHYMDLQPEPTDLYLYXKOLNDSSEED-ETDGPAGAEPPDRAHNYIVTFC 59
Db      1 MRGNPPTLRREYIIDLHPEPTDLFCFEQICDSSDEDEIGLDPDQAQAPATANYIVTCY 60
        60 KCDSTLRLCVOSTHVDRIETLEDLMGTLGVYXPCSQK 97
        61 TCGTTRLCINSTATVEVTLQQLIMGTCTVCPSCAQO 98

RESULT 47
09QCZ2_HPV58 PRELIMINARY; PRT; 98 AA.
AC      09QCZ2_HPV58
DT      01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT      01-MAY-2000, sequence version 1.
DT      07-FEB-2006, entry version 16.
DE      E7 protein.
OS      Human papillomavirus type 58.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Alphapapillomavirus.
CX      NCBI_TaxId=10598;
[1]
RN      NUCLEOTIDE SEQUENCE.
RP      STRAIN=E7-HK-1;
RC      Chan P.K.S., Lam C.W., Chan M.Y.M., Li W.W.H., Cheung J.L.K.,
RA      Cheng A.F.;
RL      Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
[2]
RN      NUCLEOTIDE SEQUENCE.
RP      STRAIN=E6/E7-HK-2, and E6/E7-HK-6;
RC      MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RX      Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA      Cheung J.L.K., Cheng A.F.;
RL      "Association of human papillomavirus type 58 variant with the risk of
RT      cervical cancer.";
RL      J. Natl. Cancer Inst. 94:1249-1253(2002).
CC      -----
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CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL; AF192269; AAF13690.1; -; Genomic DNA.
DR      EMBL; AF478133; ALA85378.1; -; Genomic DNA.
DR      EMBL; AF478137; ALA85382.1; -; Genomic DNA.
DR      GO; GO:0005622; C:intracellular; IEA.
DR      GO; GO:0003700; F:transcription factor activity; IEA.
DR      GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR      InterPro; IPR000148; Papv1_E7.
DR      Pfam; PF00527; E7; 1.
SQ      SEQUENCE 98 AA; 10861 MW; ED3C57B911355721 CRC64;
Query Match 55.0%; Score 284.5; DB 2; Length 98;
Best Local Similarity 56.1%; Pred. No. 2.8e-25;

```

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Matches 55; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MHGDTPLHEMYMDLQPEPTTDLXXYXQLNDSSEED-EIDGPAGQAEPPRAHNYIVTFCC 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRGNPPTLRXYILDHPEPIDLFCYEQLCDSSDEDEIGLDPDGOAQPATANYIYVTCY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 60 KCDSTLRCLVOSTHVDIRTELDLMGTGIGYXPCISQK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TCSITVRLCINSTTVDRTVRLQQLLMGTCTIVCPSCAQ 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 48
Q0QSE9_HPV58 PRELIMINARY; PRT; 98 AA.
AC Q0QSE9;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DE 07-FEB-2006, entry version 11.
DE E7 protein.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E6/E7-HK-10;
RX MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
  Cheung J.L.K., Cheng A.F.;
  "Association of human papillomavirus type 58 variant with the risk of
  cervical cancer.";
  J. Natl. Cancer Inst. 94:1249-1253(2002).
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CC
CC EMBL; AF478141; AAL85386.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10833 MW; ED24DEA180BC4F8A8 CRC64;

Query Match 54.8%; Score 283.5; DB 2; Length 98;
Best Local Similarity 56.1%; Pred. No. 3.7e-25;
Matches 55; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MHGDTPLHEMYMDLQPEPTTDLXXYXQLNDSSEED-EIDGPAGQAEPPRAHNYIVTFCC 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRGNPPTLRXYILDHPEPIDLFCYEQLCDSSDEDEIGLDPDGOAQPATANYIYVTCY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 60 KCDSTLRCLVOSTHVDIRTELDLMGTGIGYXPCISQK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TCSITVRLCINSTTVDRTVRLQQLLMGTCTIVCPSCAQ 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 49
Q0QSE8_HPV58 PRELIMINARY; PRT; 98 AA.
AC Q0QSE8;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE E7 protein.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=10598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E6/E7-HK-13;
RX MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;

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RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
  Cheung J.L.K., Cheng A.F.;
  "Association of human papillomavirus type 58 variant with the risk of
  cervical cancer.";
  J. Natl. Cancer Inst. 94:1249-1253(2002).
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CC
CC EMBL; AF478144; AAL85389.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10998 MW; D70C8D4620711D12 CRC64;

Query Match 54.4%; Score 281.5; DB 2; Length 98;
Best Local Similarity 56.1%; Pred. No. 6.3e-25;
Matches 55; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MHGDTPLHEMYMDLQPEPTTDLXXYXQLNDSSEED-EIDGPAGQAEPPRAHNYIVTFCC 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRGNPPTLRXYILDHPEPIDLFCYEQLCDSSDEDEIGLDPDGOAQPATANYIYVTCY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 60 KCDSTLRCLVOSTHVDIRTELDLMGTGIGYXPCISQK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TCHTIVRLCINSTTVDRTVRLQQLLMGTCTIVCPSCAQ 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 50
Q0QLP4_9PAPI PRELIMINARY; PRT; 98 AA.
AC Q0QLP4;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE E7.
OS Human papillomavirus type 6.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=31552;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Human papillomavirus type 6vc;
RX MEDLINE=99429608; PubMed=10501500;
RA Kovelman R., Bilter G.K., Roman A., Brown D.R., Barbosa M.S.;
  "Human papillomavirus type 6: Classification of clinical isolates and
  functional analysis of E2 proteins.";
  J. Gen. Virol. 80:2445-2451(1999).
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CC
CC EMBL; AF092932; AAF0065.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10903 MW; 74DD65095A39DDE5 CRC64;

Query Match 47.8%; Score 247; DB 2; Length 98;
Best Local Similarity 53.5%; Pred. No. 7.3e-21;
Matches 53; Conservative 14; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGDTPLHEMYMDLQPEPTTDLXXYXQLNDSSEED-DEIDGPAGQAEPPRAHNYIVTFCC 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGRHNTVTKDIVDLQPPDVGHLHCYEQLVDSSEDEVDDGQ--DSQPLKQHYQIVTCC 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 59 CKDSTLRCLVOSTHVDIRTELDLMGTGIGYXPCISQK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 CGDPSNVRLVQCTETDIREVQQLLGTITIVPICAPK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 51
VE7_HPV11 STANDARD; PRT; 98 AA.
AC P04020;
DT 23-OCT-1986, integrated into UniProtKB/Swiss-Prot.
DT 23-OCT-1986, sequence version 1.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 11.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=10580;
[1]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP MEDLINE=86181601; PubMed=3008427;
RA Dartmann K., Schwarz E., Gissmann L., Zur Hausen H.;
RT "The nucleotide sequence and genome organization of human papilloma
virus type 11."
RL Virology 151:124-130(1986).
[2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Fife K.H., Fan L., Fritsch M.H., Bryan J., Brown D.R.;
RT "Association of human papillomavirus 11 DNA with squamous-cell
carcinoma of the tongue."
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family;
CC -----
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CC -----
DR EMBL: M4119; AAA46928.1; -; Genomic_DNA.
DR EMBL: L36108; AAA21704.1; -; Genomic_DNA.
DR PIR: A03690; W7ML1.
DR InterPro: IPR00148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
DR DNA-binding; Early protein; Oncogene; Transcription;
KM Transcription regulation.
FT CHAIN 1 98 Protein E7.
FT MOTIF 58 61 /FTID=PRO_0000133410.
FT MOTIF 91 94 C-XX-C motif-1.
FT MOTIF 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 10889 MW; AACAA9A6C933E1F6 CRC64;

Query Match 47.4%; Score 245; DB 1; Length 98;
Best Local Similarity 53.0%; Pred. No. 1.3e-20;
Matches 53; Conservative 14; Mismatches 29; Indels 4; Gaps 3;

QY 1 MGGDTPLHEVMDLQ-PETTDLYXXQLNDSEER-DEIDGAGQAPPRARYNYTFC 58
DB 1 MGRSLVTLKDIYDLPPDPVGLHCYQLVDSSEDEVKQD--KQDAQLPHTGHQITCC 58
QY 59 CKGDSLTRLCVOSTHVDIRLTDLMTGLTGIYXPCISOK 98
DB 59 CGCDSNRLVVECTDGIROQLDLGLTINIVCPICAPKE 98

RESULT 52
VE7_HPV6B STANDARD; PRT; 98 AA.
AC P04664;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1988, sequence version 1.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 6b.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.

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OX NCBI_TaxID=10600;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP MEDLINE=84131949; PubMed=6321162;
RA Schwarz E., Durr M., Demankowski C., Laternmann O., Zech R.,
RA Wolfepberger E., Suhai S., Zur Hausen H.;
RT "DNA sequence and genome organization of genital human papillomavirus
type 6b."
RL EMBL J. 2:2341-2348(1983).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family;
CC -----
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CC -----
DR EMBL: X00203; CAA25019.1; -; Genomic_DNA.
DR PIR: D20558; W7ML6.
DR InterPro: IPR00148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
DR DNA-binding; Early protein; Oncogene; Transcription;
KM Transcription regulation.
FT CHAIN 1 98 Protein E7.
FT MOTIF 58 61 /FTID=PRO_0000133405.
FT MOTIF 91 94 C-XX-C motif-1.
FT MOTIF 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 10887 MW; 997CB5095A35C4CD CRC64;

Query Match 47.0%; Score 243; DB 1; Length 98;
Best Local Similarity 52.5%; Pred. No. 2.2e-20;
Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

QY 1 MGGDTPLHEVMDLQ-PETTDLYXXQLNDSEER-DEIDGAGQAPPRARYNYTFC 58
DB 1 MGRSLVTLKDIYDLPPDPVGLHCYQLVDSSEDEVKQD--DSQPLKHQFQVTC 58
QY 59 CKGDSLTRLCVOSTHVDIRLTDLMTGLTGIYXPCISOK 97
DB 59 CGCDSNRLVVECTDGIROQLDLGLTINIVCPICAPK 97

RESULT 53
VE7_HPV6A STANDARD; PRT; 98 AA.
AC Q84292;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 6a.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=37122;
[1]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP MEDLINE=95297152; PubMed=778283;
RA Hofmann K.U., Cook J.C., Joyce J.G., Brown D.R., Schultz L.D.,
RA George H.A., Rosolowsky M., Fife K.H., Jansen K.U.;
RT "Sequence determination of human papillomavirus type 6a and assembly
of virus-like particles in Saccharomyces cerevisiae."
RL Virology 209:506-518(1995).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family;
CC -----
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CC -----
DR EMBL: L41216; AAU4212.1; -; Genomic_DNA.
DR InterPro: IPR00148; Papyl_E7.
DR Pfam: PF00527; E7; 1.
KM DNA-binding; Early protein; Oncogene; Transcription;

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KM Transcription regulation.
FT CHAIN 1 98 /FTid=PRO_0000133404.
FT MOTIF 58 61 C-XX-C motif-1.
FT MOTIF 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 10888 MW; 997CBDBA5A39C4CD CRC64;

Query Match 46.8%; Score 242; DB 1; Length 98;
Best Local Similarity 52.5%; Pred. No. 2.8e-20;
Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

QY 1 MHGDTPTLHEMYMDLQ-PTETDLYXXQLNDSEED-DEIDGPAQAEPRRAHYNYVTF 58
DB 1 MHGKPEVQVIDLKPTETEDLVCYSL-DNSEDEBETDSHL-ERQAEGQWYIVTDCS 58
QY 59 CKCDSTLRCLCVQSTHVDIRTEEDLIMGTLGIXPICSQK 97
DB 59 CGCDNVRLVVOCTETREVOQLLGLTDLVCPICAPK 97

RESULT 54
VE7_HPV34 STANDARD; PRT; 97 AA.
AC P36828;
AT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1994, sequence version 1.
DT 07-FEB-2006, entry version 32.
DE Protein E7.
GN Name=E7.
OS Human papillomavirus type 34.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333764;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC -----
EMBL: X74476; CA52556.1; -; Genomic_DNA.
DR PTR; S36516; S36516.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
KM DNA-binding; Early protein; Oncogene; Transcription;
KM Transcription regulation.
FT CHAIN 1 97 Protein E7.
FT MOTIF 57 60 /FTid=PRO_0000133432.
FT MOTIF 90 93 C-XX-C motif-1.
FT MOTIF 93 93 C-XX-C motif-2.
SQ SEQUENCE 97 AA; 10985 MW; 19B3C9D1F12BF4F6 CRC64;

Query Match 43.0%; Score 222.5; DB 1; Length 97;
Best Local Similarity 49.0%; Pred. No. 5.5e-16;
Matches 46; Conservative 18; Mismatches 29; Indels 3; Gaps 3;

QY 1 MHGDTPTLHEMYMDLQ-PTETDLYXXQLNDSEEDIDGPAQAEPRRAHYNYVTF 59
DB 1 MHGKPEVQVIDLKPTETEDLVCYSL-DNSEDEBETDSHL-ERQAEGQWYIVTDCS 58
QY 60 KCDSTLRCLCVQSTHVDIRTEEDLIMGTLGIXPICSQK 97
DB 59 RCGSTVCLTTESTADLVLIEDLIMGALKIVCPICSR 96

RESULT 55
Q8JNA0_9PAPI

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ID Q8JNA0_9PAPI PRELIMINARY; PRT; 98 AA.
AC Q8JNA0;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Putative transforming protein E7.
OS Human papillomavirus - cand90.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333769;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22079881; PubMed=12085327; DOI=10.1086/340824;
RA Terai M., Burk R.D.;
RT "Identification and characterization of 3 novel genital human
RT papillomaviruses by overlapping polymerase chain reaction: candHPV89,
RT candHPV90, and candHPV91."
RL J. Infect. Dis. 185:1794-1797(2002).
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CC -----
EMBL: AY057438; AL14205.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10944 MW; 4978F2A03847E5A2 CRC64;

Query Match 42.8%; Score 221.5; DB 2; Length 98;
Best Local Similarity 45.9%; Pred. No. 7.4e-18;
Matches 45; Conservative 17; Mismatches 33; Indels 3; Gaps 2;

QY 1 MHGDTPTLHEMYMDLQ-PTETDLYXXQLNDSEEDIDG--PAGQAEPRRAHYNYVTF 57
DB 1 MHGKPEVQVIDLKPTETEDLVCYSL-DNSEDEBETDSHL-ERQAEGQWYIVTDCS 60
QY 58 CKCDSTLRCLCVQSTHVDIRTEEDLIMGTLGIXPICSQK 95
DB 61 CCRCCCTVRLVSGHAEITROQLBLLGALHYCPICLA 98

RESULT 56
Q91194_HPV16 PRELIMINARY; PRT; 43 AA.
ID Q91194_HPV16
AC Q91194;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Truncated E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhao M., Wu X.X., Ding X.H.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: AF93782; AAK84003.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 43 AA; 4903 MW; 19A57D4E52F814D6 CRC64;

Query Match 42.7%; Score 221; DB 2; Length 43;
Best Local Similarity 95.3%; Pred. No. 3.1e-18;

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Matches 41; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEHYMDLQPETTDLYXXYQLNDSSEEDIDGPAG 43
DB 1 MHGDTPTLHEHYMDLQPETTDLYCYEQNLNDSSEEDIDGPAG 43

RESULT 57
VE7_RHPV1 STANDARD; PRT; 113 AA.
AC P2161;
DT 01-AUG-1991, integrated into UniProtKB/Swiss-Prot.
DT 07-FEB-2006, entry version 32.
DE Protein E7.
GN Name=E7;
OS Rhesus papillomavirus type 1 (Rhpv 1).
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10570;
[1]

RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX MEDLINE=9135018; PubMed=1847267;
RA Ostrow R.S., Labresh K.V., Faras A.J.;
RT "Characterization of the complete RHPV 1 genomic sequence and an
integration locus from a metastatic tumor.";
RL Virology 181:424-429(1991).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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EMBL: M60184; AAA79312.1; -; Genomic_DNA.
DR PIR: B38503; WTMLE1.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1 113 Protein E7.
FT MOTIF 73 76 /FTID=PRO_0000133470.
FT MOTIF 106 109 C-XX-C motif-2.
SQ SEQUENCE 113 AA; 12818 MW; 9C404BDAC1298306 CRC64;

Query Match 42.3%; Score 218.5; DB 1; Length 113;
Best Local Similarity 43.8%; Pred. No. 2e-17;
Matches 49; Conservative 13; Mismatches 35; Indels 15; Gaps 2;

QY 1 MHGDTPTLHEHYMDLQPETTDLYXXYQLNDSSEEDIDGPAGQAEPRAH----- 51
DB 1 MIGKPTLEIDIVDLQPFPGQPDVLMCYEQLSDSSDEDEVDHNNHNNQCHQHARPEV 60

QY 52 -----INIVTFCKCKDSTLRCTVOSTHVDIRTELDLMTGLGIVXPCSK 97
DB 61 PEDGDCYRIVSDCYSCCKPRLVVAVSSHELRLVEDLMLGTLDIVCSCASR 112

RESULT 58
Q9WHG1_9PAPI PRELIMINARY; PRT; 108 AA.
AC Q9WHG1;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 17.
DE Putative transforming protein E7.
OS Human papillomavirus - cand85.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=151757;
[1]
FT CHAIN 1 106 Protein E7.
FT MOTIF 106 /FTID=PRO_0000133442.

RA MEDLINE=20047972; PubMed=10580054;
RA Chow V.T., Leong P.W.;
RT "Complete nucleotide sequence, genomic organization and phylogenetic
analysis of a novel genital human papillomavirus type, HLT474-S.";
RL J. Gen. Virol. 80:2923-2929(1999).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RA Chow V.T.K., Leong W.F.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
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EMBL: AF131950; MAD2482.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 108 AA; 12355 MW; B1F84D7DA0F384FB CRC64;

Query Match 41.8%; Score 216; DB 2; Length 108;
Best Local Similarity 39.0%; Pred. No. 3.7e-17;
Matches 41; Conservative 22; Mismatches 32; Indels 10; Gaps 2;

QY 1 MHGDTPTLHEHYMDLQPETTDLYXXYQLNDSSEEDIDGPAGQAEPR-----DRA 50
DB 1 MHGKPTLEIDIVDLQPFPGQPDVLMCYEQLSDSSDEDEVDHNNHNNQCHQHARPELQ 60

QY 51 HNIVTFCKCKDSTLRCTVOSTHVDIRTELDLMTGLGIVXPCIS 95
DB 61 RHITCCVCKCKEASLQLVSSAADRLDQQLPLGTISFLCPICA 105

RESULT 59
VE7_HPVA5 STANDARD; PRT; 106 AA.
AC P21736;
DT 01-MAY-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1994, sequence version 2.
DT 07-FEB-2006, entry version 33.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 45.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10593;
[1]

RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX MEDLINE=94255501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
RN [2]

RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RA Kaplan J.B., Burk R.D.;
RL Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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EMBL: X74479; CA452574.1; -; Genomic_DNA.
DR EMBL: M38198; AAA46974.1; -; Genomic_DNA.
DR PIR: S36562; S36562.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1 106 Protein E7.
FT MOTIF 106 /FTID=PRO_0000133442.

Best Local Similarity 48.5%; Pred. No. 1,1e-16;
Matches 47; Conservative 10; Mismatches 37; Indels 3; Gaps 1;

QY 1 MHGDTPLHBYMLDLOPETDLYXXYQNLDSSEEDIDEPAGQAPDRAHYNITFECK 60
DB 1 MHGKVPFLKRIVQLQDPDVGLLCNEQDLSSEEDVDEL---ATQATQHTQPPYQIVTCCEV 57
QY 61 CDSTLRKCVOSTHVDIRTDLEDLMGTGIGYXPCISOK 97
DB 58 CNRSRLRVQCTGPDINNHLTLGLTLVCPICAPK 94

RESULT 63

VE7_HPVS30 STANDARD; PRT; 105 AA.

AC P36826;
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1994, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 30.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=10611;

RN [1]
RX NUCLEOTIDE SEQUENCE (GENOMIC DNA).
MEDLINE=94265501; PubMed=8205838;

RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";

RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating activities.

CC -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.

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CC EMBL: X74474; CAAS2544.1; -; Genomic_DNA.

DR PIR: S36504; S36504.
DR InterPro: IPR000148; Papv1_E7.

DR Pfam: PF00527; E7; 1.
KM DNA-binding; Early protein; Oncogene; Transcription;

KW Transcription regulation.
FT CHAIN 1 105 Protein E7.

FT MOTIF 65 68 /FTid=PRO_0000133428.
FT MOTIF 98 101 C-XX-C motif-1.
FT MOTIF 98 101 C-XX-C motif-2.

SQ SEQUENCE 105 AA; 12001 MW; 6166758B14B4D67 CRC64;

Query Match 40.5%; Score 209.5; DB 1; Length 105;
Best Local Similarity 45.2%; Pred. No. 2.1e-16;
Matches 47; Conservative 17; Mismatches 33; Indels 7; Gaps 4;

QY 1 MHGDTPLHBYMLDLOPETDLYXXYQNLDSSEEDIDEPAGQAPDRAH--YN 53
DB 1 MHGKVPFLKRIVQLQDPDVGLLCNEQDLSSEEDVDEL---ATQATQHTQPPYQIVTCCEV 57
QY 54 IYVFCKKCDSTLRKCVOSTHVDIRTDLEDLMGTGIGYXPCISOK 97
DB 61 INTQCCRCESLVQALVQVSTKEKRLALQOMLMGALVELCPICATR 104

RESULT 64

VE7_HPVS30 STANDARD; PRT; 105 AA.

AC P36832;
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.

DT 01-JUN-1994, sequence version 1.
DT 07-FEB-2006, entry version 32.
DE Protein E7.

GN Name=E7;
OS Human papillomavirus type 53.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333765;

RN [1]
RX NUCLEOTIDE SEQUENCE (GENOMIC DNA).
MEDLINE=94265501; PubMed=8205838;

RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";

RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating activities.

CC -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.

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CC EMBL: X74482; CAAS2592.1; -; Genomic_DNA.

DR PIR: S36528; S36528.
DR InterPro: IPR000148; Papv1_E7.

DR Pfam: PF00527; E7; 1.
KM DNA-binding; Early protein; Oncogene; Transcription;

KW Transcription regulation.
FT CHAIN 1 105 Protein E7.

FT MOTIF 65 68 /FTid=PRO_0000133449.
FT MOTIF 98 101 C-XX-C motif-1.
FT MOTIF 98 101 C-XX-C motif-2.

SQ SEQUENCE 105 AA; 12162 MW; DEAYE2B8D0C1F7EC CRC64;

Query Match 40.3%; Score 208.5; DB 1; Length 105;
Best Local Similarity 43.3%; Pred. No. 2.7e-16;
Matches 45; Conservative 23; Mismatches 29; Indels 7; Gaps 4;

QY 1 MHGDTPLHBYMLDLOPETDLYXXYQNLDSSEEDIDEPAGQAPDRAH--YN 53
DB 1 MHGKVPFLKRIVQLQDPDVGLLCNEQDLSSEEDVDEL---ATQATQHTQPPYQIVTCCEV 57
QY 54 IYVFCKKCDSTLRKCVOSTHVDIRTDLEDLMGTGIGYXPCISOK 97
DB 61 INTQCCRCESLVQALVQVSTKEKRLALQOMLMGALVELCPICATR 104

RESULT 65

056947_9PAPI PRELIMINARY; PRT; 90 AA.

AC O56947;
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.

DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 20.

DE E7 protein.
OS Human papillomavirus type 77.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.

OX NCBI_TaxId=69966;
RN [1]
RX NUCLEOTIDE SEQUENCE.

RA Delius H., Saegling B., Bergmann K., Shamin V., de Villiers E.M.;
RT "The genomes of three of four novel HPV types, defined by differences

RT of their L1 genes, show high conservation of the E7 gene and the

RT UTR.";
RL Virology 240:359-365(1998).

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CC EMBL: Y15175; CAAT5464.1; -; Genomic_DNA.

DR GO: 0005562; C:intracellular; IEA.
DR GO: 0003700; F:transcription factor activity; IEA.
DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 90 AA; 9971 MW; ABAB4EADABACF33B CRC64;

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Query Match      40.1%; Score 207.5; DB 2; Length 90;
Best Local Similarity 49.5%; Pred. No. 3e-16;
Matches 47; Conservative 11; Mismatches 33; Indels 5; Gaps 2;

Qy      1 MHGPTPLHEXMDLQPTTDLXXQLNDSSEBDEIDGPAQAEPDRAHNYITFCCK 60
Db      1 MHGKPTVKDLELPLAEVAPLCLNEQL-DSSDEDCID----VVEPAQCAVRVTLCTK 55

Qy      61 CDSLTRLCVOSTHVDIRTELDLMTGLGIVXPIC 95
Db      56 CSSTLRLVESSEADIRAFQELLRTLTIVCPRC 90

RESULT 66
Q82006 HPV73 PRELIMINARY; PRT; 97 AA.
AC Q82006;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE E7 protein.
OS Human papillomavirus type 73.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=51033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96213783; PubMed=6635859;
RX DOI=10.1002/(SICI)1097-0215(19960516)66:4<453::AID-IC73.0.CO;2-V;
RA Voelter C., He Y., Delius H., Roy-Burman J.S.,
RA Greenspan D., de Villiers E.-M.;
RT "Novel HPV types present in oral papillomatous lesions from patients
RT with HIV infection.";
RL Int. J. Cancer 66:453-456(1996).

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CC -----
EMBL: X94165; CAA63883.1; -; Genomic DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 97 AA; 10970 MW; 651D0345D048F022 CRC64;

Query Match      40.1%; Score 207.5; DB 2; Length 97;
Best Local Similarity 48.5%; Pred. No. 3.2e-16;
Matches 47; Conservative 14; Mismatches 33; Indels 3; Gaps 3;

Qy      1 MHGPTPLHEXMDLQPTTDLXXQLNDSSEBDEIDGPAQAEPDRAHNYITFCCK 59
Db      1 MHGKPTVKDLELPLAEVAPLCLNEQL-DSSDEDCID----VVEPAQCAVRVTLCTK 58

Qy      60 KCDSTLRVCVOSTHVDIRTELDLMTGLGIVXPIC 96
Db      59 KCQCTVCAIESNKADLRVIEELMTGLGIVCPIC 95

RESULT 67
Q6E808_9PAPI PRELIMINARY; PRT; 94 AA.
AC Q6E808;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Putative transforming protein E7.
GN Name=E7;
OS Human papillomavirus type 71.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=120686;
RN [1]

```

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RP NUCLEOTIDE SEQUENCE.
RP STRAIN=Qv22792;
RC PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
RX Narechania A., Chen Z., Desalle R., Burk R.D.;
RT "Phylogenetic incongruence among Oncogenic Genital Alpha Human
RT Papillomaviruses.";
RL J. Virol. 79:15503-15510(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RP STRAIN=Qv22792;
RC PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
RX Narechania A., Chen Z., Desalle R., Burk R.D.;
RT "Phylogenetic incongruence among Oncogenic Genital Alpha Human
RT Papillomaviruses.";
RL J. Virol. 79:15503-15510(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RP Fu L., Burk R.D.;
RT "Correction of HPV1 sequences.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RP Fu L., Burk R.D.;
RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RA Fu L., Burk R.D.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: AY330621; AAQ95185.1; -; Genomic DNA.
DR EMBL: AY330623; AAQ95199.1; -; Genomic DNA.
DR EMBL: AY330620; AAQ95178.1; -; Genomic DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 94 AA; 10571 MW; 04C1C6DC3E0DB9C CRC64;

Query Match      39.9%; Score 206.5; DB 2; Length 94;
Best Local Similarity 44.7%; Pred. No. 4.1e-16;
Matches 42; Conservative 15; Mismatches 36; Indels 1; Gaps 1;

Qy      1 MHGPTPLHEXMDLQPTTDLXXQLNDSSEBDEIDGPAQAEPDRAHNYITFCCK 60
Db      1 MRGQCTKIDIVQLQPEVVDLYCHEQFASSEBDEIDGPAQAEPDRAHNYITFCCK 59

Qy      61 CDSLTRVCVOSTHVDIRTELDLMTGLGIVXPIC 94
Db      60 CCRVRLVSESEADIRAFQELLRTLTIVCPIC 93

RESULT 68
Q2VUC6_9PAPI PRELIMINARY; PRT; 95 AA.
AC Q2VUC6;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein.
OS Human papillomavirus type 106.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=338326;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP STRAIN=Qv28897;
RC PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
RX Narechania A., Chen Z., Desalle R., Burk R.D.;
RT "Phylogenetic incongruence among Oncogenic Genital Alpha Human
RT Papillomaviruses.";
RL J. Virol. 79:15503-15510(2005).
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP Fu L., Burk R.D.;
RT "Correction of HPV1 sequences.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RA Fu L., Burk R.D.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
EMBL: DQ080082; AA329514.1; -; Genomic DNA.
DR EMBL: DQ080082; AA329514.1; -; Genomic DNA.
SQ SEQUENCE 95 AA; 10541 MW; FDD5E210EE230741 CRC64;

Query Match      39.8%; Score 206; DB 2; Length 95;
Best Local Similarity 41.7%; Pred. No. 4.7e-16;

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DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cervix;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Sculter G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Datsenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Umed T.B., Toshimiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL, BC056907; AAHS6907.1; mRNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000146; Papv1_E7.
DR Pfam; PF00527; E7; 1.
DR Hypothetical protein.
KW SEQUENCE 105 AA; 11995 MW; 2CDB119534D0186A CRC64;
SQ
Query Match 39.2%; Score 202.5; DB 2; Length 105;
Best Local Similarity 39.6%; Pred. No. 1.4e-15;
Matches 42; Conservative 21; Mismatches 32; Indels 11; Gaps 3;
QY 1 MHGDTPLHEXMDLOPET--TDLYXXYQINDSSEEDIDG-----PAGQAEPRRAH 51
DB 1 MHGPKATLQDIVLHLEPQNEIPVDLLCHEQSDSEEDDEIDGVNHQHLPARRAEPQR-- 58
QY 52 YNITPCCKCDSTRLCVOSTHVDIRTELDLMGTGIVPICGOK 97
DB 59 HTMLCMCCCKEARIKLVESADDLRAFPQQLFNTLSFVCPWCASQ 104
RESULT 72
VE7_HPV13
ID_VE7_HPV13 STANDARD; PRT; 101 AA.
AC Q02271;
DT 01-APR-1993, integrated into UniProtKB/Swiss-Prot.
DT 01-APR-1993, sequence version 1.
DT 07-FEB-2006, entry version 33.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 13.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=10573;
OX NCBI_TaxID=10573;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=92391075; PubMed=1325697;
RA van Ranst M., Fuse A., Filten P., Beuken E., Pieter H., Burk R.D.,
RA Opendakker G.;
RT "Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type
RT 1: comparison of the genome organizations.";
RL Virology 190:587-596(1992).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC
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CC
CC EMBL; X62843; CAA44648.1; -; Genomic DNA.
DR PIR; B42955; W7WL13.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1
FT MOTIF 61 /FTID=PRO_0000133412.
FT MOTIF 94 C-XX-C motif-1.
FT MOTIF 97 C-XX-C motif-2.
SQ SEQUENCE 101 AA; 11049 MW; 380E5D4B2B0472 CRC64;
Query Match 38.8%; Score 200.5; DB 1; Length 101;
Best Local Similarity 44.7%; Pred. No. 2.3e-15;
Matches 46; Conservative 13; Mismatches 35; Indels 9; Gaps 2;
QY 1 MHGDTPLHEXMDLOPETTDLYXXYQINDSSEEDIDGPAQAEPRRAH-----YNI 54
DB 1 MHGKPYPLKQIVLELTDPDVLHCHNEQLDSS--EDEVDAQATQATGATGSHLLGCTCYOI 57
QY 55 VTFPCCKCDSTRLCVOSTHVDIRTELDLMGTGIVPICGOK 97
DB 58 LTSCSKCNSVRLVVECTGPDIDHDLHLLGTINIVCPKAPK 100
RESULT 73
Q76296_HPV18
ID_Q76296_HPV18 PRELIMINARY; PRT; 105 AA.
AC Q76296;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333761;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15306621; DOI=10.1126/JVI.79.24.15503-15510.2005;
RA Narechania A., Chen Z., Desalle R., Burk R.D.,
RT "Phylogenetic Incongruence among Oncogenic Genital Alpha Human
RT Papillomaviruses.";
RL J. Virol. 79:15503-15510(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21568387; PubMed=11711624;
RX DOI=10.1126/JVI.75.24.12339-12346.2001;
RA Shera K.A., Shera C.A., McDougall J.K.;
RT "Small tumor virus genomes are integrated near nuclear matrix
RT attachment regions in transformed cells.";
RL J. Virol. 75:12339-12346(2001).
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DR EMBL; AY262282; AAP20595.1; -; Genomic_DNA.
DR EMBL; AF339139; AAL34458.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papyl_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 11996 MW; 24799BB534D0186A CRC64;

Query Match 38.8%; Score 200.5; DB 2; Length 105;
Best Local Similarity 39.6%; Pred. No. 2.4e-15;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

QY 1 MHGDTPLHEHYMDLQEPET---TDLYXXYQNDSSSEEDIDG-----PAGQAPDRAH 51
DB 1 MHGPKATLDIVVHLBPQNEIPVDLCHQGLSDSSEENDEIDGVNHQHLPARAPQR-- 58
QY 52 YNIVTFCKCDSTLRCLCVOSTHVDIRTLIEDLMLGTGLGYXPIC 97
DB 59 HTMLCMCKCKEARIELVBSADLRAFQQLFNTLSFVCPWCASQ 104

RESULT 74
Q6EGQ1_9PAP1 PRELIMINARY; PRT; 94 AA.
Q6EGQ1_9PAP1
ID Q6EGQ1_9PAP1 PRELIMINARY; PRT; 94 AA.
AC Q6EGQ1_9PAP1
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Putative transforming protein E7.
OS Human papillomavirus type 71.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=120686;
RN NCBI_TaxID=120686;
RP NUCLEOTIDE SEQUENCE.
RA Fu L., Burk R.D.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY330622; AAG95192.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papyl_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 94 AA; 10499 MW; 07A1C6DC1E2DB9E CRC64;

Query Match 38.6%; Score 199.5; DB 2; Length 94;
Best Local Similarity 43.6%; Pred. No. 2.7e-15;
Matches 41; Conservative 15; Mismatches 37; Indels 1; Gaps 1;

QY 1 MHGDTPLHEHYMDLQEPETTDLYXXYQNDSSSEEDIDGAPGAPDRAHYNVTFCK 60
DB 1 MRGQCCCTKQIVVQLQPEVVDLYCHQEPASDDEGDNVDGQ-PTSPAQA YRVVSYCGR 59
QY 61 CDSTLRCLCVOSTHVDIRTLIEDLMLGTGLGYXPIC 94
DB 60 CCRVRLVBSDEADIRALQQLLGLTITVCPI 93

RESULT 75
Q9QNP7_HPV18 PRELIMINARY; PRT; 105 AA.
Q9QNP7_HPV18
ID Q9QNP7_HPV18 PRELIMINARY; PRT; 105 AA.
AC Q9QNP7_HPV18
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE E7 protein.

```

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OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=333761;
RN NCBI_TaxID=333761;
RP NUCLEOTIDE SEQUENCE.
RA Laaseri M., Gul'ko L., Vinokurova S., Kissel'jova N., Velko V.,
RA Kissel'jov P.,
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RT Transformation Potential of E7 Gene and its Mutants.";
RT Virus Genes 182:139-149(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Velko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL; Y18491; CAB53097.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papyl_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 105 AA; 12010 MW; 24799BB534D4496A CRC64;

Query Match 38.4%; Score 198.5; DB 2; Length 105;
Best Local Similarity 39.6%; Pred. No. 4.1e-15;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

QY 1 MHGDTPLHEHYMDLQEPET---TDLYXXYQNDSSSEEDIDG-----PAGQAPDRAH 51
DB 1 MHGPKATLDIVVHLBPQNEIPVDLCHQGLSDSSEENDEIDGVNHQHLPARAPQR-- 58
QY 52 YNIVTFCKCDSTLRCLCVOSTHVDIRTLIEDLMLGTGLGYXPIC 97
DB 59 HTMLCMCKCKEARIELVBSADLRAFQQLFNTLSFVCPWCASQ 104

RESULT 76
Q705H9_HPV43 PRELIMINARY; PRT; 99 AA.
Q705H9_HPV43
ID Q705H9_HPV43 PRELIMINARY; PRT; 99 AA.
AC Q705H9_HPV43
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE E7 protein.
OS Human papillomavirus type 43.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OC NCBI_TaxID=10591;
RN NCBI_TaxID=10591;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98259065; PubMed=2542593;
RA Loerincz A.T., Quinn A.P., Goldborough M.D., Schmidt B.J.,
RA Temple G.F.;
RT "Cloning and partial DNA sequencing of two new human papillomavirus
RT types associated with condylomas and low-grade cervical neoplasia.";
RL J. Virol. 63:2829-2833(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Matsukura T., Delius H., Sugase M.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA de Villiers E.M.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL; AJ620205; CAF05784.1; -; Genomic_DNA.

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DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 99 AA; 11187 MW; CA98EACB2C34EB3 CRC64;

Query Match
Best Local Similarity 38.8%; Score 198; DB 2; Length 99;
Matches 44; Conservative 14; Mismatches 36; Indels 2; Gaps 2;

Qy 1 MHGDTPLHEMYLDLPETDLYXXQLNDSSEEDIDGAGQAEPRAH-VNIITFCC 59
Db 1 MHGKPTIRDVYLTMOEPRSLTCNEQL-DSSEDEREQPTQDQVNLQVRYVTECT 59

Qy 60 KCDSTRLCVQSTHVDIRTLIEDLMGTLGIVXPIC 95
Db 60 SCLCVIRLVQCSDSIDIKEDLLGLTKIVCPLECT 95

RESULT 77
Q9QNP6 HPV18 PRELIMINARY; PRT; 105 AA.
AC Q9QNP6;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 14.
DE E7 protein.
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333761;
RN NUCLEOTIDE SEQUENCE.
RA Laaseri M., Gulko L., Vinokurova S., Kisseljoova N., Velko V.,
RA Kisseljev F.;
RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
RT Transfection Potential of E7 Gene and its Mutants.";
RL Virus Genes 182:139-149(1999).
RN NUCLEOTIDE SEQUENCE.
RA Velko V.P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: Y18492; CAB53098.1; -; Genomic DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 105 AA; 12009 MW; C4979555DDA4A960 CRC64;

Query Match
Best Local Similarity 38.0%; Score 196.5; DB 2; Length 105;
Matches 42; Conservative 19; Mismatches 34; Indels 11; Gaps 3;

Qy 1 MHGDTPLHEMYLDLPETDLYXXQLNDSSEEDIDGAGQAEPRAH 51
Db 1 MHGKATLQNLVHLBPONELPYVLLCHEQLSDSEEDIDGAGNQHLPARRAEPOR-- 58

Qy 52 YNIITFCCDSTRLCVQSTHVDIRTLIEDLMGTLGIVXPIC 97
Db 59 HTMLCMCKCEARIELVVESSADDLRAFOQLFLTLISFVCWCASQ 104

RESULT 78
Q81965 HPV59 PRELIMINARY; PRT; 107 AA.
AC Q81965;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.

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DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE ORF putative E7 protein.
GN Name=ORF putative E7;
OS Human papillomavirus type 59.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=37115;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=9430322; PubMed=8030272;
RA Kuo J., Roy-Burman A., Kim H., de Villiers E.-M., Matsukura T.,
RA Choe J.;
RT "Nucleotide sequence and phylogenetic classification of human
RT papillomavirus type 59.";
RL Virology 203:158-161(1994).
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CC -----
DR EMBL: X77858; CA54850.1; -; Genomic DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 107 AA; 12042 MW; A8F2B6973D727163 CRC64;

Query Match
Best Local Similarity 37.8%; Score 195.5; DB 2; Length 107;
Matches 46; Conservative 17; Mismatches 30; Indels 13; Gaps 4;

Qy 1 MHGDTPLHEMYLDLPETDLYXXQLNDSSEEDIDGAGQAEPR 49
Db 1 MHGKATLQNLVHLBPONELPYVLLCHEQLSDSEEDIDGAGNQHLPARRAEPOR 60

Qy 50 AHYNIITFCCDSTRLCVQSTHVDIRTLIEDLMGTLGIVXPIC 95
Db 61 --HNIVCVCKCCKNNQQLVETSDQGRALQQLFMDTLISFVCBLCA 104

RESULT 79
VE7_PCPV1 STANDARD; PRT; 98 AA.
ID VE7_PCPV1
AC Q02272;
DT 01-APR-1993, integrated into UniProtKB/Swiss-Prot.
DT 01-APR-1993, sequence version 1.
DT 07-FEB-2006, entry version 34.
DE Protein E7.
GN Name=E7;
OS Pygmy chimpanzee papillomavirus type 1.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10576;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP MEDLINE=92391075; PubMed=1325697;
RX van Ranst M., Fuse A., Filten P., Beuken E., Pfister H., Burk R.D.,
RA Odenakker G.;
RT "Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type
RT 1: comparison of the genome organizations.";
RL Virology 190:587-596(1992).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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CC -----
DR EMBL: X62844; CA444656.1; -; Genomic DNA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Transcription;

```

KW Transcription regulation.
 FT CHAIN 1 98 Protein E7.
 FT /FTID=PRO_0000133464.
 FT MOTIF 58 61 C-XX-C motif-1.
 FT MOTIF 91 94 C-XX-C motif-2.
 SQ SEQUENCE 98 AA; 10742 MW; E67165CFBD7BAFA6 CRC64;

Query Match 37.5%; Score 194; DB 1; Length 98;
 Best Local Similarity 46.4%; Pred. No. 1.3e-14;
 Matches 45; Conservative 13; Mismatches 35; Indels 4; Gaps 2;

QY 1 MHGDTPLHEHYMDLOPETDLYXXYQXQNDSEEDIDGPAQAEPRD--RAHNYITFC 58
 DB 1 MHGKTTTLKDIIVDLSPDVGKCNEDL--SSEDEVDQATQATQTQHTQIVTCC 58
 59 CKDCSTLRLCVOSTHVDIRTELLMGTGIVXPIC 95
 59 GQCDSNVRLVVDCTGSDIQHLHKLGLSLNIVCPICA 95

Db 59 CKDCSTLRLCVOSTHVDIRTELLMGTGIVXPIC 95
 59 GQCDSNVRLVVDCTGSDIQHLHKLGLSLNIVCPICA 95

RESULT 80
 ID Q8V9K9 HPV18 PRELIMINARY; PRT; 105 AA.
 AC Q8V9K9;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2002, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE E7 protein.
 GN Name=E7;
 OS Human Papillomavirus type 18.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxID=333761;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21568387; PubMed=11711624;
 RX DOI=10.1128/JVI.75.24.12339-12346.2001;
 RA Shera K.A., Shera C.A., McDougall J.K.;
 RT "Small Tumor Virus Genomes Are Integrated near Nuclear Matrix
 Attachment Regions in Transformed Cells.";
 RT J. Virol. 75:12339-12346(2001).
 RL J. Virol. 75:12339-12346(2001).
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DR EMBL; AF339137; AL34455.1; -; Genomic DNA.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000148; Papv1_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 105 AA; 12036 MW; 2528DEA165850C71 CRC64;

Query Match 37.2%; Score 192.5; DB 2; Length 105;
 Best Local Similarity 38.7%; Pred. No. 2.1e-14;
 Matches 41; Conservative 21; Mismatches 33; Indels 11; Gaps 3;

QY 1 MHGDTPLHEHYMDLOPET--TDLYXXYQXQNDSEEDIDG-----PAGQAEPRAH 51
 DB 1 MYGKATLQDIIVLHLEPQNEIPVDLCHQGLSDEENDELIDGNNHQLPRARAEPR-- 58
 52 YNIVTFCCDCSTLRLCVOSTHVDIRTELLMGTGIVXPIC 97
 59 HTMLCMCKCEARIELVVESSADLRAFOQLFKTLSEFVCEWCA 104

Db 59 HTMLCMCKCEARIELVVESSADLRAFOQLFKTLSEFVCEWCA 104

RESULT 81
 ID Q8B5X6 HPV54 PRELIMINARY; PRT; 95 AA.
 AC Q8B5X6;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 11.

DE Putative transforming protein E7.
 GN Name=E7;
 OS Human Papillomavirus type 54.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxID=333766;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
 RA Narechanla A., Chen Z., Desalle R., Burk R.D.;
 RT "Phylogenetic Incongruence among Oncogenic Genital Alpha Human
 Papillomaviruses.";
 RT J. Virol. 79:15503-15510(2005).
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RA Terai M., Burk R.D.;
 RT "Cervical HPV in Evolution; Genomic sequence of AB9, a subtype of
 HPV54.";
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF36129; AA015449.1; -; Genomic DNA.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000148; Papv1_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 95 AA; 10433 MW; 2B18F84E1BDAD3C8 CRC64;

Query Match 37.0%; Score 191.5; DB 2; Length 95;
 Best Local Similarity 40.8%; Pred. No. 2.4e-14;
 Matches 42; Conservative 17; Mismatches 31; Indels 13; Gaps 4;

QY 1 MHGDTPLHEHYMDLOPETDLYXXYQXQNDSEEDIDGPAQAEPRAHYINVT---- 56
 DB 1 MHGKATIEDIIVDLHPECDLYCREGLSDADE-----TAVIQDKQAFKVLSCGG 55
 57 FCCKCDSTLRLCVOSTHVDIRTELLMGTGIVXPIC 98
 56 VCKK--TVRLCVYSTHTGIRVLQELHGLALEIVCPICSRP 95

Db 57 FCCKCDSTLRLCVOSTHVDIRTELLMGTGIVXPIC 98
 56 VCKK--TVRLCVYSTHTGIRVLQELHGLALEIVCPICSRP 95

RESULT 82
 ID Q8QNP5 HPV18 PRELIMINARY; PRT; 105 AA.
 AC Q8QNP5;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 14.
 DE E7 protein.
 OS Human papillomavirus type 18.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxID=333761;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Laessli M., Gul'ko L., Vinokurova S., Kissel'jova N., Veiko V.,
 RA Laessli F.;
 RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and
 RT Transformation Potential of E7 Gene and Its Mutants.";
 RT Virus Genes 18:139-149(1999).
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RA Veiko V.P.;
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

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DR EMBL; Y18493; CAB53099.1; -; Genomic DNA.
 DR GO; GO:0005622; C:intracellular; IEA.

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DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.1952 MW; 247BF448A6BB84FA CRC64;
SQ SEQUENCE 105 AA; 11055 MW; 247BF448A6BB84FA CRC64;

Query Match
Best Local Similarity 37.0%; Score 191.5; DB 2; Length 105;
Matches 41; Conservative 20; Mismatches 34; Indels 11; Gaps 3;

QY 1 MHGDTPTLHEMYMDLOPETTDLYXXYXQLNDSSEEDIDGPAQ--PAGQAEPRRAH 51
DB 1 MHGKATLQDVLVLEPQNEIPVGLCHQQLDSSEEDIDGVNHQHLPARAPQR-- 58

QY 52 YNITPCCKCDSTLRLCVQSTHVDIRTLIEDLLMGTLGIYXPICSQK 97
DB 59 HTMLCKCKCEARIELVVESSADDLRAQQLFLKTLISVVCWCSQ 104

RESULT 83
Q8BTG7_9PAPI PRELIMINARY; PRT; 98 AA.
AC Q8BTG7_9PAPI
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE E7.
OS Human papillomavirus - cand91.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=202352;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2079881; PubMed=12085327; DOI=10.1086/340824;
RA Terai M, Burk R.D.;
RT Identification and characterization of 3 novel genital human
RT papillomaviruses by overlapping polymerase chain reaction: candHPV99,
RT candHPV90, and candHPV91.
RL J. Infect. Dis. 185:1794-1797(2002).
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CC -----
DR EMBL: AF419318; AAM69131.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11055 MW; E6874FA881797E4 CRC64;

Query Match
Best Local Similarity 36.9%; Score 191; DB 2; Length 98;
Matches 44; Conservative 16; Mismatches 34; Indels 2; Gaps 2;

QY 1 MHGDTPTLHEMYMDLOPETTDLYXXYXQLNDSSEEDIDGPAQ-AEPRRAHYNIVTFCC 59
DB 1 MYGKEPTLRDYLVLQEPERSLTCDEQL-DSSEDEDESGTQDDQVLDVYKVTECT 59

QY 60 KCDSTLRLCVQSTHVDIRTLIEDLLMGTLGIYXPIC 95
DB 60 SCYCSIRLVNVCSSDIKTELLIGTLQIVCPDCT 95

RESULT 84
Q212S3_HPV13 PRELIMINARY; PRT; 98 AA.
AC Q212S3;
DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, sequence version 1.
DT 07-MAR-2006, entry version 1.
DE E7.
GN Name=E7;

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OS Human papillomavirus type 13.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=10573;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Borborema-Santos C.M., Santos P.J.B., Talhari S., Azeiteiro-Filho S.;
RT "Sequencing and genome analysis of HPV type 13 isolated in the
RT Amazon."
RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: DQ344807; ABC79058.1; -; Genomic_DNA.
SQ SEQUENCE 98 AA; 10738 MW; 97D6627C57CF896D CRC64;

Query Match
Best Local Similarity 36.8%; Score 190; DB 2; Length 98;
Matches 45; Conservative 12; Mismatches 37; Indels 6; Gaps 2;

QY 1 MHGDTPTLHEMYMDLOPETTDLYXXYXQLNDSSEEDIDGPAQAEPRRA--HYNIVTF 57
DB 1 MHGQYTLKQIVLDLTPDPVGLHCHNEQLDS--EDVDQAQTQATGHTLQCTQILTS 57

QY 58 CCKCDSTLRLCVQSTHVDIRTLIEDLLMGTLGIYXPICSQK 97
DB 58 CSKCCSNVRLVVECTGPDHLDLHLLGTLNIVCPDCAK 97

RESULT 85
Q98005_9PAPI PRELIMINARY; PRT; 96 AA.
AC Q98005;
DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.
DT 01-FEB-1997, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE E7 protein.
OS Human papillomavirus type 74.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=44028;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96379050; PubMed=8784613;
RA Longuet M., Cassemonet P., Orch G.;
RT "A novel genital human papillomavirus (HPV), HPV type 74, found in
RT immunosuppressed patients."
RL J. Clin. Microbiol. 34:1859-1862(1996).
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CC -----
DR EMBL: U40822; AAC55128.1; -; Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 96 AA; 10522 MW; 8DF8480CE5CCEA3 CRC64;

Query Match
Best Local Similarity 36.6%; Score 189; DB 2; Length 96;
Matches 45; Conservative 12; Mismatches 37; Indels 4; Gaps 2;

QY 1 MHGDTPTLHEMYMDLOPETTDLYXXYXQLNDSSEEDIDGPAQAEPRRAH-YNIVTFCC 59
DB 1 MHGKYSTLKEIVLELQDPVGLCHNEQLDSSEEDVBL--ATQATQQLTQAIVQIVTCG 57

QY 60 KCDSTLRLCVQSTHVDIRTLIEDLLMGTLGIYXPICSQK 97
DB 58 VCNRSIRLVVQCTGPDINNHTLILGTLNIVCPDCAK 95

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RESULT 86
VE7_HPV28      STANDARD;      PRT;      87 AA.
AC P50783;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Protein E7.
GN Name=E7;
OS Human Papillomavirus type 28.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=37111;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP Delius H.;
RA Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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CC -----
DR EMBL: U31783; AAA79423.1; -, Genomic_DNA.
DR InterPro: IPR00148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Transcription;
KM Transcription regulation.
FT CHAIN 1 87 Protein E7.
FT MOTIF 50 53 /FTId=PRO_0000133426.
FT MOTIF 83 86 C-XX-C motif-1.
FT MOTIF 83 86 C-XX-C motif-2.
SQ SEQUENCE 87 AA; 9625 MW; 4A3692CED16BCD60 CRC64;

Query Match 36.0%; Score 186; DB 1; Length 87;
Best Local Similarity 44.8%; Pred. No. 9.7e-14;
Matches 43; Conservative 11; Mismatches 30; Indels 12; Gaps 3;

QY 1 MGGDTPLHEMYLDLPETTDLYXXQLNDSSEED--SIDGPAQAEPDRAHYNIYVTF 58
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1 MGGHPHVKVDIELSLAEDVPV---QCVOQDDEDTNVNBPQAQ-----YRVTLIC 50
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 59 CCKCDSTLRLCVQSTHVDIRLTEDLMGTIGIYXPC 94
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 51 PKCSSPLRLVCECSHADIRALEQLLGLTLTVVCPRC 86
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 87
VE7_HPV42      STANDARD;      PRT;      93 AA.
AC P27231;
DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1992, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE Protein E7.
GN Name=E7;
OS Human Papillomavirus type 42.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=10590;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP MEDLINE:92087479; PubMed:1309278;
RA Philipp W., Honore N., Sapp M., Cole S.T., Streeck R.E.;
RT "Human papillomavirus type 42: new sequences, conserved genome
RT organization.";
RL Virology 186:331-334 (1992).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----

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CC -----
DR EMBL: M73236; AAA47042.1; ALT_INIT; Genomic_DNA.
DR PIR: F39451; M7ML42.
DR InterPro: IPR00148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Transcription;
KM Transcription regulation.
FT CHAIN 1 93 Protein E7.
FT MOTIF 53 56 /FTId=PRO_0000133440.
FT MOTIF 86 89 C-XX-C motif-1.
FT MOTIF 86 89 C-XX-C motif-2.
SQ SEQUENCE 93 AA; 10679 MW; 829D1E24071F7A53 CRC64;

Query Match 35.5%; Score 183.5; DB 1; Length 93;
Best Local Similarity 44.4%; Pred. No. 2.1e-13;
Matches 44; Conservative 17; Mismatches 27; Indels 11; Gaps 4;

QY 1 MGGDTPLHEMYLDLP--ET-TDLYXXQLNDSSEEDSIDGPAQAEPDRAHYNIYVTF 57
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1 MGGHPHVKVDIELSLAEDVPV---QCVOQDDEDTNVNBPQAQ-----YRVTLICV 52
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 58 CCKCDSTLRLCVQSTHVDIRLTEDLMGTIGIYXPCSQ 96
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 53 CTQCYKSVKLVQCTEADIRNLQOMLGTIDIVCPICAR 91
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 88
VE7_HPV66      STANDARD;      PRT;      105 AA.
AC Q80956;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Protein E7.
GN Name=E7;
OS Human Papillomavirus type 66.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=37119;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP PubMed:1663515;
RA Tawheed A.R., Beaudenon S., Favre M., Orth G.;
RT "Characterization of human papillomavirus type 66 from an invasive
RT carcinoma of the uterine cervix.";
RL J. Clin. Microbiol. 29:2656-2660 (1991).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC -----
DR EMBL: M75123; -, NOT ANNOTATED CDS; Genomic_DNA.
DR EMBL: U31794; AAA79500.1; -, Genomic_DNA.
DR PIR: B44890; B44890.
DR InterPro: IPR00148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Transcription;
KM Transcription regulation.
FT CHAIN 1 105 Protein E7.
FT MOTIF 66 69 /FTId=PRO_0000133459.
FT MOTIF 98 101 C-XX-C motif-1.
FT MOTIF 98 101 C-XX-C motif-2.
SQ SEQUENCE 105 AA; 11912 MW; C09339FA2F62AFAA CRC64;

Query Match 35.5%; Score 183.5; DB 1; Length 105;

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Best Local Similarity 42.7%; Pred. No. 2.4e-13;
Matches 44; Conservative 17; Mismatches 33; Indels 9; Gaps 4;

QY 1 MHGPTPLHEMYMLDLPET--TDLYXXYXQNDSSSEEDIDGPAGQAEPRAHYVVT 52
DB 1 MHGVPPLQEVILELAPTEIDLCNEQLDSSSEDEDEDEHLLERPOQARQAQHC-Y 59
QY 53 NIVTFCCCKDSTLRCLVOSTHVDIRTEEDLLMGTGLGVXPCIS 95
DB 60 LIHPCCCKCELIVQDIDISTKEELRVVQQLMGALVTVCPLCA 102

RESULT 89
037386 CCPV1 PRELIMINARY; PRT; 99 AA.
AC 037386,
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DE 07-FEB-2006, entry version 20.
DE E7.
OS Common chimpanzee papillomavirus type 1.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae; primate Papillomaviruses;
OC Common chimpanzee papillomavirus.
OX NCBI_Taxid=66261;
RN NUCLEOTIDE SEQUENCE.
RA Schiavarello F., Soza I., Brasky K.M., Hilliard J.K.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
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DR EMBL: AF020905; AAB71705.1; -: Genomic_DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
DR SEQUENCE 99 AA; 10856 MW; 7385003547E87AFE CRC64;

Query Match 34.9%; Score 180.5; DB 2; Length 99;
Best Local Similarity 42.4%; Pred. No. 5e-13;
Matches 42; Conservative 18; Mismatches 32; Indels 7; Gaps 2;

QY 1 MHGPTPLHEMYMLDLPETTDLYXXYXQNDSSSEEDIDGPAGQAEPRAHYVVT 56
DB 1 MHGVPPLQEVILELAPTEIDLCNEQLDSSSEDEDEDEHLLERPOQARQAQHC-Y 57

QY 57 FCCCKDSTLRCLVOSTHVDIRTEEDLLMGTGLGVXPCIS 95
DB 58 SCGHGNNTVRLVVECTGPDIGHLNHLGLSLNIVCPPLCA 96

RESULT 90
VE7_HPV54 STANDARD; PRT; 95 AA.
ID VE7_HPV54
AC 081019,
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 54.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333766;
RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RP Delius H.;
RA Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RL FUNCTION: E7 protein has both transforming and trans-activating
CC activities.

CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC -----
DR EMBL: U37488; AAA79188.1; -: Genomic_DNA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KM DNA-binding; Early protein; Oncogene; Transcription;
KM Transcription regulation.
FT CHAIN 1 95 Protein E7.
FT /FTID=PRO_0000133450.
FT MOTIF 88 91 C-XX-C motif-2.
FT SEQUENCE 95 AA; 10565 MW; 6A543269F2561891 CRC64;

Query Match 34.7%; Score 179.5; DB 1; Length 95;
Best Local Similarity 39.2%; Pred. No. 6.3e-13;
Matches 40; Conservative 18; Mismatches 31; Indels 13; Gaps 4;

QY 1 MHGPTPLHEMYMLDLPETTDLYXXYXQNDSSSEEDIDGPAGQAEPRAHYVVT 56
DB 1 MHGVPPLQEVILELAPTEIDLCNEQLDSSSEDEDEDEHLLERPOQARQAQHC-Y 55

QY 57 FCCCKDSTLRCLVOSTHVDIRTEEDLLMGTGLGVXPCIS 97
DB 56 VCCCKDSTLRCLVOSTHVDIRTEEDLLMGTGLGVXPCIS 94

RESULT 91
VE7_HPV70 STANDARD; PRT; 109 AA.
ID VE7_HPV70
AC P50785,
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 70.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=39457;
RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RP MEDLINE=96249586; PubMed=8815087;
RX Forslund O., Hansson B.G.;
RA "Human papillomavirus type 70 genome cloned from overlapping PCR
RT products: complete nucleotide sequence and genomic organization.";
RL J. Clin. Microbiol. 34:802-809 (1996).
RN [2]

RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX MEDLINE=97060129; PubMed=8904450;
RA Longuet M., Beaudenon S., Orch G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
RT related to the potentially oncogenic HPV39.";
RL J. Clin. Microbiol. 34:738-744 (1996).
CC -1- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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CC -----
DR EMBL: U21941; AAC54851.1; -: Genomic_DNA.
DR EMBL: U22461; AAC54881.1; -: Genomic_DNA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
KM DNA-binding; Early protein; Oncogene; Transcription;
KM Transcription regulation.
FT CHAIN 1 109 Protein E7.
FT /FTID=PRO_0000133462.
FT MOTIF 66 69 C-XX-C motif-1.
FT MOTIF 101 104 C-XX-C motif-2.
FT SEQUENCE 109 AA; 12657 MW; 2FD3C643DFAF891 CRC64;

Query Match 34.6%; Score 179; DB 1; Length 109;
 Best Local Similarity 40.2%; Pred. No. 8.5e-13;
 Matches 43; Conservative 14; Mismatches 36; Indels 14; Gaps 3;

QY 1 MGGDTPLHEMYMDLQ-----ETTDLYXXYQLNDSSEEDIDP-----AGQAEPD 48
 DB 1 MGGPRPLQIVDLVYNEIQPVLYCHQLEDSDNETEPHVVNHQQLARRRPFQ 60

QY 49 RAHNYIVTFCCDSTRLCVQSTHVDIRTLMDLMTGLGIYXPCIS 95
 DB 61 R-HKICQWCKKNTLHLVVEASQENLRSLQLFMETLSFVCPWCA 105

RESULT 92
 VE7_HPV57 STANDARD; PRT; 92 AA.
 AC P22160;
 DT 01-AUG-1991, integrated into UniProtKB/Swiss-Prot.
 DT 07-FEB-2006, entry version 34.
 DE Protein E7.
 GN Name=E7;
 OS Human papillomavirus type 57.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 NCBI_TaxID=333753;
 RN [1]
 RP MEDLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=91188699; PubMed=1964523; DOI=10.1016/0168-1702(90)90091-O;
 RA Hirsch-Behnam A., Dellus H., de Villiers E.M.;
 RT "A comparative sequence analysis of two human papillomavirus (HPV)
 types 2a and 57.";
 RL Virus Res. 18:81-98(1990).
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating
 activities.
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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 CC -----
 CC EMBL: X55965; CA39431.1; -; Genomic_DNA.
 CC DR PIR: S15622; S15622.
 DR InterPro: IPR000148; Papv1_E7.
 DR Pfam: PF00527; E7; 1.
 KW DNA-binding; Early protein; Oncogene; Transcription;
 KM Transcription regulation.
 FT CHAIN 1 92 Protein E7.
 FT MOTIF 55 58 /FTID=PRO_0000133453.
 FT MOTIF 88 91 C-XX-C motif-2.
 FT MOTIF 91 C-XX-C motif-2.
 SQ SEQUENCE 92 AA; 10376 MW; DB56C16916257B13 CRC64;

Query Match 34.5%; Score 178.5; DB 1; Length 92;
 Best Local Similarity 43.3%; Pred. No. 7.9e-13;
 Matches 42; Conservative 15; Mismatches 31; Indels 9; Gaps 3;

QY 1 MGGDTPLHEMYMDLQ-----PETTDLYXXYQLNDSSEEDIDPAGQAEPPRAHNYIVTF 57
 DB 1 MGGPRPLQIVDLVYNEIQPVLYCHQLEDSDNETEPHVVNHQQLARRRPFQ 60

QY 58 CCKCDSTRLCVQSTHVDIRTLMDLMTGLGIYXPCIS 94
 DB 55 CCKCHSTVRLVVEGADIRHLEQLFNTLTIVCPRC 91

RESULT 93
 VE7_HPV56 STANDARD; PRT; 105 AA.
 AC P36833;
 DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-1994, sequence version 1.
 DT 07-FEB-2006, entry version 31.

DE Protein E7.
 GN Name=E7;
 OS Human papillomavirus type 56.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 NCBI_TaxID=10596;
 RN [1]
 RP MEDLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=94265501; PubMed=8205838;
 RA Dellus H., Hofmann B.;
 RT "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating
 activities.
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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 CC -----
 CC EMBL: X74463; CA52477.1; -; Genomic_DNA.
 CC DR PIR: S36585; S36585.
 DR InterPro: IPR000148; Papv1_E7.

Query Match 34.5%; Score 178.5; DB 1; Length 105;
 Best Local Similarity 40.8%; Pred. No. 9.3e-13;
 Matches 42; Conservative 17; Mismatches 35; Indels 9; Gaps 3;

QY 1 MGGDTPLHEMYMDLQPEETDLYXXYQLNDSSEEDIDPAGQAEPPRAHNYIVTF 52
 DB 1 MGGPRPLQIVDLVYNEIQPVLYCHQLEDSDNETEPHVVNHQQLARRRPFQ 60

QY 53 NIVTFCCDSTRLCVQSTHVDIRTLMDLMTGLGIYXPCIS 95
 DB 60 LHVPCCECKFVVQLDIQSTKEDLRVQQLMGALTVTCPLCA 102

RESULT 94
 VE7_HPV07 STANDARD; PRT; 111 AA.
 AC P36816;
 DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-1994, sequence version 1.
 DT 07-FEB-2006, entry version 31.
 DE Protein E7.
 GN Name=E7;
 OS Human papillomavirus type 7.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 NCBI_TaxID=10620;
 RN [1]
 RP MEDLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=94265501; PubMed=8205838;
 RA Dellus H., Hofmann B.;
 RT "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating
 activities.
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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 CC -----
 CC EMBL: X74463; CA52477.1; -; Genomic_DNA.
 CC DR PIR: S36585; S36585.
 DR InterPro: IPR000148; Papv1_E7.

DR Pfam; PF00527; E7; 1.
 KM DNA-binding; Early protein; Oncogene; Transcription;
 KM Transcription regulation.
 FT CHAIN 1 111 Protein E7.
 FT MOTIF 71 74 /FTid=PRO_0000133406.
 FT MOTIF 104 107 C-XX-C motif-1.
 FT MOTIF 107 C-XX-C motif-2.
 SQ SEQUENCE 111 AA; 12460 MW; 830ADCA5F912BF1A CRC64;

Query Match 34.5%; Score 178.5; DB 1; Length 111;
 Best Local Similarity 39.8%; Pred. No. 9.9e-13;
 Matches 45; Conservative 12; Mismatches 33; Indels 23; Gaps 3;

QY 1 MHGDPPTLHEHYMLDLPETTDLYXXYQANDSSEEDFIDGPAQAEPDRAH-----YNTV 51
 DB 1 MHGERTPGDIDVLDQPEPVLSCHQQL-DSSDSDDHE-----QDQDSSINRQREQPTQ 55

QY 52 -----YNTVPCKCSDTLRLCVOSTHVDIRLTLEDLLMGTIGVXPICS 95
 DB 56 QDLQVNLQSPKIVTHCVFCHGLVRLVHCTATDIRQVQLMGLTNIIVCPNCA 108

RESULT 95

VE7_HPV51 STANDARD; PRT; 101 AA.

AC P26558;
 DT 01-AUG-1992, integrated into UniProtKB/Swiss-Prot.
 DT 01-AUG-1992, sequence version 1.
 DT 07-FEB-2006, entry version 31.
 DE Protein E7.
 GN Name=E7;
 OS Human Papillomavirus type 51.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxId=10595;

RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RA MEDLINE=91303675; PubMed=1649326;
 RA Lungu O., Crum C.P., Silverstein S.J.;

RT "Biologic properties and nucleotide sequence analysis of human
 RT papillomavirus type 51.";

RL J. Virol. 65:4216-4225(1991).

CC -1- FUNCTION: E7 protein has both transforming and trans-activating
 CC activities.

CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.

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CC EMBL; M62877; -; NOT_ANNOTATED_CDS; Genomic_DNA.

DR PIR; F40415; W7ML51.
 DR InterPro: IPR000148; Papv1_E7.

DR Pfam; PF00527; E7; 1.
 KM DNA-binding; Early protein; Oncogene; Transcription;
 KM Transcription regulation.

KW CHAIN 1 101 Protein E7.
 FT MOTIF 62 65 /FTid=PRO_0000133447.
 FT MOTIF 95 98 C-XX-C motif-1.
 FT MOTIF 98 C-XX-C motif-2.

SQ SEQUENCE 101 AA; 11339 MW; 65E85C534099801A CRC64;

Query Match 34.4%; Score 178; DB 1; Length 101;
 Best Local Similarity 41.0%; Pred. No. 1e-12;
 Matches 41; Conservative 16; Mismatches 37; Indels 6; Gaps 3;

QY 1 MHGDPPTLHEHYMLDLPETTDLYXXYQANDSSEEDFIDGPAQAEPDRAH-----YNTV 55
 DB 1 MRGNVPDLKDVVLTHTPTETIDLCYEQF-DSSSEEDVDNMRRQLPERRAQAATCYRIE 59

QY 56 TPCCKCDSTLRLCVOSTHVDIRLTLEDLLMGTIGVXPICS 95
 DB 60 APCCRSSVVQDLAVSSGDTLRVVQOMLMBLSLVCPCA 99

RESULT 96
 VE7_HPV55 STANDARD; PRT; 97 AA.
 AC Q80935;
 DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 30.
 DE Protein E7.
 GN Name=E7;
 OS Human Papillomavirus type 55.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxId=37114;
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Delius H.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating
 CC activities.

CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.

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DR EMBL; U31791; AAA79479.1; -; Genomic_DNA.
 DR InterPro: IPR000148; Papv1_E7.

DR Pfam; PF00527; E7; 1.
 KM DNA-binding; Early protein; Oncogene; Transcription;
 KM Transcription regulation.

KW CHAIN 1 97 Protein E7.
 FT MOTIF 57 60 /FTid=PRO_0000133451.
 FT MOTIF 90 93 C-XX-C motif-1.
 FT MOTIF 93 C-XX-C motif-2.

SQ SEQUENCE 97 AA; 10621 MW; E2997616BC647D42 CRC64;

Query Match 34.1%; Score 176.5; DB 1; Length 97;
 Best Local Similarity 44.4%; Pred. No. 1.5e-12;
 Matches 44; Conservative 14; Mismatches 36; Indels 5; Gaps 3;

QY 1 MHGDPPTLHEHYMLDLPETTDLYXXYQANDSSEEDFIDGPAQAEPDRAH-YNTVFC 58
 DB 1 MHGVPPLKEIKVIELDPDPVGLHCNEQLDSS--EDEVBLATQATQDTPQYQIVTTC 57

QY 59 CKCDSTLRLCVOSTHVDIRLTLEDLLMGTIGVXPICSOK 97
 DB 58 GTCNRNRYLVVQCTGTIDICQHTLLLSLEILCPVCAPK 96

RESULT 97
 VE7_HPV2A STANDARD; PRT; 92 AA.
 AC P25495;
 DT 01-MAY-1992, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-1992, sequence version 1.
 DT 07-FEB-2006, entry version 32.
 DE Protein E7.
 GN Name=E7;
 OS Human Papillomavirus type 2a.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxId=10584;
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RP MEDLINE=91188699; PubMed=1964523; DOI=10.1016/0168-1702(90)90091-O;
 RA Hirsch-Bennett A., Delius H., de Villiers E.M.;

RT "A comparative sequence analysis of two human papillomavirus (HPV)
 RT types 2a and 57.";

RL Virus Res. 18:81-98(1990).

CC -1- FUNCTION: E7 protein has both transforming and trans-activating
 CC activities.

CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.

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DR EMBL; M62877; -; NOT_ANNOTATED_CDS; Genomic_DNA.

DR PIR; F40415; W7ML51.
 DR InterPro: IPR000148; Papv1_E7.

DR Pfam; PF00527; E7; 1.
 KM DNA-binding; Early protein; Oncogene; Transcription;
 KM Transcription regulation.

KW CHAIN 1 101 Protein E7.
 FT MOTIF 62 65 /FTid=PRO_0000133447.
 FT MOTIF 95 98 C-XX-C motif-1.
 FT MOTIF 98 C-XX-C motif-2.

SQ SEQUENCE 101 AA; 11339 MW; 65E85C534099801A CRC64;

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 CC EMBL; X55964; -; NOT_ANNOTATED_CDS; Genomic_DNA.
 DR PIR; S15615; S15615.
 DR InterPro; IPR000148; Papyl_E7.
 DR Pfam; PF00527; E7; 1.
 DR DNA-binding; Early protein; Oncogene; Transcription;
 KM Transcription regulation.
 FT CHAIN 1 92
 FT Protein E7.
 FT /Fric=PRO 0000133400.
 FT MOTIF 55 58 C-XX-C motif-1.
 FT MOTIF 88 91 C-XX-C motif-2.
 SQ SEQUENCE 92 AA; 10369 MW; 0C412DF9C7A9EBA CRC64;

Query Match 33.9%; Score 175.5; DB 1; Length 92;
 Best Local Similarity 43.3%; Pred. No. 1.8e-12;
 Matches 42; Conservative 13; Mismatches 35; Indels 7; Gaps 3;

QY 1 MGGDTPLTLEH--YMLDLPETTDLYXXQLNDSSSEEDIDGPAQAEPRAHNYIVTFC 58
 DB 1 MGGNRSPLKDITLIDELIPEIVDLHCDEGF--DSSSEENHQ---LTPDVQAYGVVTC 55
 59 CKCDSTRLCVQSTHVDIRTLMDLMTGLTGIYXPICS 95
 DB 56 CKCGTRTLVBCGQDLRELEQLFKTLTLVCPHCA 92

RESULT 98
 Q9IR58 HPV82 PRELIMINARY; PRT; 100 AA.
 AC Q9IR58;
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2000, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE E7 protein.
 OS Human papillomavirus type 82.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxId=129724;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20087389; PubMed=10618284;
 RA Kuno N., Sata T., Sato Y., Sugase M., Matukura T.;
 RT "Molecular cloning and nucleotide sequence analysis of a novel human
 RT papillomavirus (type 82) associated with vaginal intraepithelial
 RT neoplasia";
 RL Clin. Diagn. Lab. Immunol. 7:91-95(2000).
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 CC EMBL; AB027021; BAA90736.1; -; Genomic_DNA.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000148; Papyl_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 100 AA; 11325 MW; 47E8C0D0F67A81D CRC64;

Query Match 33.9%; Score 175.5; DB 2; Length 100;
 Best Local Similarity 40.0%; Pred. No. 2e-12;
 Matches 40; Conservative 18; Mismatches 35; Indels 7; Gaps 4;

QY 1 MGGDTPLTLEHMDLPE--TTDLXXYQLNDSSSEEDIDG---PQAQEPRAHNYIV 55
 DB 1 MGGNRSPLKDITLIDELIPEIVDLHCDEGF--DSSSEENHQ---LTPDVQAYGVVTC 55
 56 CKCDSTRLCVQSTHVDIRTLMDLMTGLTGIYXPICS 95
 DB 59 VHCRCSSVQVLAVSSGSLRIFQQLGLDLSLVCPWCA 98

RESULT 99
 Q2VJB9 9PAPI PRELIMINARY; PRT; 96 AA.
 ID Q2VJB9;
 AC Q2VJB9;
 DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 10-JAN-2006, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE E7 protein.
 OS Human papillomavirus type 102.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxId=338327;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=QV340771;
 RX PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
 RA Narechania A., Chen Z., Desalle R., Burk R.D.;
 RT "Phylogenetic incongruence among Oncogenic Genital Alpha Human
 RT Papillomaviruses";
 RL J. Virol. 79:15503-15510(2005).
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC EMBL; DQ080083; AAZ39521.1; -; Genomic_DNA.
 SQ SEQUENCE 96 AA; 10594 MW; E791B4A9BA885F CRC64;

Query Match 33.8%; Score 174.5; DB 2; Length 96;
 Best Local Similarity 42.7%; Pred. No. 2.5e-12;
 Matches 41; Conservative 13; Mismatches 41; Indels 1; Gaps 1;

QY 1 MGGDTPLTLEHMDLPE--TTDLXXYQLNDSSSEEDIDGPAQA--EPRAHNYIVTFC 59
 DB 1 MGGNRSPLKDITLIDELIPEIVDLHCDEGF--DSSSEENHQ---LTPDVQAYGVVTC 55
 60 KCDSTRLCVQSTHVDIRTLMDLMTGLTGIYXPICS 95
 DB 61 MCGQSLRLVLCGDDIRLQELVAVAVIVCPSCA 96

RESULT 100
 VE7 HPV10 STANDARD; PRT; 86 AA.
 ID VE7 HPV10
 AC P36818;
 DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-1994, sequence version 1.
 DT 07-FEB-2006, entry version 32.
 DE Protein E7.
 GN Name=E7;
 OS Human papillomavirus type 10.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxId=333759;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=94265501; PubMed=8205838;
 RA Delius H., Holman B.;
 RT "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating
 CC activities.
 CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC EMBL; X74465; CAAS2490.1; -; Genomic_DNA.
 DR PIR; S36533; S36533.
 DR InterPro; IPR000148; Papyl_E7.
 DR Pfam; PF00527; E7; 1.
 KM DNA-binding; Early protein; Oncogene; Transcription;
 FT CHAIN 1 86 Protein E7.

FT MOTIF 49 52 /FtId=PRO_0000133409.
 FT MOTIF 82 85 C-XX-C motif-1.
 SQ SEQUENCE 86 AA: 9541 MW: E597B895A4125090 CRC64;

Query Match 33.6%; Score 173.5; DB 1; Length 86;
 Best Local Similarity 42.6%; Pred. No. 2.8e-12;
 Matches 40; Conservative 10; Mismatches 35; Indels 9; Gaps 2;

QY 1 MHGDTPLHEYM LLOPBTVDLYXXQLNDSSFEDEIDGPAGQAEPPRAHNYIVTFCK 60
 DB 1 MHGPHPTVKDIELSLAPEDIPV-----CNVQLDEBDYTD-----VEPAQQA YRVVTECTK 51
 QY 61 CDSTLR LCVOSTHVDIRTLIEDL LMGTLGIYXPIC 94
 DB 52 CSLPLRLV ECGSHADIRALBQLLGTLKLVCPRC 85

Search completed: May 27, 2006, 05:16:26
 Job time : 154.133 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:16:46 ; Search time 28.7309 Seconds
(without alignments)
298.563 Million cell updates/sec

Title: US-10-530-253-14ED

Perfect score: 517
Sequence: 1 MHGDTPTLHXYMDLQPEPT.....LEDLHMGTLGVXPCSQKP 98

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
Issued Patents AA:*
1: /BMC_Ceitera_SIDS3/prodata/2/iaa/5 COMB.pep:*
2: /BMC_Ceitera_SIDS3/prodata/2/iaa/6 COMB.pep:*
3: /BMC_Ceitera_SIDS3/prodata/2/iaa/7 COMB.pep:*
4: /BMC_Ceitera_SIDS3/prodata/2/iaa/H COMB.pep:*
5: /BMC_Ceitera_SIDS3/prodata/2/iaa/PCUS COMB.pep:*
6: /BMC_Ceitera_SIDS3/prodata/2/iaa/RE COMB.pep:*
7: /BMC_Ceitera_SIDS3/prodata/2/iaa/bckfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	99.2	220	2	US-09-485-885-8
2	512	99.0	98	1	US-08-406-248-6
3	512	99.0	98	2	US-08-075-541D-42
4	512	99.0	98	2	US-09-382-616A-1
5	512	99.0	98	2	US-08-944-368A-4
6	512	99.0	98	2	US-09-820-764-4
7	512	99.0	98	2	US-09-986-118A-4
8	512	99.0	98	2	US-09-728-466-1
9	512	99.0	98	2	US-09-824-017-4
10	512	99.0	98	2	US-09-637-746-3
11	512	99.0	98	2	US-09-501-097A-7
12	512	99.0	98	2	US-09-980-523A-12
13	512	99.0	121	2	US-09-613-303-12
14	512	99.0	121	2	US-10-267-311-12
15	512	99.0	198	2	US-09-613-303-35
16	512	99.0	198	2	US-10-267-311-35
17	512	99.0	220	2	US-09-485-885-1
18	512	99.0	253	2	US-08-485-885-12
19	512	99.0	253	1	US-08-459-818-20
20	512	99.0	253	1	US-08-889-666-20
21	512	99.0	253	1	US-08-465-078-20
22	512	99.0	253	1	US-08-725-776-20
23	512	99.0	263	1	US-08-488-062-20
24	512	99.0	263	1	US-08-117-083-9
25	512	99.0	266	2	US-08-860-165-10
26	512	99.0	266	2	US-09-359-382-10
27	512	99.0	266	2	US-09-367-309A-1
28	512	99.0	287	2	US-09-501-097A-25
29	512	99.0	295	2	US-09-613-303-33
30	512	99.0	295	2	US-10-267-311-33
31	512	99.0	324	2	US-09-613-303-25
32	512	99.0	324	2	US-10-267-311-25
33	512	99.0	371	2	US-09-485-885-6
34	512	99.0	390	2	US-09-485-885-14
35	512	99.0	493	2	US-09-613-303-19
36	512	99.0	493	2	US-10-267-311-19
37	512	99.0	639	2	US-09-613-303-17
38	512	99.0	639	2	US-10-267-311-17
39	512	99.0	641	2	US-09-613-303-51
40	512	99.0	641	2	US-10-267-311-51
41	512	99.0	647	2	US-09-613-303-53
42	512	99.0	647	2	US-10-267-311-53
43	507	98.1	98	2	US-09-566-420-19
44	507	98.1	98	2	US-10-201-764-19
45	503	97.3	98	2	US-09-613-303-8
46	503	97.3	98	2	US-10-267-311-8
47	503	97.3	648	2	US-09-613-303-29
48	503	97.3	648	2	US-10-267-311-29
49	503	97.3	711	2	US-09-613-303-41
50	503	97.3	711	2	US-10-267-311-41
51	503	97.3	724	2	US-09-613-303-45
52	503	97.3	724	2	US-10-267-311-45
53	500	96.7	420	2	US-09-501-097A-22
54	500	96.7	723	2	US-09-501-097A-20
55	478	92.5	185	2	US-09-462-993-2
56	353	68.3	172	2	US-08-860-165-12
57	353	68.3	172	2	US-09-359-382-12
58	345	66.7	172	2	US-08-860-165-14
59	345	66.7	172	2	US-09-359-382-14
60	247	47.8	601	1	US-08-606-288-7
61	247	47.8	601	1	US-08-606-288-10
62	247	47.8	601	2	US-09-347-483-7
63	247	47.8	601	2	US-09-347-483-10
64	243	47.0	1587	2	US-09-000-094-46
65	243	47.0	1587	2	US-10-011-749-46
66	240	46.4	375	2	US-09-000-094-42
67	240	46.4	375	2	US-10-011-749-42
68	240	46.4	465	2	US-09-000-094-24
69	240	46.4	465	2	US-10-011-749-24
70	209	40.4	38	2	US-09-501-097A-6
71	201.5	39.0	227	2	US-09-485-885-19
72	200.5	38.8	272	1	US-08-117-083-13
73	200.5	38.8	383	2	US-09-485-885-23
74	192.5	37.2	227	1	US-09-485-885-16
75	171	33.1	30	2	US-08-934-915-52
76	171	33.1	30	2	US-09-486-394-3
77	162	31.3	30	1	US-08-934-915-53
78	154	29.8	30	2	US-09-486-394-1
79	153	29.6	30	1	US-08-934-915-51
80	153	29.6	30	2	US-09-486-394-5
81	150.5	29.1	32	2	US-08-075-541D-7
82	148	28.6	30	2	US-09-828-645-7
83	147	28.4	30	1	US-08-363-586-1
84	147	28.4	30	2	US-09-828-645-3
85	146	28.2	30	1	US-08-934-915-54
86	145	28.0	30	2	US-09-486-394-2
87	143	27.7	25	2	US-08-075-541D-47
88	137	26.5	28	2	US-09-486-394-5
89	136	26.3	25	1	US-08-363-586-2
90	126	24.4	26	2	US-08-075-541D-40
91	122	23.6	30	1	US-08-934-915-71
92	121	23.4	23	2	US-09-980-523A-14
93	120	23.2	20	2	US-08-075-541D-10
94	118	22.8	20	1	US-08-934-915-48
95	118	22.8	20	2	US-09-980-177A-73
96	116	22.4	20	2	US-09-980-177A-74
97	114	22.1	19	2	US-08-075-541D-3
98	113	21.9	20	1	US-08-934-915-46
99	112	21.7	20	2	US-08-075-541D-43

100 112 21.7 20 2 US-09-980-177A-69

Sequence 69, Appl1

ALIGNMENTS

RESULT 1

US-09-485-885-8
; Sequence 8, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 8
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-8

Query Match 99.2%; Score 513; DB 2; Length 220;
Best Local Similarity 96.9%; Pred. No. 1.8e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYXQINDSSEEDIDGPAQAEPBRAHNYITVFCK 60
Db 114 MHGDTPLHEYMLDLPETTDLYGYQINDSSEEDIDGPAQAEPBRAHNYITVFCK 173
Qy 61 CDSTRLCVOSTHVDIRLTEDLLMGTLGIYVPICSQKP 98
Db 174 CDSTRLCVOSTHVDIRLTEDLLMGTLGIYVPICSQKP 211

RESULT 2

US-08-406-248-6
; Sequence 6, Application US/08406248
; Patent No. 5736318
; GENERAL INFORMATION:
; APPLICANT: Munger, Karl
; APPLICANT: Jones, D. Leanne
; TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
; TITLE OF INVENTION: TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,248
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: McDanielis, Patricia A.

; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: HAZ-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-406-248-6

Query Match 99.0%; Score 512; DB 1; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYXQINDSSEEDIDGPAQAEPBRAHNYITVFCK 60
Db 1 MHGDTPLHEYMLDLPETTDLYCYEQINDSSEEDIDGPAQAEPBRAHNYITVFCK 60
Qy 61 CDSTRLCVOSTHVDIRLTEDLLMGTLGIYVPICSQKP 98
Db 61 CDSTRLCVOSTHVDIRLTEDLLMGTLGIYVPICSQKP 98

RESULT 3

US-08-075-541D-42
; Sequence 42, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZ JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU Pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pcc/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-075-541D-42

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPFLHEYMULDQPETTDLYXXYXQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60
DB 1 MHGDPFLHEYMULDQPETTDLYCYEQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60

QY 61 CDSTLRFCVOSTHVDIRTLBLLMGTLGIVXPCISQKP 98
DB 61 CDSTLRFCVOSTHVDIRTLBLLMGTLGIVXPCISQKP 98

RESULT 4
US-09-382-616A-1

Sequence 1, Application US/09382616A
Patent No. 6200746
GENERAL INFORMATION:

APPLICANT: Fisher, Christopher

APPLICANT: He, Wanxia

TITLE OF INVENTION: Methods to Identify Anti-Viral Agents

FILE REFERENCE: 28341/6216

CURRENT FILING DATE: 1999-08-25

PRIOR APPLICATION NUMBER: 09/382,616

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 98

TYPE: PRT

ORGANISM: Papillomavirus sylvilagi

US-09-382-616A-1

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPFLHEYMULDQPETTDLYXXYXQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60
DB 1 MHGDPFLHEYMULDQPETTDLYCYEQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60

QY 61 CDSTLRFCVOSTHVDIRTLBLLMGTLGIVXPCISQKP 98
DB 61 CDSTLRFCVOSTHVDIRTLBLLMGTLGIVXPCISQKP 98

RESULT 5

US-08-944-368A-4

Sequence 4, Application US/08944368A

Patent No. 6228368

GENERAL INFORMATION:

APPLICANT: Giesman, et al.

TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: 233 South Wacker Drive, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,368A

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27013/34028

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-944-368A-4

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPFLHEYMULDQPETTDLYXXYXQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60
DB 1 MHGDPFLHEYMULDQPETTDLYCYEQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60

QY 61 CDSTLRFCVOSTHVDIRTLBLLMGTLGIVXPCISQKP 98
DB 61 CDSTLRFCVOSTHVDIRTLBLLMGTLGIVXPCISQKP 98

RESULT 6
US-09-820-764-4

Sequence 4, Application US/09820764
Patent No. 6352696
GENERAL INFORMATION:

APPLICANT: BURGER, Alexander

APPLICANT: HALPER, Michael

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESSES:

ADDRESS: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/820,764

FILING DATE: 30-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/026,896

FILING DATE: 20-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-820-764-4

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMULDQPEPTTDLVYXXQANDSSEDEIDGPAQAEPDRAHNYIVTFCK 60
Db 1 MHGDPPTLHEYMULDQPEPTTDLVYXXQANDSSEDEIDGPAQAEPDRAHNYIVTFCK 60
61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIVPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIVPCISQKP 98

RESULT 7

US-09-986-118A-4
; Sequence 4, Application US/09986118A
; Patent No. 6562351
; GENERAL INFORMATION:

APPLICANT: BURGER, Alexander
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/986,118A
FILING DATE: 07-NO. 6562351-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-986-118A-4

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMULDQPEPTTDLVYXXQANDSSEDEIDGPAQAEPDRAHNYIVTFCK 60
Db 1 MHGDPPTLHEYMULDQPEPTTDLVYXXQANDSSEDEIDGPAQAEPDRAHNYIVTFCK 60
61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIVPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIVPCISQKP 98

RESULT 8

US-09-728-466-1
; Sequence 1, Application US/09728466
; Patent No. 6641994
; GENERAL INFORMATION:

APPLICANT: Fisher, Christopher
APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/728,466
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sv1v1agi
US-09-728-466-1

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60; 3; Indels 0; Gaps 0;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMULDQPEPTTDLVYXXQANDSSEDEIDGPAQAEPDRAHNYIVTFCK 60
Db 1 MHGDPPTLHEYMULDQPEPTTDLVYXXQANDSSEDEIDGPAQAEPDRAHNYIVTFCK 60
61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIVPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIVPCISQKP 98

RESULT 9

US-09-824-017-4
; Sequence 4, Application US/09824017
; Patent No. 6649167
; GENERAL INFORMATION:

APPLICANT: BURGER, Alexander
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,017
FILING DATE: 03-Apr-2001
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-824-017-4

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60; 3; Indels 0; Gaps 0;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDSIDGPAGAEPRRAHYNIVTFCK 60
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DB 1 MHGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDSIDGPAGAEPRRAHYNIVTFCK 60

QY 61 CDSTLRFCVOSTHYDRTLEDLMGTIGIYXPCISQKP 98
|||||
DB 61 CDSTLRFCVOSTHYDRTLEDLMGTIGIYXPCISQKP 98

RESULT 10
US-09-637-746-3
Sequence 3, Application US/09637746
Patent No. 6727079
GENERAL INFORMATION:
APPLICANT: Thorngelsson, Snorri S.
APPLICANT: Moltach, Joseph T.
APPLICANT: Zhang, Minghuang
TITLE OF INVENTION: CDNA ENCODING A GENE BOG (BST OVER-EXPRESSED GENE) AND ITS PROTEIN
TITLE OF INVENTION: PRODUCT
FILE REFERENCE: 11613.29USW1
CURRENT APPLICATION NUMBER: US/09/637,746
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: PCT/US99/04142
PRIOR FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: US 60/079,567
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/075,922
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 98
TYPE: PRT
ORGANISM: Human papillomavirus
US-09-637-746-3

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60; 3; Indels 0; Gaps 0;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDSIDGPAGAEPRRAHYNIVTFCK 60
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DB 1 MHGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDSIDGPAGAEPRRAHYNIVTFCK 60

QY 61 CDSTLRFCVOSTHYDRTLEDLMGTIGIYXPCISQKP 98
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DB 61 CDSTLRFCVOSTHYDRTLEDLMGTIGIYXPCISQKP 98

RESULT 11
US-09-501-097A-7
Sequence 7, Application US/09501097A
Patent No. 6734173
GENERAL INFORMATION:
APPLICANT: Tzyy-Chou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
CURRENT APPLICATION NUMBER: US/09/501,097A
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7

LENGTH: 98
TYPE: PRT
ORGANISM: human papillomavirus
US-09-501-097A-7

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60; 3; Indels 0; Gaps 0;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDSIDGPAGAEPRRAHYNIVTFCK 60
|||||
DB 1 MHGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDSIDGPAGAEPRRAHYNIVTFCK 60

QY 61 CDSTLRFCVOSTHYDRTLEDLMGTIGIYXPCISQKP 98
|||||
DB 61 CDSTLRFCVOSTHYDRTLEDLMGTIGIYXPCISQKP 98

RESULT 12
US-09-980-523A-12
Sequence 12, Application US/09980523A
Patent No. 6783763
GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WO1 NO. INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: FR 99/07012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 98
TYPE: PRT
ORGANISM: Human Papillomavirus
US-09-980-523A-12

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60; 3; Indels 0; Gaps 0;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDSIDGPAGAEPRRAHYNIVTFCK 60
|||||
DB 1 MHGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDSIDGPAGAEPRRAHYNIVTFCK 60

QY 61 CDSTLRFCVOSTHYDRTLEDLMGTIGIYXPCISQKP 98
|||||
DB 61 CDSTLRFCVOSTHYDRTLEDLMGTIGIYXPCISQKP 98

RESULT 13
US-09-613-303-12
Sequence 12, Application US/09613303
Patent No. 6495347
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08

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; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-12
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Query Match          99.0%; Score 512; DB 2; Length 121;
Best Local Similarity 96.9%; Pred. No. 1.1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 MHGDTPLHEYMLDLPETTTDLYXXQLNDSSEDEIDGPAQAEPDRAHNYITVFCK 60
    |||||||
Db 24 MHGDTPLHEYMLDLPETTTDLYCYEQLNDSSEDEIDGPAQAEPDRAHNYITVFCK 83
    |||||||
Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVXPICQKP 98
    |||||||
Db 84 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICQKP 121
    |||||||
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```
RESULT 14
US-10-267-311-12
; Sequence 12, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-12
```

```
Query Match          99.0%; Score 512; DB 2; Length 121;
Best Local Similarity 96.9%; Pred. No. 1.1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
Qy 1 MHGDTPLHEYMLDLPETTTDLYXXQLNDSSEDEIDGPAQAEPDRAHNYITVFCK 60
    |||||||
Db 24 MHGDTPLHEYMLDLPETTTDLYCYEQLNDSSEDEIDGPAQAEPDRAHNYITVFCK 83
    |||||||
Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVXPICQKP 98
    |||||||
Db 84 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICQKP 121
    |||||||
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RESULT 15
US-09-613-303-35
; Sequence 35, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
```

```
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-35
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```
Query Match          99.0%; Score 512; DB 2; Length 198;
Best Local Similarity 96.9%; Pred. No. 2.1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 MHGDTPLHEYMLDLPETTTDLYXXQLNDSSEDEIDGPAQAEPDRAHNYITVFCK 60
    |||||||
Db 101 MHGDTPLHEYMLDLPETTTDLYCYEQLNDSSEDEIDGPAQAEPDRAHNYITVFCK 160
    |||||||
Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVXPICQKP 98
    |||||||
Db 161 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICQKP 198
    |||||||
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```
RESULT 16
US-10-267-311-35
; Sequence 35, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-35
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```
Query Match          99.0%; Score 512; DB 2; Length 198;
Best Local Similarity 96.9%; Pred. No. 2.1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
Qy 1 MHGDTPLHEYMLDLPETTTDLYXXQLNDSSEDEIDGPAQAEPDRAHNYITVFCK 60
    |||||||
Db 101 MHGDTPLHEYMLDLPETTTDLYCYEQLNDSSEDEIDGPAQAEPDRAHNYITVFCK 160
    |||||||
Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVXPICQKP 98
    |||||||
Db 161 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICQKP 198
    |||||||
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```
RESULT 17
US-09-485-885-1
; Sequence 1, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cadezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
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Query Match	99.0%	Score 512;	DB 2;	Length 220;
Best Local Similarity	96.9%	Pred. No. 2.4e-59;		
Matches 95;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

Dy 1 MHGDTPTLHEYMLDLPETTDLYXXYYQINDSEEBEDIDGPAGQAEPBRAHNYIVTFCKK 60
|||
Db 114 MHGDTPTLHEYMLDLPETTDLYCYEQINDSEEBEEDIDGPAGQAEPBRAHNYIVTFCKK 173

QY	61 CDSTLRACVSTHVDIRITLEDLMGTGLGVXPCISQKP 98
Dd	174 CDSTLRACVSTHVDIRITLEDLMGTGLGVXPCISQKP 211

```

RESULT 18
US-09-485-885-12
; Sequence 12, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernan
; APPLICANT: Gerard, Catherine Marie Ghisla
; APPLICANT: Lombard-Benckelkh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485, 885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0.C
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-12

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Query Match	99.0%	Score 512	DB 2	length 239
Best Local Similarity	96.9%	Pred. No. 2.7e-59		
Matches 95	Conservative	0	Mismatches 3	Indels 0
			Gaps	0

Dy 1 MHGDLPTLHEFMLDLPETTDLYXXHQINDSSSEDEIDGPAGQAEPRRAHNYITVFCCK 60

Db 133 MHGDLPTLHEFMLDLPETTDLYCYEQINDSSSEDEIDGPAGQAEPRRAHNYITVFCCK 199

Oy 61 CDSTLRFCVSTHVDIRITLEDLNGTLGVXPCISQKP 98
| | | | | | | | | | | | | | | | | | | | |
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Db 193 CDSTLRFCVSTHVDIRITLEDLNGTLGVXPCISQKP 230

RESULT 19
US-08-459-818-20
; Sequence 20, Application US/08459818

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Query Match	99.0%	Score 512	DB 1	Length 253
Best Local Similarity	96.9%	Pred. No. 2.9e-59		
Matches 95	Conservative 0	Mismatches 3	Indels 0	Gaps 0

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Qy      1 MHGDTPTLHEYMDLQPETTDLXXHXQLNDSSSEEBEIDGAGQAEBDRAHNIIVTFCK 60
        |||||
Db      156 MHGDTPTLHEYMDLQPETTDLXCYQLNDSSSEEBEIDGAGQAEBDRAHNIIVTFCK 215

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Qy 61 CDSTRLCVGSTHVDIRLTEDLMGTGLGVPCISQKP 98
 |||||
Db 216 CDSTRLCVGSTHVDIRLTEDLMGTGLGVPCISQKP 253
 |||||

RESULT 20
US-08-889-666-20
Sequence 20, Application US/08889666
Patent No. 588579
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Dame, Ntin K.
APPLICANT: Brady, William
APPLICANT: Kienert, Peter A.
TITLE OF INVENTION: CTL4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,666
FILING DATE: 08-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-889-666-20

Query Match 99.0%; Score 512; DB 1; Length 253;
Best Local Similarity 96.9%; Pred. No. 2.9e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEHYMLDQPEPTTDLXXYXQLNDSSEDEIDGPAGQAEPPRAHNYIVTFCK 60
Db 156 MHGDPPTLHEHYMLDQPEPTTDLXXYXQLNDSSEDEIDGPAGQAEPPRAHNYIVTFCK 215
Qy 61 CDSTRLCVQSTHVDIRLTEDLMLGTLGIYXPCSQKP 98
Db 216 CDSTRLCVQSTHVDIRLTEDLMLGTLGIYXPCSQKP 253

RESULT 21
US-08-465-078-20
Sequence 20, Application US/08465078
Patent No. 5885796
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Dame, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kienner, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,078
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-078-20

Query Match 99.0%; Score 512; DB 1; Length 253;
Best Local Similarity 96.9%; Pred. No. 2.9e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEHYMLDQPEPTTDLXXYXQLNDSSEDEIDGPAGQAEPPRAHNYIVTFCK 60
Db 156 MHGDPPTLHEHYMLDQPEPTTDLXXYXQLNDSSEDEIDGPAGQAEPPRAHNYIVTFCK 215
Qy 61 CDSTRLCVQSTHVDIRLTEDLMLGTLGIYXPCSQKP 98
Db 216 CDSTRLCVQSTHVDIRLTEDLMLGTLGIYXPCSQKP 253

RESULT 22
US-08-725-776-20
Sequence 20, Application US/08725776
Patent No. 5968510
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Dame, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kienner, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

;; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
;; FILE REFERENCE: 17227/130
;; CURRENT APPLICATION NUMBER: US/08/860,165A
;; CURRENT FILING DATE: 1997-09-22
;; EARLIER APPLICATION NUMBER: PCT/AU95/00868
;; EARLIER FILING DATE: 1995-12-20
;; EARLIER APPLICATION NUMBER: AU PNO157
;; EARLIER FILING DATE: 1994-12-20
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 10
;; LENGTH: 266
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 99.0%; Score 512; DB 2; Length 266;
Best Local Similarity 96.9%; Pred. No. 3.2e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPEETDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 60
Db 161 MHGDTPLHEYMDLQPEETDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 220
Qy 61 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCSQKP 98
Db 221 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCSQKP 258

RESULT 26
US-09-359-382-10
;; Sequence 10, Application US/09359382
;; Patent No. 6306397
;; GENERAL INFORMATION:
;; APPLICANT: EDWARDS, Scitling John
;; APPLICANT: COX, John Cooper
;; APPLICANT: WEBB, Elizabeth Ann
;; APPLICANT: PRATER, Ian
;; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
;; FILE REFERENCE: 017227/0148
;; CURRENT APPLICATION NUMBER: US/09/359,382
;; CURRENT FILING DATE: 1999-07-23
;; EARLIER APPLICATION NUMBER: US 08/860,165
;; EARLIER FILING DATE: 1997-09-22
;; EARLIER APPLICATION NUMBER: PCT/AU95/00868
;; EARLIER FILING DATE: 1995-12-20
;; EARLIER APPLICATION NUMBER: AU PNO157/94
;; EARLIER FILING DATE: 1994-12-20
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 10
;; LENGTH: 266
;; TYPE: PRT
;; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 99.0%; Score 512; DB 2; Length 266;
Best Local Similarity 96.9%; Pred. No. 3.2e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MHGDTPLHEYMDLQPEETDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 60
Db 161 MHGDTPLHEYMDLQPEETDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 220
Qy 61 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCSQKP 98
Db 221 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCSQKP 258

RESULT 27
US-09-367-309A-1

;; Sequence 1, Application US/09367309A
;; Patent No. 6428807
;; GENERAL INFORMATION:
;; APPLICANT: MACFARLAN, RODERICK I.
;; APPLICANT: MALLIKOS, JIM
;; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
;; FILE REFERENCE: 017227/0149
;; CURRENT APPLICATION NUMBER: US/09/367,309A
;; CURRENT FILING DATE: 1999-08-11
;; PRIOR APPLICATION NUMBER: PCT/AU98/00080
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: AU PO 5178
;; PRIOR FILING DATE: 1997-02-19
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 266
;; TYPE: PRT
;; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 99.0%; Score 512; DB 2; Length 266;
Best Local Similarity 96.9%; Pred. No. 3.2e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPEETDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 60
Db 161 MHGDTPLHEYMDLQPEETDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 220
Qy 61 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCSQKP 98
Db 221 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCSQKP 258

RESULT 28
US-09-501-097A-25
;; Sequence 25, Application US/09501097A
;; Patent No. 6734173
;; GENERAL INFORMATION:
;; APPLICANT: Tzyy-Chiou Wu
;; APPLICANT: Chien-Fu Hung
;; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
;; FILE REFERENCE: 2240-169349
;; CURRENT APPLICATION NUMBER: US/09/501,097A
;; CURRENT FILING DATE: 2000-02-09
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 25
;; LENGTH: 287
;; TYPE: PRT
;; ORGANISM: Human papillomavirus/Mouse
US-09-501-097A-25

Query Match 99.0%; Score 512; DB 2; Length 287;
Best Local Similarity 96.9%; Pred. No. 3.5e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MHGDTPLHEYMDLQPEETDLYXXQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 60
Db 190 MHGDTPLHEYMDLQPEETDLYCYEQLNDSSEDEIDGPAGAEPRRAHYNIVTFCK 249
Qy 61 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCSQKP 98
Db 250 CDSTLRICVOSTHVDIRLTEDLMGTIGIYXPCSQKP 287

RESULT 29
US-09-613-303-33
;; Sequence 33, Application US/09613303
;; Patent No. 6495347
;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Marvin
;; APPLICANT: Chu, N. Randall

APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 295
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-09-613-303-33

Query Match 99.0%; Score 512; DB 2; Length 295;
Best Local Similarity 96.9%; Pred. No. 3,6e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMLDLPETTDLYXXQLNDSSEEDSIDGPAGAEPRAHYNIIVTFCK 60
DB 198 MHGDTPLHRYMLDLPETTDLYCYEQLNDSSEEDSIDGPAGAEPRAHYNIIVTFCK 257
QY 61 CDSTLRFCVOSTHVDIRTLBEDLMGTIGIVPCISQKP 98
DB 258 CDSTLRFCVOSTHVDIRTLBEDLMGTIGIVPCISQKP 295

RESULT 30
US-10-267-311-33
Sequence 33, Application US/10267311
Patent No. 6657055
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 295
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-267-311-33

Query Match 99.0%; Score 512; DB 2; Length 295;
Best Local Similarity 96.9%; Pred. No. 3,6e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMLDLPETTDLYXXQLNDSSEEDSIDGPAGAEPRAHYNIIVTFCK 60
DB 198 MHGDTPLHRYMLDLPETTDLYCYEQLNDSSEEDSIDGPAGAEPRAHYNIIVTFCK 257
QY 61 CDSTLRFCVOSTHVDIRTLBEDLMGTIGIVPCISQKP 98
DB 258 CDSTLRFCVOSTHVDIRTLBEDLMGTIGIVPCISQKP 295

RESULT 31
US-09-613-303-25
Sequence 25, Application US/09613303
Patent No. 6495347

GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 324
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-09-613-303-25

Query Match 99.0%; Score 512; DB 2; Length 324;
Best Local Similarity 96.9%; Pred. No. 4,1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMLDLPETTDLYXXQLNDSSEEDSIDGPAGAEPRAHYNIIVTFCK 60
DB 227 MHGDTPLHRYMLDLPETTDLYCYEQLNDSSEEDSIDGPAGAEPRAHYNIIVTFCK 286
QY 61 CDSTLRFCVOSTHVDIRTLBEDLMGTIGIVPCISQKP 98
DB 287 CDSTLRFCVOSTHVDIRTLBEDLMGTIGIVPCISQKP 324

RESULT 32
US-10-267-311-25
Sequence 25, Application US/10267311
Patent No. 6657055
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 324
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-267-311-25

Query Match 99.0%; Score 512; DB 2; Length 324;
Best Local Similarity 96.9%; Pred. No. 4,1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMLDLPETTDLYXXQLNDSSEEDSIDGPAGAEPRAHYNIIVTFCK 60
DB 227 MHGDTPLHRYMLDLPETTDLYCYEQLNDSSEEDSIDGPAGAEPRAHYNIIVTFCK 286
QY 61 CDSTLRFCVOSTHVDIRTLBEDLMGTIGIVPCISQKP 98
DB 287 CDSTLRFCVOSTHVDIRTLBEDLMGTIGIVPCISQKP 324

RESULT 33

```
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485, 885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9711953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match          99.0%; Score 512; DB 2; Length 371;
Best Local Similarity 96.9%; Pred. No. 5e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPLHEYMLDLPETTDLYXXYXOLNDSSEEDIDGPAGAEPRAHYNIIVTFCK 60
DB 265 MHGDPPLHEYMLDLPETTDLYCYEQUNDSEEDIDGPAGAEPRAHYNIIVTFCK 324

QY 61 CDSTLRFCVOSTHVDIRTLBDMGLTGIYVPCISQRP 98
DB 325 CDSTLRFCVOSTHVDIRTLBDMGLTGIYVPCISQRP 362

RESULT 34
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485, 885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9711953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match          99.0%; Score 512; DB 2; Length 390;
Best Local Similarity 96.9%; Pred. No. 5.4e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

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DB 344 CDSTLRFCVOSTHVDIRTLBDMGLTGIYVPCISQRP 381

RESULT 35
US-09-613-303-19
; Sequence 19, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-19

Query Match          99.0%; Score 512; DB 2; Length 493;
Best Local Similarity 96.9%; Pred. No. 7.4e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPLHEYMLDLPETTDLYXXYXOLNDSSEEDIDGPAGAEPRAHYNIIVTFCK 60
DB 396 MHGDPPLHEYMLDLPETTDLYCYEQUNDSEEDIDGPAGAEPRAHYNIIVTFCK 455

QY 61 CDSTLRFCVOSTHVDIRTLBDMGLTGIYVPCISQRP 98
DB 456 CDSTLRFCVOSTHVDIRTLBDMGLTGIYVPCISQRP 493

RESULT 36
US-10-267-311-19
; Sequence 19, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-19

Query Match          99.0%; Score 512; DB 2; Length 493;
Best Local Similarity 96.9%; Pred. No. 7.4e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPLHEYMLDLPETTDLYXXYXOLNDSSEEDIDGPAGAEPRAHYNIIVTFCK 60
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Db 396 MHGDTPLHEMYMDLQPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 455
Qy 61 CDSTLRFCVOSTHVDIRTLLEDLMGTGIVXPCISQKP 98
Db 456 CDSTLRFCVOSTHVDIRTLLEDLMGTGIVCPCISQKP 493

RESULT 37
US-09-613-303-17
; Sequence 17, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-17

Query Match 99.0%; Score 512; DB 2; Length 639;
Best Local Similarity 96.9%; Pred. No. 1,1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMDLQPETTDLYXXQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 542 MHGDTPLHEMYMDLQPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 601
Qy 61 CDSTLRFCVOSTHVDIRTLLEDLMGTGIVXPCISQKP 98
Db 602 CDSTLRFCVOSTHVDIRTLLEDLMGTGIVCPCISQKP 639

RESULT 38
US-10-267-311-17
; Sequence 17, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-17

Query Match 99.0%; Score 512; DB 2; Length 639;
Best Local Similarity 96.9%; Pred. No. 1,1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEMYMDLQPETTDLYXXQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 542 MHGDTPLHEMYMDLQPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 601
Qy 61 CDSTLRFCVOSTHVDIRTLLEDLMGTGIVXPCISQKP 98
Db 602 CDSTLRFCVOSTHVDIRTLLEDLMGTGIVCPCISQKP 639

RESULT 39
US-09-613-303-51
; Sequence 51, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-51

Query Match 99.0%; Score 512; DB 2; Length 641;
Best Local Similarity 96.9%; Pred. No. 1,1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEMYMDLQPETTDLYXXQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 544 MHGDTPLHEMYMDLQPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 603
Qy 61 CDSTLRFCVOSTHVDIRTLLEDLMGTGIVXPCISQKP 98
Db 604 CDSTLRFCVOSTHVDIRTLLEDLMGTGIVCPCISQKP 641

RESULT 40
US-10-267-311-51
; Sequence 51, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-51
```

```
Query Match          99.0%; Score 512; DB 2; Length 641;
Best Local Similarity 96.9%; Pred. No. 1.1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPTTDLXXYXQNDSSSEDEIDGPAGQAEPRAHYNIYTFCK 60
Db 544 MHGDTPLHEYMDLQPTTDLXXYXQNDSSSEDEIDGPAGQAEPRAHYNIYTFCK 603

Qy 61 CDSTRLCVOSTHYDITLEDLIMGTIGIYXPCSQKP 98
Db 604 CDSTRLCVOSTHYDITLEDLIMGTIGIYXPCSQKP 641

RESULT 41
US-09-613-303-53
; Sequence 53, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; US-09-613-303-53

Query Match          99.0%; Score 512; DB 2; Length 647;
Best Local Similarity 96.9%; Pred. No. 1.1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPTTDLXXYXQNDSSSEDEIDGPAGQAEPRAHYNIYTFCK 60
Db 550 MHGDTPLHEYMDLQPTTDLXXYXQNDSSSEDEIDGPAGQAEPRAHYNIYTFCK 609

Qy 61 CDSTRLCVOSTHYDITLEDLIMGTIGIYXPCSQKP 98
Db 610 CDSTRLCVOSTHYDITLEDLIMGTIGIYXPCSQKP 647

RESULT 42
US-10-267-311-53
; Sequence 53, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: fusion sequence
US-10-267-311-53

Query Match          99.0%; Score 512; DB 2; Length 647;
Best Local Similarity 96.9%; Pred. No. 1.1e-58;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPTTDLXXYXQNDSSSEDEIDGPAGQAEPRAHYNIYTFCK 60
Db 550 MHGDTPLHEYMDLQPTTDLXXYXQNDSSSEDEIDGPAGQAEPRAHYNIYTFCK 609

Qy 61 CDSTRLCVOSTHYDITLEDLIMGTIGIYXPCSQKP 98
Db 610 CDSTRLCVOSTHYDITLEDLIMGTIGIYXPCSQKP 647

RESULT 43
US-09-566-420-19
; Sequence 19, Application US/09566420
; Patent No. 6500641
; GENERAL INFORMATION:
; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
; FILE REFERENCE: TBA
; CURRENT APPLICATION NUMBER: US/09/566,420
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,752
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
; US-09-566-420-19

Query Match          98.1%; Score 507; DB 2; Length 98;
Best Local Similarity 95.9%; Pred. No. 3.7e-59;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPTTDLXXYXQNDSSSEDEIDGPAGQAEPRAHYNIYTFCK 60
Db 1 MHGDTPLHEYMDLQPTTDLXXYXQNDSSSEDEIDGPAGQAEPRAHYNIYTFCK 60

Qy 61 CDSTRLCVOSTHYDITLEDLIMGTIGIYXPCSQKP 98
Db 61 CDSTRLCVOSTHYDITLEDLIMGTIGIYXPCSQKP 98

RESULT 44
US-10-201-764-19
; Sequence 19, Application US/10201764
; Patent No. 6716623
; GENERAL INFORMATION:
; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
; FILE REFERENCE: TBA
; CURRENT APPLICATION NUMBER: US/10/201,764
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/566,420
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,752
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 98
```

```
; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
US-10-201-764-19

Query Match
Best Local Similarity 98.1%; Score 507; DB 2; Length 98;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDIDGPAGAEPPDRAHYNIVTFCK 60
DB 1 MGGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDIDGPAGAEPPDRAHYNIVTFCK 60

QY 61 CDSTLRVCVSTHVDIRTLIEDLMGTLGIYXPCISQKP 98
DB 61 CDSTLRVCVSTHVDIRTLIEDLMGTLGIYXPCISQKP 98

RESULT 45
US-09-613-303-8
; Sequence 8, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-8

Query Match
Best Local Similarity 97.3%; Score 503; DB 2; Length 98;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDIDGPAGAEPPDRAHYNIVTFCK 60
DB 1 MGGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDIDGPAGAEPPDRAHYNIVTFCK 60

QY 61 CDSTLRVCVSTHVDIRTLIEDLMGTLGIYXPCISQKP 98
DB 61 CDSTLRVCVSTHVDIRTLIEDLMGTLGIYXPCISQKP 98

RESULT 46
US-10-267-311-8
; Sequence 8, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
```

```
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-8

Query Match
Best Local Similarity 97.3%; Score 503; DB 2; Length 98;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDIDGPAGAEPPDRAHYNIVTFCK 60
DB 1 MGGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDIDGPAGAEPPDRAHYNIVTFCK 60

QY 61 CDSTLRVCVSTHVDIRTLIEDLMGTLGIYXPCISQKP 98
DB 61 CDSTLRVCVSTHVDIRTLIEDLMGTLGIYXPCISQKP 98

RESULT 47
US-09-613-303-29
; Sequence 29, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-29

Query Match
Best Local Similarity 97.3%; Score 503; DB 2; Length 648;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGGDTPLHEHYMDLQPEETDLYXXQLNDSSEEDIDGPAGAEPPDRAHYNIVTFCK 60
DB 1 MGGDTPLHEHYMDLQPEETDLYCYEQLNDSSEEDIDGPAGAEPPDRAHYNIVTFCK 60

QY 61 CDSTLRVCVSTHVDIRTLIEDLMGTLGIYXPCISQKP 98
DB 61 CDSTLRVCVSTHVDIRTLIEDLMGTLGIYXPCISQKP 98

RESULT 48
US-10-267-311-29
; Sequence 29, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
```

```
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-29
```

```
Query Match          97.3%; Score 503; DB 2; Length 648;
Best Local Similarity 95.9%; Pred. No. 1.7e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 MHGDTPLHEHYMLDLOPETTDLYXXYXOLNDSSEBEDIIDGPAQAEPDRAHYNIVTFCK 60
    |||||||
DB 1 MDGDTPLHEHYMLDLOPETTDLYCYEQNLNDSSEBEDIIDGPAQAEPDRAHYNIVTFCK 60
```

```
QY 61 CDSTLRFCVOSTHVDIRTLBEDLGMGTIGIYXPCISQKP 98
    |||||||
DB 61 CDSTLRFCVOSTHVDIRTLBEDLGMGTIGIYXPCISQKP 98
```

```
RESULT 49
US-09-613-303-41
; Sequence 41, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-41
```

```
Query Match          97.3%; Score 503; DB 2; Length 711;
Best Local Similarity 95.9%; Pred. No. 1.9e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 MHGDTPLHEHYMLDLOPETTDLYXXYXOLNDSSEBEDIIDGPAQAEPDRAHYNIVTFCK 60
    |||||||
DB 1 MDGDTPLHEHYMLDLOPETTDLYCYEQNLNDSSEBEDIIDGPAQAEPDRAHYNIVTFCK 60
```

```
QY 61 CDSTLRFCVOSTHVDIRTLBEDLGMGTIGIYXPCISQKP 98
    |||||||
DB 61 CDSTLRFCVOSTHVDIRTLBEDLGMGTIGIYXPCISQKP 98
```

```
RESULT 50
US-10-267-311-41
; Sequence 41, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
```

```
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-41
```

```
Query Match          97.3%; Score 503; DB 2; Length 711;
Best Local Similarity 95.9%; Pred. No. 1.9e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 MHGDTPLHEHYMLDLOPETTDLYXXYXOLNDSSEBEDIIDGPAQAEPDRAHYNIVTFCK 60
    |||||||
DB 1 MDGDTPLHEHYMLDLOPETTDLYCYEQNLNDSSEBEDIIDGPAQAEPDRAHYNIVTFCK 60
```

```
QY 61 CDSTLRFCVOSTHVDIRTLBEDLGMGTIGIYXPCISQKP 98
    |||||||
DB 61 CDSTLRFCVOSTHVDIRTLBEDLGMGTIGIYXPCISQKP 98
```

```
RESULT 51
US-09-613-303-45
; Sequence 45, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-45
```

```
Query Match          97.3%; Score 503; DB 2; Length 724;
Best Local Similarity 95.9%; Pred. No. 1.9e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 MHGDTPLHEHYMLDLOPETTDLYXXYXOLNDSSEBEDIIDGPAQAEPDRAHYNIVTFCK 60
    |||||||
DB 1 MDGDTPLHEHYMLDLOPETTDLYCYEQNLNDSSEBEDIIDGPAQAEPDRAHYNIVTFCK 60
```

```
QY 61 CDSTLRFCVOSTHVDIRTLBEDLGMGTIGIYXPCISQKP 98
    |||||||
DB 61 CDSTLRFCVOSTHVDIRTLBEDLGMGTIGIYXPCISQKP 98
```

```
RESULT 52
US-10-267-311-45
; Sequence 45, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
```

;; CURRENT APPLICATION NUMBER: US/10/267,311
;; CURRENT FILING DATE: 2002-10-09
;; PRIOR APPLICATION NUMBER: US/09/613,303
;; PRIOR FILING DATE: 2000-07-10
;; PRIOR APPLICATION NUMBER: US 60/143,757
;; PRIOR FILING DATE: 1999-07-08
;; NUMBER OF SEQ ID NOS: 55
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 45
;; LENGTH: 724
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: fusion sequence
US-10-267-311-45

Query Match 97.3%; Score 503; DB 2; Length 724;
Best Local Similarity 95.9%; Pred. No. 1,9e-57;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPEETDLYXXYQLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEHYMDLQPEETDLYXXYQLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
Qy 61 CDSTLRICVQSTHVDIRLTEDLMGTIGIYXPCISQK 98
Db 61 CDSTLRICVQSTHVDIRLTEDLMGTIGIYXPCISQK 98

RESULT 53
US-09-501-097A-22

;; Sequence 22, Application US/09501097A
;; Patent No. 6734173
;; GENERAL INFORMATION:
;; APPLICANT: Tzyy-Chou Wu
;; APPLICANT: Chien-Fu Hung
;; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
;; FILE REFERENCE: 2240-169349
;; CURRENT APPLICATION NUMBER: US/09/501,097A
;; CURRENT FILING DATE: 2000-02-09
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 22
;; LENGTH: 420
;; TYPE: PRT
;; ORGANISM: Mouse/Pseudomonas
US-09-501-097A-22

Query Match 96.7%; Score 500; DB 2; Length 420;
Best Local Similarity 96.9%; Pred. No. 2,3e-57;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPEETDLYXXYQLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
Db 317 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSEDEIDGPAGAEPPRAHYNIVTFCK 376
Qy 61 CDSTLRICVQSTHVDIRLTEDLMGTIGIYXPCISQ 96
Db 377 CDSTLRICVQSTHVDIRLTEDLMGTIGIYXPCISQ 412

RESULT 54
US-09-501-097A-20

;; Sequence 20, Application US/09501097A
;; Patent No. 6734173
;; GENERAL INFORMATION:
;; APPLICANT: Tzyy-Chou Wu
;; APPLICANT: Chien-Fu Hung
;; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
;; FILE REFERENCE: 2240-169349
;; CURRENT APPLICATION NUMBER: US/09/501,097A
;; CURRENT FILING DATE: 2000-02-09
;; NUMBER OF SEQ ID NOS: 25

;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 20
;; LENGTH: 723
;; TYPE: PRT
;; ORGANISM: human papillomavirus/mycobacterium tuberculosis
US-09-501-097A-20

Query Match 96.7%; Score 500; DB 2; Length 723;
Best Local Similarity 96.9%; Pred. No. 4,8e-57;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPEETDLYXXYQLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
Qy 61 CDSTLRICVQSTHVDIRLTEDLMGTIGIYXPCISQ 96
Db 61 CDSTLRICVQSTHVDIRLTEDLMGTIGIYXPCISQ 96

RESULT 55
US-09-462-993-2

;; Sequence 2, Application US/09462993
;; Patent No. 6884786
;; GENERAL INFORMATION:
;; APPLICANT: KIENY, Marie-Paule
;; APPLICANT: BALLOUL, Jean-Marc
;; APPLICANT: BIZOUARNE, Nadine
;; TITLE OF INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNOGENIC
;; TITLE OF INVENTION: POLYPEPTIDE WITH MODIFIED CELL LOCATION
;; FILE REFERENCE: 01753-122
;; CURRENT APPLICATION NUMBER: US/09/462,993
;; CURRENT FILING DATE: 2000-04-17
;; PRIOR APPLICATION NUMBER: PCT/FR98/01576
;; PRIOR FILING DATE: 1998-07-17
;; PRIOR APPLICATION NUMBER: FR 97/09152
;; PRIOR FILING DATE: 1997-07-18
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: Patencin Ver. 2.2
;; SEQ ID NO 2
;; LENGTH: 185
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Derived from human papillomavirus, strain
;; OTHER INFORMATION: HPV-16, E7 fusion signals of the rabies
;; OTHER INFORMATION: glycoprotein, clone E7*TMR.
US-09-462-993-2

Query Match 92.5%; Score 478; DB 2; Length 185;
Best Local Similarity 92.9%; Pred. No. 6e-55;
Matches 91; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

Qy 1 MHGDTPLHEHYMDLQPEETDLYXXYQLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
Db 26 MHGDTPLHEHYMDLQPEETDLYCYEQNDSSEDEIDGPAGAEPPRAHYNIVTFCK 79
Qy 61 CDSTLRICVQSTHVDIRLTEDLMGTIGIYXPCISQK 98
Db 80 CDSTLRICVQSTHVDIRLTEDLMGTIGIYXPCISQK 117

RESULT 56
US-08-860-165-12

;; Sequence 12, Application US/08860165A
;; Patent No. 6004557
;; GENERAL INFORMATION:
;; APPLICANT: EDWARDS, Stirling John
;; APPLICANT: COX, John Cooper
;; APPLICANT: WEBB, Elizabeth Ann
;; APPLICANT: FRAZER, Ian
;; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
;; FILE REFERENCE: 17227/130

```
; CURRENT APPLICATION NUMBER: US/08/860.165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match          68.3%; Score 353; DB 2; Length 172;
Best Local Similarity 97.0%; Pred. No. 1.8e-38;
Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDLPQETTDLYXXYXOLNDSSEEDSIDGPAGQAEPRRAHYNIVTFCK 60
    |||||
Db 99 MHGDTPLHEYMLDLPQETTDLYCYEQUNDSEEDSIDGPAGQAEPRRAHYNIVTFCK 158

QY 61 CDSTLR 66
    |||||
Db 159 CDSTLR 164

RESULT 57
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359.382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860.165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match          68.3%; Score 353; DB 2; Length 172;
Best Local Similarity 97.0%; Pred. No. 1.8e-38;
Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDLPQETTDLYXXYXOLNDSSEEDSIDGPAGQAEPRRAHYNIVTFCK 60
    |||||
Db 99 MHGDTPLHEYMLDLPQETTDLYCYEQUNDSEEDSIDGPAGQAEPRRAHYNIVTFCK 158

QY 61 CDSTLR 66
    |||||
Db 159 CDSTLR 164

RESULT 58
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
```

```
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860.165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match          66.7%; Score 345; DB 2; Length 172;
Best Local Similarity 98.5%; Pred. No. 2e-37;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 EDEIDGPAGQAEPRRAHYNIVTFCKCDSTLRCLVQSTHVDIRTELDLMTGLGIVXPI 93
    |||||
Db 2 EDEIDGPAGQAEPRRAHYNIVTFCKCDSTLRCLVQSTHVDIRTELDLMTGLGIVCPI 61

QY 94 CSQKP 98
    |||||
Db 62 CSQKP 66

RESULT 59
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359.382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860.165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match          66.7%; Score 345; DB 2; Length 172;
Best Local Similarity 98.5%; Pred. No. 2e-37;
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 EDEIDGPAGQAEPRRAHYNIVTFCKCDSTLRCLVQSTHVDIRTELDLMTGLGIVXPI 93
    |||||
Db 2 EDEIDGPAGQAEPRRAHYNIVTFCKCDSTLRCLVQSTHVDIRTELDLMTGLGIVCPI 61

QY 94 CSQKP 98
    |||||
Db 62 CSQKP 66
```


Db 62 CSQKP 66

RESULT 60
US-08-606-288-7
Sequence 7, Application US/08606288
Patent No. 5955087
GENERAL INFORMATION:
APPLICANT: Whittle, N.R.
APPLICANT: Carmichael, J.P.
APPLICANT: Connor, S.E.
APPLICANT: Thompson, H.S.G.
APPLICANT: Wilson, M.J.
TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic
TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Suite 3400, Four Embarcadero Center
CITY: San Francisco
STATE: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,288
FILING DATE: 23-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9503786.7
FILING DATE: 24-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000034
FILING DATE: 08-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9515478.7
FILING DATE: 28-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Walter H. Dregger
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63284/WHD
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-288-7

Query Match 47.8%; Score 247; DB 1; Length 601;
Best Local Similarity 53.5%; Pred. No. 1e-23;
Matches 53; Conservative 14; Mismatches 28; Indels 4; Gaps 3;

Db 493 MGRHVTLKDIIVDLQPPDVGHLCEQLVDSSEDEVDDGQ--DSQPLKHQIVTCC 550
QY 1 MGGDTPLHEMYMLDQ-PETTDLYXXYQLNDSSEER-DEIDGPAQAEPRAHNYITFC 58
59 CKKDSIRLCVOSTHVDIRTELDLMGTGLGVXPIGSOX 97
551 CGCDSNVRLVVOCTETDIRVQQLLGLTNIIVCPICAPK 589

RESULT 61
US-08-606-288-10
Sequence 10, Application US/08606288
Patent No. 5955087
GENERAL INFORMATION:
APPLICANT: Whittle, N.R.

APPLICANT: Carmichael, J.P.
APPLICANT: Connor, S.E.
APPLICANT: Thompson, H.S.G.
APPLICANT: Wilson, M.J.
TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic
TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Suite 3400, Four Embarcadero Center
CITY: San Francisco
STATE: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,288
FILING DATE: 23-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9503786.7
FILING DATE: 24-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000034
FILING DATE: 08-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9515478.7
FILING DATE: 28-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Walter H. Dregger
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63284/WHD
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-606-288-10

Query Match 47.8%; Score 247; DB 1; Length 601;
Best Local Similarity 53.5%; Pred. No. 1e-23;
Matches 53; Conservative 14; Mismatches 28; Indels 4; Gaps 3;

Db 493 MGRHVTLKDIIVDLQPPDVGHLCEQLVDSSEDEVDDGQ--DSQPLKHQIVTCC 550
QY 1 MGGDTPLHEMYMLDQ-PETTDLYXXYQLNDSSEER-DEIDGPAQAEPRAHNYITFC 58
59 CKKDSIRLCVOSTHVDIRTELDLMGTGLGVXPIGSOX 97
551 CGCDSNVRLVVOCTETDIRVQQLLGLTNIIVCPICAPK 589

RESULT 62
US-09-347-483-7
Sequence 7, Application US/09347483
Patent No. 6123948
GENERAL INFORMATION:
APPLICANT: Whittle, N.R.
APPLICANT: Carmichael, J.P.
APPLICANT: Connor, S.E.
APPLICANT: Thompson, H.S.G.
APPLICANT: Wilson, M.J.
TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic
TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation
NUMBER OF SEQUENCES: 10

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Teet, Albritton & Herbert
STREET: Suite 3400, Four Embarcadero Center
CITY: San Francisco
STATE: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/347,483
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/606,288
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000034
FILING DATE: 08-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9515478.7
FILING DATE: 28-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Walter H. Dreger
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63284/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-347-483-7

Query Match 47.8%; Score 247; DB 2; Length 601;
Best Local Similarity 53.5%; Pred. No. 1e-23;
Matches 53; Conservative 14; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGPTPLHEMLDQ-PETTDLYXXKLNDSSEEE-DEINGPACQAPDRRAHYIYFC 58
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 493 MHGHNVTKLDVLDQPPDPVGLHCEGLVDSSEDEVBEVDQG--DSQPLKHQIVITVC 550
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 59 CKCDSTLRLCVOSTHVDIRTEBDLLMGTLGIYXPICSOK 97
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 551 CGCDSNVRLVVQCETETDIRREVQQLLGTLNIVCPICAKK 589
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 63
US-09-347-483-10
Sequence 10, Application US/09347483
Patent No. 6123948
GENERAL INFORMATION:
APPLICANT: Whittle, N.R.
APPLICANT: Carmichael, J.P.
APPLICANT: Connor, S.E.
APPLICANT: Thompson, H.S.G.
APPLICANT: Wilson, M.J.
TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic
TITLE OF INVENTION: Agents, and Methods of Polypeptide Preparation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Teet, Albritton & Herbert
STREET: Suite 3400, Four Embarcadero Center
CITY: San Francisco
STATE: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

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      1  MHGPTPLHEWMLDLO-PETTDLXXYYQANDSSBEE-DEIDGPAQGEPPDRAHYNYVFC 58
      2  47.8%; Score 247, DB 2, Length 601;
      3  Best Local Similarity 53.5%; Pred. No. 1e-23;
      4  Matches 53; Conservative 14; Mismatches 28; Indels 4; Gaps 3
      5
      6  QY 1
      7  493 MHGHVTLTKDVLDPDPVGLHCYEQLVDSSEDEVDVGQ--DSQPLKHQIQTIC 550
      8  59 CKCDSTLRLCVQSTHVDIRLTEDLLMGTLGIVXPICSOX 97
      9  551 CGCDSNVRLVQCETETDIRVQQLLTGTLNIVCPICAPK 589
      10
      11  Db
      12
      13  RESULT 64
      14  US-09-000-094-46
      15  ; Sequence 46, Application US/09000094
      16  ; Patent No. 6365160
      17  ; GENERAL INFORMATION:
      18  APPLICANT: WEBB, Elizabeth Ann
      19  MARGETTS, Mary Brigid
      20  COX, John Cooper
      21  FRAZER, Ian
      22  MCMILLAN, Nigel Alan John
      23  WILLIAMS, Mark Philip
      24  MOLONEY, Margaret Bridget
      25  Holland
      26  EDWARDS, Stirling John
      27  TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
      28  NUMBER OF SEQUENCES: 50
      29  CORRESPONDENCE ADDRESSES:
      30  ADDRESSEE: FOLEY & LARDNER
      31  STREET: 3000 K Street, N.W.
      32  CITY: Washington
      33  STATE: D.C.
      34  COUNTRY: U.S.A.
      35  ZIP: 20007-5109
      36  COMPUTER READABLE FORM:
      37  MEDIUM TYPE: Floppy disk
      38  COMPUTER: IBM PC compatible
      39  OPERATING SYSTEM: PC-DOS/MS-DOS
      40  SOFTWARE: PatentIn Release #1.0, Version #1.30
      41  CURRENT APPLICATION DATA:
      42
      43  OPERATING SYSTEM: PC-DOS/MS-DOS
      44  SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
      45  CURRENT APPLICATION DATA:
      46  APPLICATION NUMBER: US/09/347,483
      47  FILING DATE:
      48  PRIOR APPLICATION DATA:
      49  APPLICATION NUMBER: US 08/606,288
      50  FILING DATE:
      51  PRIOR APPLICATION DATA:
      52  APPLICATION NUMBER: US 60/000034
      53  FILING DATE: 08-JUN-1995
      54  PRIOR APPLICATION DATA:
      55  APPLICATION NUMBER: GB 9515478.7
      56  FILING DATE: 28-JUL-1995
      57  ATTORNEY/AGENT INFORMATION:
      58  NAME: Walter H. Dreger
      59  REGISTRATION NUMBER: 24,190
      60  REFERENCE/DOCKET NUMBER: A-63284/WHD
      61  TELECOMMUNICATION INFORMATION:
      62  TELEPHONE: (415) 781-1989
      63  TELEFAX: (415) 398-3249
      64  INFORMATION FOR SEQ ID NO: 10:
      65  SEQUENCE CHARACTERISTICS:
      66  LENGTH: 601 amino acids
      67  TYPE: amino acid
      68  TOPOLOGY: linear
      69  MOLECULE TYPE: Protein
      70  HYPOTHEITICAL: NO
      71  ANTI-SENSE: NO
      72  US-09-347-483-10

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APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1587 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-000-094-46

Query Match 47.0%; Score 243; DB 2; Length 1587;
Best Local Similarity 52.5%; Pred. No. 1.3e-22;
Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

QY 1 MHGDTPIHEVM-DLQ-PEITDLYXXYQUNDSEEE-DEIDGPAGAEPPRAHNYITFC 58
DB 839 MGRHVTLKIVDLPDPDVGLHCYBQLVDSSEDEVYDQ--DSQPKQHPIVTC 896

QY 59 CKCDSTRLCVQSTHVDIRITDLMLGTLGIYXPCSQK 97
DB 897 CGCDSNRLVQCTETDIRVQQLLGLTINIVCPICAPK 935

RESULT 65
US-10-011-749-46
Sequence 46, Application US/10011749
Patent No. 6726912
GENERAL INFORMATION:
APPLICANT: WEBB, Elizabeth Ann
MARGETS, Mary Brigid
COX, John Cooper
FRAZER, Ian
MCWILLIAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
Holland
EDWARDS, Scirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,749
FILING DATE: 11-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473

FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1587 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-011-749-46

Query Match 47.0%; Score 243; DB 2; Length 1587;
Best Local Similarity 52.5%; Pred. No. 1.3e-22;
Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

QY 1 MHGDTPIHEVM-DLQ-PEITDLYXXYQUNDSEEE-DEIDGPAGAEPPRAHNYITFC 58
DB 839 MGRHVTLKIVDLPDPDVGLHCYBQLVDSSEDEVYDQ--DSQPKQHPIVTC 896

QY 59 CKCDSTRLCVQSTHVDIRITDLMLGTLGIYXPCSQK 97
DB 897 CGCDSNRLVQCTETDIRVQQLLGLTINIVCPICAPK 935

RESULT 66
US-09-000-094-22
Sequence 22, Application US/09000094
Patent No. 6365160
GENERAL INFORMATION:
APPLICANT: WEBB, Elizabeth Ann
MARGETS, Mary Brigid
COX, John Cooper
FRAZER, Ian
MCWILLIAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
Holland
EDWARDS, Scirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137

Query Match 46.4%; Score 240; DB 2; Length 465;
Best Local Similarity 51.5%; Pred. No. 6.1e-23;
Matches 51; Conservative 16; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGDTPLHERYMDLQ-PETTDLYXXYQXNDSSSEER-DEIDGPAGQAPPRAHYNIYVFC 58
152 LHGRHTLKDVIYDLQPPDPVGLHCYEQVLDSSSEDEVDGQ--DSQPLKQHFIYVTC 209

Db 152 LHGRHTLKDVIYDLQPPDPVGLHCYEQVLDSSSEDEVDGQ--DSQPLKQHFIYVTC 209

Qy 59 CKCDSTLRCLCVGQSTHVDIRTEDLMLGTLGIVXPICSQK 97
210 CGCDSNVRLVQCTETREVDREVQQLLGLTINIVCPICAPK 248

Db 210 CGCDSNVRLVQCTETREVDREVQQLLGLTINIVCPICAPK 248

RESULT 69
US-10-011-749-24
; Sequence 24, Application US/10011749
; Patent No. 6726912
; GENERAL INFORMATION:
; APPLICANT: WEBB, Elizabeth Ann
; MARGITTS, Mary Bridgid
; COX, John Cooper
; FRAZER, Ian
; MCWILLIAM, Nigel Alan John
; WILLIAMS, Mark Philip
; MOLONEY, Margaret Bridget
; Holland
; EDWARDS, Scirling John
; TITLE OF INVENTION: PAPILLOMAVIRUS POLYPEPTIDE CONSTRUCTS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011.749
; FILING DATE: 11-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/000.094
; FILING DATE: 21-Apr-1998
; APPLICATION NUMBER: WO PCT/AU96/00473
; FILING DATE: 26-JUL-1996
; APPLICATION NUMBER: AU PN 4439/95
; FILING DATE: 27-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 017227/0137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-011-749-24

Query Match 46.4%; Score 240; DB 2; Length 465;
Best Local Similarity 51.5%; Pred. No. 6.1e-23;
Matches 51; Conservative 16; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGDTPLHERYMDLQ-PETTDLYXXYQXNDSSSEER-DEIDGPAGQAPPRAHYNIYVFC 58

Db 152 LHGRHTLKDVIYDLQPPDPVGLHCYEQVLDSSSEDEVDGQ--DSQPLKQHFIYVTC 209

Qy 59 CKCDSTLRCLCVGQSTHVDIRTEDLMLGTLGIVXPICSQK 97
210 CGCDSNVRLVQCTETREVDREVQQLLGLTINIVCPICAPK 248

Db 210 CGCDSNVRLVQCTETREVDREVQQLLGLTINIVCPICAPK 248

RESULT 70
US-09-501-097A-6
; Sequence 6, Application US/09501097A
; Patent No. 6734173
; GENERAL INFORMATION:
; APPLICANT: Tzyy-Chou Wu
; APPLICANT: Chien-Fu Hung
; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
; FILE REFERENCE: 2240-169349
; CURRENT APPLICATION NUMBER: US/09/501,097A
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 38
; TYPE: PRT
; ORGANISM: human papillomavirus
US-09-501-097A-6

Query Match 40.4%; Score 209; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.4e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 DSSEEDRIDGPAGQAPPRAHYNIYVFCCKCDSTLR 67
1 DSSEEDRIDGPAGQAPPRAHYNIYVFCCKCDSTLR 38

Db 1 DSSEEDRIDGPAGQAPPRAHYNIYVFCCKCDSTLR 38

RESULT 71
US-09-485-885-19
; Sequence 19, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Gislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-19

Query Match 39.0%; Score 201.5; DB 2; Length 227;
Best Local Similarity 39.6%; Pred. No. 2.8e-18;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

Qy 1 MHGDTPLHERYMDLQPET--TDLYXXYQXNDSSSEERIDG-----PAGQAPPRAH 51
114 MHGKATLQDIVVHLEPQNEIPVLLGHQQLSDSEENDEIDGVNHQHPARRAPOR-- 171

Db 114 MHGKATLQDIVVHLEPQNEIPVLLGHQQLSDSEENDEIDGVNHQHPARRAPOR-- 171

Qy 52 YNIYVFCCKCDSTLRCLCVGQSTHVDIRTEDLMLGTLGIVXPICSQK 97
172 HTMLCMCKCKEARIELVYESSADDLRAFQQLFNTLSFVCPWCASQ 217

Db 172 HTMLCMCKCKEARIELVYESSADDLRAFQQLFNTLSFVCPWCASQ 217


```

; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MASON & ASSOCIATES, P. A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-52

Query Match      33.1%; Score 171; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      44 QAEPRAHNYIVTFCCCKDSTLRICVOSTH 73
Db      1 QAEPRAHNYIVTFCCCKDSTLRICVOSTH 30

RESULT 76
US-09-486-394-3
; Sequence 3, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT: Hopfl, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; FILE REFERENCE: 032929-001
; CURRENT APPLICATION NUMBER: US/09/486,394
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
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; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: E7 peptide.
; US-09-486-394-3

Query Match      33.1%; Score 171; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      41 PQAQAEPRAHNYIVTFCCCKDSTLRICVQ 70
Db      1 PQAQAEPRAHNYIVTFCCCKDSTLRICVQ 30

RESULT 77
US-08-934-915-53
; Sequence 53, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MASON & ASSOCIATES, P. A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-53

Query Match      31.3%; Score 162; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      58 CCKCDSTLRICVOSTHYDITLTLDMGTL 87
Db      1 CCKCDSTLRICVOSTHYDITLTLDMGTL 30

RESULT 78
```


COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2291
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-7

Query Match 29.1%; Score 150.5; DB 2; Length 32;
Best Local Similarity 56.6%; Pred. No. 1e-12; 2; Indels 21; Gaps 1;
Matches 30; Conservative 0; Mismatches 2;

QY 10 EYMLDLPETTDLYXXYQLNDSSEEDIDGPAQAPDRAHYIVTFCCKCD 62
Db 1 EYMLD-----GIDGPAQAPDRAHYIVTFCCKCD 32

RESULT 82
US-09-828-645-7
Sequence 7, Application US/09828645
Patent No. 6743593
GENERAL INFORMATION:
APPLICANT: Hu, Yao Xiong
TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
FILE REFERENCE: 146-1-002
CURRENT APPLICATION NUMBER: US/09/828,645
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/194,796
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from the E7 early region of HPV-16
NAME/KEY: misc feature
LOCATION: (19)-(19)
OTHER INFORMATION: Xaa = L-carboxymethylcysteine
US-09-828-645-7

Query Match 28.6%; Score 148; DB 2; Length 30;
Best Local Similarity 96.7%; Pred. No. 2e-12;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTLHEVMDLPETTDLYXXYQLNDSSEEE 35
Db 1 PTLHEVMDLPETTDLYXXYQLNDSSEEE 30

RESULT 83

US-08-363-586-1
Sequence 1, Application US/08363586
Patent No. 5629161
GENERAL INFORMATION:
APPLICANT: Mueller, Martin
APPLICANT: Giesmann, Lutz
TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,586
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/909,296
FILING DATE: 09-JUL-1992
APPLICATION NUMBER: EP 91111720.8
FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02481-1195-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-363-586-1

Query Match 28.4%; Score 147; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 2.7e-12;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PTLHEVMDLPETTDLYXXYQLNDSSEEE 35
Db 1 PTLHEVMDLPETTDLYCYEQLNDSSEEE 30

RESULT 84
US-09-828-645-3
Sequence 3, Application US/09828645
Patent No. 6743593
GENERAL INFORMATION:
APPLICANT: Hu, Yao Xiong
TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
FILE REFERENCE: 146-1-002
CURRENT APPLICATION NUMBER: US/09/828,645
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/194,796
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Derived from the E7 early region of HPV-16
US-09-828-645-3

Query Match 28.4%; Score 147; DB 2; Length 30;
Best Local Similarity 93.3%; Pred. No. 2.7e-12;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PTLHEVMDLPETDLYXXQLNDSSEE 35
Db 1 PTLHEVMDLPETDLYXXQLNDSSEE 30

RESULT 85
US-08-934-915-54
Sequence 54, Application US/08934915
Patent No. 5932412

GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LEVA
APPLICANT: CHENG, HWEI-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MASON & ASSOCIATES, P. A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S. A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Fouch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-54

Query Match 28.2%; Score 146; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 3.7e-12;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 69 VOSTHVDIRTLEDLIMGTGLGVXPCISQXP 98
Db 1 VOSTHVDIRTLEDLIMGTGLGVXPCISQXP 30

RESULT 86
US-09-486-394-2
Sequence 2, Application US/09486394

Patent No. 6478749
GENERAL INFORMATION:
APPLICANT: Hopfl, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 30
TYPE: PRT
ORGANISM: Human papillomavirus type 16
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(30)
OTHER INFORMATION: E7 peptide.
US-09-486-394-2

Query Match 28.0%; Score 145; DB 2; Length 30;
Best Local Similarity 93.3%; Pred. No. 5e-12;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 21 DLYXXQLNDSSEEDIDGPAQAEPRDA 50
Db 1 DLYXXQLNDSSEEDIDGPAQAEPRDA 30

RESULT 87
US-08-075-541D-47
Sequence 47, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PANITCH SCHWARZ JACOBS & NADEL, P. C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-47

Query Match 27.7%; Score 143; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 AHNYIVFCKCKDSTLRLCVQSTHV 74
DB 1 AHNYIVFCKCKDSTLRLCVQSTHV 25

RESULT 88
US-09-486-394-5
Sequence 5, Application US/09486394
Patent No. 6478749
GENERAL INFORMATION:
APPLICANT: Hopfl, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 28
TYPE: PRT
ORGANISM: Human papillomavirus type 16
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(28)
OTHER INFORMATION: E7 peptide.
US-09-486-394-5

Query Match 26.5%; Score 137; DB 2; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.2e-11;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 71 STHYDRTLDLMLGTGLGVXPICSOKP 98
DB 1 STHYDRTLDLMLGTGLGVXPICSOKP 28

RESULT 89
US-08-363-586-2
Sequence 2, Application US/08363586
Patent No. 5629161
GENERAL INFORMATION:
APPLICANT: Mueller, Martin
APPLICANT: Giesmann, Lutz
TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
TITLE OF INVENTION: Peptides for the Diagnostic Purpose
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,586
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/909,296
FILING DATE: 09-JUL-1992
APPLICATION NUMBER: EP 9111720.8
FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02481-1195-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-363-586-2

Query Match 26.3%; Score 136; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 NDSSEEDRIDGPAGAEPPRAHYN 53
DB 1 NDSSEEDRIDGPAGAEPPRAHYN 25

RESULT 90
US-08-075-541D-40
Sequence 40, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZ JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-40

Query Match 24.4%; Score 126; DB 2; Length 26;
Best Local Similarity 96.2%; Pred. No. 1.3e-09;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 THVDIRLTEDLMGTGIVPICGOK 97
Db 1 THVDIRLTEDLMGTGIVPICGOK 26

RESULT 91
US-08-934-915-71
Sequence 71, Application US/08934915

Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-71

Query Match 23.6%; Score 122; DB 1; Length 30;
Best Local Similarity 75.9%; Pred. No. 5.5e-09;
Matches 22; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 58 CCKCDSTLRCLCVOSTHVDIRLTEDLMGT 86

Db 1 CCKCDSTLRCLCVOSTHVDIRLTEDLMGT 29

RESULT 92
US-09-980-523A-14
Sequence 14, Application US/09980523A
Patent No. 6783763
GENERAL INFORMATION:
APPLICANT: CHOIPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCES
APPLICANT: FERRIS, ESTELLE
TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WO/98/01513
CURRENT FILING DATE: 2002-04-29
CURRENT APPLICATION NUMBER: US/09/980,523A
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 23
TYPE: PRT
ORGANISM: Human Papillomavirus
US-09-980-523A-14

Query Match 23.4%; Score 121; DB 2; Length 23;
Best Local Similarity 95.7%; Pred. No. 5.2e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDTPTLHEVMDLQPETTDLYXY 25
Db 1 GDTPTLHEVMDLQPETTDLYCY 23

RESULT 93
US-08-075-541D-10
Sequence 10, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575

```

; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-075-541D-10

Query Match      23.2%; Score 120; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5,8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      43  GQAEPRAHYIVTFCKCD 62
Db      1  GQAEPRAHYIVTFCKCD 20

RESULT 94
US-08-934-915-48
; Sequence 48, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILNER, JOAKIM
; APPLICANT: DILNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNODIAGNOSIS FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946,6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-48

Query Match      22.8%; Score 118; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      47  PDRAHYIVTFCKCDSTLR 66
Db      1  PDRAHYIVTFCKCDSTLR 20

RESULT 95
US-09-980-177A-73
; Sequence 73, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochims, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; US-09-980-177A-73

Query Match      22.8%; Score 118; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      45  AEPDRAHYIVTFCKCDST 64
Db      1  AEPDRAHYIVTFCKCDST 20

RESULT 96
US-09-980-177A-74
; Sequence 74, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochims, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; US-09-980-177A-74

Query Match      22.4%; Score 116; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 56 TFCCKDSTLRCLVQSTHVD 75
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Db 1 TFCCKDSTLRCLVQSTHVD 20

RESULT 97

US-08-075-541D-3
Sequence 3, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075, 541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pcc/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2920
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-3

Query Match 22.1%; Score 114; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 QAEPPRAHYNIVTFCCKD 62
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Db 1 QAEPPRAHYNIVTFCCKD 19

RESULT 98

US-08-934-915-46
Sequence 46, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-46

Query Match 21.9%; Score 113; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGDPTLHEYMLDQPEPTD 21
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Db 1 HGDPTLHEYMLDQPEPTD 20

RESULT 99
US-08-075-541D-43
Sequence 43, Application US/0807541D
Patent No. 6183745

GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075, 541D
FILING DATE: 10-JUN-1993

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-08-075-541D-43

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Query Match          21.7%; Score 112; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 MHGDTPLHEYMLDLQPEPT 20
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Db      1 MHGDTPLHEYMLDLQPEPT 20

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RESULT 100
US-09-980-177A-69
; Sequence 69, Application US/09980177A
; Patent No. 683084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
;
US-09-980-177A-69

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Query Match          21.7%; Score 112; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 MHGDTPLHEYMLDLQPEPT 20
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Db      1 MHGDTPLHEYMLDLQPEPT 20

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Job time : 30.7309 secs

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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:33:17 ; Search time 101.936 Seconds
(without alignments)
445.330 Million cell updates/sec

Title: US-10-530-253-14ED
Perfect score: 517
Sequence: 1 MHGDTPLHEWMLDLPETT.....LEDLMGTGIVPICSQKP 98

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues
Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

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- 2: /EMC_Celextra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celextra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celextra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celextra_SIDS3/prodata/2/pubppaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celextra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	514	99.4	248 5	US-10-530-253-11 Sequence 11, Appl
2	513	99.2	220 4	US-10-000-903-8 Sequence 8, Appl
3	513	99.2	220 5	US-10-899-771-8 Sequence 8, Appl
4	513	99.2	248 5	US-10-530-253-9 Sequence 9, Appl
5	513	99.2	805 4	US-10-367-095-9 Sequence 9, Appl
6	513	99.2	805 4	US-10-368-046-9 Sequence 9, Appl
7	513	99.2	805 4	US-10-367-367-9 Sequence 9, Appl
8	513	99.2	805 4	US-10-918-337-9 Sequence 9, Appl
9	512	99.0	98 3	US-09-728-466-1 Sequence 1, Appl
10	512	99.0	98 3	US-09-820-765-4 Sequence 4, Appl
11	512	99.0	98 3	US-09-824-017-4 Sequence 4, Appl
12	512	99.0	98 3	US-09-986-118A-4 Sequence 8, Appl
13	512	99.0	98 4	US-10-177-390-8 Sequence 8, Appl
14	512	99.0	98 4	US-10-654-129-4 Sequence 4, Appl
15	512	99.0	98 4	US-10-772-988-3 Sequence 3, Appl
16	512	99.0	98 4	US-10-479-541-5 Sequence 5, Appl
17	512	99.0	98 5	US-10-042-526A-4 Sequence 4, Appl
18	512	99.0	98 5	US-10-657-399-1 Sequence 1, Appl
19	512	99.0	98 5	US-10-858-384-12 Sequence 12, Appl
20	512	99.0	98 5	US-10-343-448-5 Sequence 5, Appl
21	512	99.0	98 5	US-10-367-057-17 Sequence 17, Appl
22	512	99.0	98 5	US-10-530-253-14 Sequence 14, Appl
23	512	99.0	98 6	US-11-077-939-5 Sequence 5, Appl
24	512	99.0	98 6	US-11-179-478-4 Sequence 4, Appl
25	512	99.0	121 4	US-10-267-311-12 Sequence 12, Appl
26	512	99.0	121 5	US-10-679-956-12 Sequence 12, Appl
27	512	99.0	198 4	US-10-267-311-35 Sequence 35, Appl

28	512	99.0	198 5	US-10-679-956-35 Sequence 35, Appl
29	512	99.0	220 4	US-10-000-903-1 Sequence 1, Appl
30	512	99.0	220 5	US-10-899-771-1 Sequence 1, Appl
31	512	99.0	239 4	US-10-000-903-12 Sequence 12, Appl
32	512	99.0	239 5	US-10-899-771-12 Sequence 12, Appl
33	512	99.0	248 5	US-10-530-253-7 Sequence 7, Appl
34	512	99.0	256 6	US-11-192-923A-2 Sequence 2, Appl
35	512	99.0	256 6	US-09-367-309A-1 Sequence 1, Appl
36	512	99.0	205 4	US-10-267-311-33 Sequence 33, Appl
37	512	99.0	255 5	US-10-679-956-33 Sequence 25, Appl
38	512	99.0	324 4	US-10-267-311-25 Sequence 25, Appl
39	512	99.0	334 5	US-10-679-956-25 Sequence 10, Appl
40	512	99.0	334 4	US-10-472-724A-10 Sequence 6, Appl
41	512	99.0	371 4	US-10-000-903-6 Sequence 6, Appl
42	512	99.0	371 5	US-10-899-771-6 Sequence 14, Appl
43	512	99.0	330 4	US-10-000-903-14 Sequence 14, Appl
44	512	99.0	330 5	US-10-899-771-14 Sequence 7, Appl
45	512	99.0	421 4	US-10-296-770-7 Sequence 19, Appl
46	512	99.0	493 4	US-10-267-311-19 Sequence 19, Appl
47	512	99.0	493 5	US-10-679-956-19 Sequence 17, Appl
48	512	99.0	639 4	US-10-267-311-17 Sequence 17, Appl
49	512	99.0	639 5	US-10-679-956-17 Sequence 11, Appl
50	512	99.0	641 4	US-10-267-311-51 Sequence 51, Appl
51	512	99.0	641 5	US-10-679-956-51 Sequence 51, Appl
52	512	99.0	647 4	US-10-267-311-53 Sequence 53, Appl
53	512	99.0	647 5	US-10-679-956-53 Sequence 5, Appl
54	511	98.8	248 5	US-10-530-253-5 Sequence 5, Appl
55	510	98.6	248 5	US-10-530-253-3 Sequence 3, Appl
56	509	98.5	248 5	US-10-530-253-1 Sequence 1, Appl
57	507	98.1	98 4	US-10-201-764-19 Sequence 19, Appl
58	507	98.1	98 4	US-10-681-410-19 Sequence 19, Appl
59	507	98.1	98 5	US-10-484-063-26 Sequence 26, Appl
60	507	98.1	111 4	US-10-472-724A-4 Sequence 4, Appl
61	504	97.5	98 4	US-10-392-113-29 Sequence 29, Appl
62	503	97.3	98 4	US-10-267-311-8 Sequence 8, Appl
63	503	97.3	98 5	US-10-679-956-8 Sequence 8, Appl
64	503	97.3	648 4	US-10-267-311-29 Sequence 29, Appl
65	503	97.3	648 5	US-10-679-956-29 Sequence 41, Appl
66	503	97.3	711 4	US-10-267-311-41 Sequence 41, Appl
67	503	97.3	711 5	US-10-679-956-41 Sequence 45, Appl
68	503	97.3	724 4	US-10-267-311-45 Sequence 45, Appl
69	503	97.3	724 5	US-10-679-956-45 Sequence 7, Appl
70	500	96.7	99 4	US-10-115-440-7 Sequence 7, Appl
71	500	96.7	289 4	US-10-115-440-5 Sequence 2, Appl
72	478	92.5	185 6	US-11-072-288-2 Sequence 2, Appl
73	381.5	73.8	99 5	US-10-530-253-30 Sequence 30, Appl
74	372	72.0	98 5	US-10-530-253-28 Sequence 28, Appl
75	295	57.1	97 5	US-10-530-253-29 Sequence 29, Appl
76	294	56.9	99 5	US-10-530-253-34 Sequence 34, Appl
77	289.5	56.0	98 5	US-10-530-253-36 Sequence 36, Appl
78	245	47.4	98 5	US-10-367-075-12 Sequence 12, Appl
79	215	41.6	117 5	US-10-751-845-126 Sequence 126, Appl
80	215	41.6	236 5	US-10-751-845-157 Sequence 157, Appl
81	215	41.6	237 5	US-10-751-845-158 Sequence 158, Appl
82	215	41.6	261 5	US-10-751-845-160 Sequence 160, Appl
83	213	41.2	106 5	US-10-530-253-32 Sequence 32, Appl
84	202.5	39.2	105 4	US-10-433-091-4 Sequence 4, Appl
85	202.5	39.2	105 5	US-10-530-253-27 Sequence 27, Appl
86	201.5	39.0	227 4	US-10-000-903-19 Sequence 19, Appl
87	201.5	39.0	227 5	US-10-899-771-19 Sequence 19, Appl
88	200.5	38.8	383 4	US-10-000-903-23 Sequence 23, Appl
89	200.5	38.8	383 5	US-10-899-771-23 Sequence 23, Appl
90	198.5	38.4	105 5	US-10-800-023-28 Sequence 28, Appl
91	196	37.9	35 6	US-11-041-993-101 Sequence 101, Appl
92	195.5	37.8	107 4	US-10-530-253-37 Sequence 37, Appl
93	195.5	37.8	118 4	US-10-472-724A-8 Sequence 8, Appl
94	192.5	37.2	227 4	US-10-000-903-16 Sequence 16, Appl
95	192.5	37.2	227 5	US-10-899-771-16 Sequence 35, Appl
96	178.5	34.5	105 5	US-10-530-253-35 Sequence 35, Appl
97	178	34.4	101 5	US-10-530-253-33 Sequence 33, Appl
98	170	32.9	109 5	US-10-530-253-31 Sequence 31, Appl
99	164.5	31.8	110 5	US-10-530-253-38 Sequence 38, Appl
100	156	30.2	517 5	US-10-475-203A-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-530-253-11
; Sequence 11, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT FILING DATE: US/10/530, 253
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-11

Query Match 99.4%; Score 514; DB 5; Length 248;
Best Local Similarity 96.9%; Pred. No. 3,3e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPIHEYMLDLOPETTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60
Db 1 MHGDPPIHEYMLDLOPETTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60

Qy 61 CDSTLRLCVOSTHVDIRLTEDLLMGTLGIYXPICSQKP 98
Db 61 CDSTLRLCVOSTHVDIRLTEDLLMGTLGIYXPICSQKP 98

RESULT 2

US-10-000-903-8
; Sequence 8, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-8

Query Match 99.2%; Score 513; DB 4; Length 220;
Best Local Similarity 96.9%; Pred. No. 3.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPIHEYMLDLOPETTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60
Db 114 MHGDPPIHEYMLDLOPETTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 173

Qy 61 CDSTLRLCVOSTHVDIRLTEDLLMGTLGIYXPICSQKP 98
Db 174 CDSTLRLCVOSTHVDIRLTEDLLMGTLGIYXPICSQKP 211

RESULT 3

US-10-899-771-8
; Sequence 8, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions comprising Human Papilloma Virus Proteins
and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeic protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and mutated E7 from Human papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-8

Query Match 99.2%; Score 513; DB 5; Length 220;
Best Local Similarity 96.9%; Pred. No. 3.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPIHEYMLDLOPETTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60
Db 114 MHGDPPIHEYMLDLOPETTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 173

Qy 61 CDSTLRLCVOSTHVDIRLTEDLLMGTLGIYXPICSQKP 98
Db 174 CDSTLRLCVOSTHVDIRLTEDLLMGTLGIYXPICSQKP 211

RESULT 4

US-10-530-253-9
; Sequence 9, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 248

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; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; US-10-530-253-9
Query Match      99.2%: Score 513; DB 5; Length 248;
Best Local Similarity 96.9%: Pred. No. 4.4e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPETTDLYXXQLNDSSEDEIDGPAGAEPRAHYNIIVTFCK 60
Db 1 MHGDTPLHEYMDLQPETTDLYGYQLNDSSEDEIDGPAGAEPRAHYNIIVTFCK 60

Qy 61 CDSTLRICVQSTHYDITRTLEDLMGTIGIYCPICSOXP 98
Db 61 CDSTLRICVQSTHYDITRTLEDLMGTIGIYCPICSOXP 98

RESULT 5
US-10-367-095-9
; Sequence 9, Application US/10367095
; Publication No. US20030228696A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; TITLE OR INVENTION: No. US20030228696A1 Insect Cell Line
; FILE REFERENCE: 44149-1US1
; CURRENT APPLICATION NUMBER: US/10/367,095
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,123
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,113
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,154
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,135
; PRIOR FILING DATE: 2002-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
; US-10-367-095-9
Query Match      99.2%: Score 513; DB 4; Length 805;
Best Local Similarity 96.9%: Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPETTDLYXXQLNDSSEDEIDGPAGAEPRAHYNIIVTFCK 60
Db 471 MHGDTPLHEYMDLQPETTDLYGYQLNDSSEDEIDGPAGAEPRAHYNIIVTFCK 530

Qy 61 CDSTLRICVQSTHYDITRTLEDLMGTIGIYCPICSOXP 98
Db 531 CDSTLRICVQSTHYDITRTLEDLMGTIGIYCPICSOXP 568

RESULT 6
US-10-368-046-9
```

```

; Sequence 9, Application US/10368046
; Publication No. US20040063188A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; APPLICANT: Victoria Cioce
; TITLE OR INVENTION: Method for Isolation and Purification of
; TITLE OR INVENTION: Expressed Gene Products In Vitro
; FILE REFERENCE: 44149-3US1
; CURRENT APPLICATION NUMBER: US/10/368,046
; PRIOR FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,123
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,113
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,154
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,135
; PRIOR FILING DATE: 2002-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
; US-10-368-046-9
Query Match      99.2%: Score 513; DB 4; Length 805;
Best Local Similarity 96.9%: Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMDLQPETTDLYXXQLNDSSEDEIDGPAGAEPRAHYNIIVTFCK 60
Db 471 MHGDTPLHEYMDLQPETTDLYGYQLNDSSEDEIDGPAGAEPRAHYNIIVTFCK 530

Qy 61 CDSTLRICVQSTHYDITRTLEDLMGTIGIYCPICSOXP 98
Db 531 CDSTLRICVQSTHYDITRTLEDLMGTIGIYCPICSOXP 568

RESULT 7
US-10-367-367-9
; Sequence 9, Application US/10367367
; Publication No. US20040121465A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; TITLE OR INVENTION: Optimization of Gene Sequences of
; TITLE OR INVENTION: Virus-Like Particles for Expression in Insect Cells
; FILE REFERENCE: 44149-2US1
; CURRENT APPLICATION NUMBER: US/10/367,367
; PRIOR FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
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PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 805
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
US-10-367-367-9

Query Match 99.2% Score 513; DB 4; Length 805;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 471 MHGDTPLHEYMLDLPETTDLYGEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 530
Qy 61 CDSTRLCVOSTHYDRTLEDLMGTGIVXPICQKP 98
Db 531 CDSTRLCVOSTHYDRTLEDLMGTGIVCPICQKP 568

RESULT 8
US-10-918-337-9
Sequence 9, Application US/10918337
Publication No. US2005011819A1
GENERAL INFORMATION:
APPLICANT: NOVAVAX, INC., et al.
TITLE OF INVENTION: Optimization of Gene Sequences of
FILE REFERENCE: 19065/2132
CURRENT APPLICATION NUMBER: US/10/918,337
PRIOR FILING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: PCT/US03/04473
PRIOR FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: US 60/356,119
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,161
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,123
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,113
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,154
PRIOR FILING DATE: 2002-02-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 805
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
US-10-918-337-9

Query Match 99.2% Score 513; DB 5; Length 805;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 471 MHGDTPLHEYMLDLPETTDLYGEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 530
Qy 61 CDSTRLCVOSTHYDRTLEDLMGTGIVXPICQKP 98
Db 531 CDSTRLCVOSTHYDRTLEDLMGTGIVCPICQKP 568

RESULT 9
US-09-728-466-1
Sequence 1, Application US/09728466
Patent No. US20010029022A1
GENERAL INFORMATION:
APPLICANT: Fleher, Christopher
FILE OF INVENTION: Methode to Identify Anti-Viral Agents
TITLE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/728,466
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 98
TYPE: PR
ORGANISM: Papillomavirus sylvilagi
US-09-728-466-1

Query Match 99.0% Score 512; DB 3; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEYMLDLPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Qy 61 CDSTRLCVOSTHYDRTLEDLMGTGIVXPICQKP 98
Db 61 CDSTRLCVOSTHYDRTLEDLMGTGIVCPICQKP 98

RESULT 10
US-09-820-765-4
Sequence 4, Application US/09820765
Publication No. US20020039584A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/820,765
FILING DATE: 30-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4

Query Match 99.0%; Score 512; DB 3; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDLPETTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60
DB 1 MHGDTPLHEYMLDLPETTDLYCYEQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60
61 CDSTLRICVOSTHYDIRTLEDLMGTIGIVPCISQKP 98
DB 61 CDSTLRICVOSTHYDIRTLEDLMGTIGIVPCISQKP 98

RESULT 11
US-09-824-017-4
Sequence 4, Application US/09824017
Publication No. US20020197668A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLER, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,017
FILING DATE: 03-Apr-2001
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4

Query Match 99.0%; Score 512; DB 3; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDLPETTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60
DB 1 MHGDTPLHEYMLDLPETTDLYCYEQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60
61 CDSTLRICVOSTHYDIRTLEDLMGTIGIVPCISQKP 98
DB 61 CDSTLRICVOSTHYDIRTLEDLMGTIGIVPCISQKP 98

RESULT 12
US-09-986-118A-4
Sequence 4, Application US/09986118A
Publication No. US20030021806A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLER, Michael

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE

NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/986,118A
FILING DATE: 07-No. US20030021806A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-986-118A-4

Query Match 99.0%; Score 512; DB 3; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDLPETTDLYXXQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60
DB 1 MHGDTPLHEYMLDLPETTDLYCYEQLNDSSEEDIDGPAGQAEPRRAHYNIVTFCK 60
61 CDSTLRICVOSTHYDIRTLEDLMGTIGIVPCISQKP 98
DB 61 CDSTLRICVOSTHYDIRTLEDLMGTIGIVPCISQKP 98

RESULT 13
US-10-177-390-8

Sequence 8, Application US/10177390
Publication No. US20030143743A1
GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with linear
FILE REFERENCE: 021505wo/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 98
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: fragment of
US-10-177-390-8

Query Match 99.0%; Score 512; DB 4; Length 98;
Best Local Similarity 96.9%; Pred. No. 1,8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPLHEYMLDLOPETTDLYXXYQNDSSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
Db 1 MHGDPPLHEYMLDLOPETTDLYCYEQNDSSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
61 CDSTLRLCVOSTHVDIRTDLEMLMGTLGIYXPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRTDLEMLMGTLGIYXPCISQKP 98

RESULT 14

US-10-654-129-4
Sequence 4, Application US/10654129
Publication No. US2004008161A1
GENERAL INFORMATION:

APPLICANT: BURGER, Alexander

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE

FORMULATIONS AND METHODS OF USE

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESS: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/654,129

FILING DATE: 04-Sep-2003

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/824,017

FILING DATE: 03-Apr-2001

APPLICATION NUMBER: 09/026,896

FILING DATE: 1998-02-20

ATTORNEY/AGENT INFORMATION:

NAME: Sandercoc, Colin G.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-654-129-4

Query Match 99.0%; Score 512; DB 4; Length 98;
Best Local Similarity 96.9%; Pred. No. 1,8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPLHEYMLDLOPETTDLYXXYQNDSSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
Db 1 MHGDPPLHEYMLDLOPETTDLYCYEQNDSSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
61 CDSTLRLCVOSTHVDIRTDLEMLMGTLGIYXPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRTDLEMLMGTLGIYXPCISQKP 98

RESULT 15

US-10-772-988-3
Sequence 3, Application US/10772988
Publication No. US20040139485A1
GENERAL INFORMATION:

APPLICANT: Thorgelsson, Snorri S.

APPLICANT: Moltach, Joseph T.

APPLICANT: Zhang, Minghuang

TITLE OF INVENTION: CDNA ENCODING A GENE BOG (BET OVER-EXPRESSED GENE) AND ITS PROTEIN

FILE REFERENCE: 11613.29USW1

CURRENT APPLICATION NUMBER: US/10/772,988

CURRENT FILING DATE: 2004-02-05

PRIOR APPLICATION NUMBER: US/09/637,746

PRIOR FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: PCT/US99/04142

PRIOR FILING DATE: 1999-02-25

PRIOR APPLICATION NUMBER: US 60/079,567

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: US 60/075,922

PRIOR FILING DATE: 1998-02-25

SOFTWARE: PatentIn version 3.1

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 3

LENGTH: 98

TYPE: PRT

ORGANISM: Human papillomavirus

US-10-772-988-3

Query Match 99.0%; Score 512; DB 4; Length 98;
Best Local Similarity 96.9%; Pred. No. 1,8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPLHEYMLDLOPETTDLYXXYQNDSSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
Db 1 MHGDPPLHEYMLDLOPETTDLYCYEQNDSSSEDEIDGPAGQAEPRRAHNYIVTFCK 60
61 CDSTLRLCVOSTHVDIRTDLEMLMGTLGIYXPCISQKP 98
Db 61 CDSTLRLCVOSTHVDIRTDLEMLMGTLGIYXPCISQKP 98

RESULT 16

US-10-479-541-5
Sequence 5, Application US/10479541
Publication No. US20040151723A1
GENERAL INFORMATION:

APPLICANT: Kirin Beer Kabushiki Kaisha

TITLE OF INVENTION: Novel E7 antigen epitope from human papillomavirus and

FILE REFERENCE: 137240PX

CURRENT APPLICATION NUMBER: US/10/479,541

;; CURRENT FILING DATE: 2003-12-04
;; PRIOR APPLICATION NUMBER: 173803/2001
;; PRIOR FILING DATE: 2001-06-08
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 5
;; LENGTH: 98
;; TYPE: PRT
;; ORGANISM: Human papillomavirus type 16
US-10-479-541-5

Query Match 99.0%; Score 512; DB 4; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHXYMDLQPEETDLYXXQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHXYMDLQPEETDLYCYEQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Qy 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICQKP 98
Db 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICQKP 98

RESULT 17
US-10-042-526A-4
; Sequence 4, Application US/10042526A
; Publication No. US20050031636A1
; GENERAL INFORMATION:
; APPLICANT: GISSMAN, et al.
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE FORMULATIONS AND METHODS OF USE
; FILE REFERENCE: 27013/38150
; CURRENT APPLICATION NUMBER: US/10/042,526A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/632,286
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 08/944,368
; PRIOR FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human Papilloma Virus
US-10-042-526A-4

Query Match 99.0%; Score 512; DB 5; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHXYMDLQPEETDLYXXQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHXYMDLQPEETDLYCYEQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Qy 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICQKP 98
Db 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICQKP 98

RESULT 18
US-10-657-399-1
; Sequence 1, Application US/10657399
; Publication No. US20050032038A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Manxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/10/657,399
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: US/09/728,466
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/382,616

;; PRIOR FILING DATE: 1999-08-25
;; NUMBER OF SEQ ID NOS: 43
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1
;; LENGTH: 98
;; TYPE: PRT
;; ORGANISM: Papillomavirus sylviaagl
US-10-657-399-1

Query Match 99.0%; Score 512; DB 5; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHXYMDLQPEETDLYXXQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHXYMDLQPEETDLYCYEQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Qy 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICQKP 98
Db 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICQKP 98

RESULT 19
US-10-858-384-12
; Sequence 12, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-12

Query Match 99.0%; Score 512; DB 5; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHXYMDLQPEETDLYXXQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHXYMDLQPEETDLYCYEQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Qy 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICQKP 98
Db 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICQKP 98

RESULT 20
US-10-343-448-5
; Sequence 5, Application US/10343448
; Publication No. US20050054820A1
; GENERAL INFORMATION:
; APPLICANT: WU, Tzy-Chou
; APPLICANT: HUNG, Chien-Fu
; TITLE OF INVENTION: MOLECULAR VACCINE LINKING AN ENDOPLASMIC RETICULUM CHAPERONE
; FILE REFERENCE: 2240-186463
; CURRENT APPLICATION NUMBER: US/10/343,448
; CURRENT FILING DATE: 2003-01-31

```
; PRIOR APPLICATION NUMBER: PCT/US01/24134
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,902
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-343-448-5
```

```
Query Match          99.0%; Score 512; DB 5; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
Db      1 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
```

```
Qy      61 CDSTLRLCVOSTHYDIRTLEDLMGTIGIVXPICSQKP 98
Db      61 CDSTLRLCVOSTHYDIRTLEDLMGTIGIVCPICSQKP 98
```

```
RESULT 21
US-10-367-057-17
```

```
; Sequence 17, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuroseqList version 0.1
; SEQ ID NO 17
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-17
```

```
Query Match          99.0%; Score 512; DB 5; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
Db      1 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
```

```
Qy      61 CDSTLRLCVOSTHYDIRTLEDLMGTIGIVXPICSQKP 98
Db      61 CDSTLRLCVOSTHYDIRTLEDLMGTIGIVCPICSQKP 98
```

```
RESULT 22
US-10-530-253-14
```

```
; Sequence 14, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
```

```
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-14
```

```
Query Match          99.0%; Score 512; DB 5; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
Db      1 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
```

```
Qy      61 CDSTLRLCVOSTHYDIRTLEDLMGTIGIVXPICSQKP 98
Db      61 CDSTLRLCVOSTHYDIRTLEDLMGTIGIVCPICSQKP 98
```

```
RESULT 23
US-11-077-939-5
```

```
; Sequence 5, Application US/11077939
; Publication No. US20050196865A1
; GENERAL INFORMATION:
; APPLICANT: Frazer, Ian Hector
; TITLE OF INVENTION: Gene Expression System Based on Codon Translation Efficiency
; FILE REFERENCE: 10338-1101
; CURRENT APPLICATION NUMBER: US/11/077,939
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/AU2003/001200
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/410410
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-11-077-939-5
```

```
Query Match          99.0%; Score 512; DB 6; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 MHGDTPTLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
Db      1 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
```

```
Qy      61 CDSTLRLCVOSTHYDIRTLEDLMGTIGIVXPICSQKP 98
Db      61 CDSTLRLCVOSTHYDIRTLEDLMGTIGIVCPICSQKP 98
```

```
RESULT 24
US-11-179-478-4
```

```
; Sequence 4, Application US/11179478
; Publication No. US20050249745A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALBEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; TITLE OF INVENTION: FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FOLEY & LARDNER
```


STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/179,478
FILING DATE: 13-JULY-2005
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/654,129
FILING DATE: 04-Sep-2003
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-11-179-478-4

Query Match 99.0%; Score 512; DB 6; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMDLQPEETDLYXXQLNDSSEDEIDDPAGQAEPRAHYNIIVTFCK 60
DB 1 MHGDTPLHRYMDLQPEETDLYCYEQLNDSSEDEIDDPAGQAEPRAHYNIIVTFCK 60
QY 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVXPICSQKP 98
DB 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVCPICSQKP 98

RESULT 25
US-10-267-311-12
Sequence 12, Application US/10267311
Publication No. US20030050469A1
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-267-311-12

Query Match 99.0%; Score 512; DB 4; Length 121;

Best Local Similarity 96.9%; Pred. No. 2.4e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMDLQPEETDLYXXQLNDSSEDEIDDPAGQAEPRAHYNIIVTFCK 60
DB 24 MHGDTPLHRYMDLQPEETDLYCYEQLNDSSEDEIDDPAGQAEPRAHYNIIVTFCK 83
QY 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVXPICSQKP 98
DB 84 CDSTLRVCVOSTHYDRTLEDLMGTGIVCPICSQKP 121

RESULT 26
US-10-679-956-12
Sequence 12, Application US/10679956
Publication No. US2005008984A1
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-679-956-12

Query Match 99.0%; Score 512; DB 5; Length 121;
Best Local Similarity 96.9%; Pred. No. 2.4e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHRYMDLQPEETDLYXXQLNDSSEDEIDDPAGQAEPRAHYNIIVTFCK 60
DB 24 MHGDTPLHRYMDLQPEETDLYCYEQLNDSSEDEIDDPAGQAEPRAHYNIIVTFCK 83
QY 61 CDSTLRVCVOSTHYDRTLEDLMGTGIVXPICSQKP 98
DB 84 CDSTLRVCVOSTHYDRTLEDLMGTGIVCPICSQKP 121

RESULT 27
US-10-267-311-35
Sequence 35, Application US/10267311
Publication No. US20030050469A1
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 198
TYPE: PRT
ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: fusion sequence
; US-10-267-311-35

Query Match          99.0%; Score 512; DB 4; Length 198;
Best Local Similarity 96.9%; Pred. No. 4,4e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMLDLPETTDLYXXQLNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 101 MHGDPPTLHEYMLDLPETTDLYCYEQUNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 160

Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTLGIYXPCISQKP 98
Db 161 CDSTRLCVOSTHVDIRLTEDLMGTLGIYXPCISQKP 198

RESULT 28
US-10-679-956-35
; Sequence 35, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; US-10-679-956-35

Query Match          99.0%; Score 512; DB 5; Length 198;
Best Local Similarity 96.9%; Pred. No. 4,4e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMLDLPETTDLYXXQLNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 101 MHGDPPTLHEYMLDLPETTDLYCYEQUNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 160

Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTLGIYXPCISQKP 98
Db 161 CDSTRLCVOSTHVDIRLTEDLMGTLGIYXPCISQKP 198

RESULT 29
US-10-000-903-1
; Sequence 1, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
```

```
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-000-903-1

Query Match          99.0%; Score 512; DB 4; Length 220;
Best Local Similarity 96.9%; Pred. No. 5e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMLDLPETTDLYXXQLNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 114 MHGDPPTLHEYMLDLPETTDLYCYEQUNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 173

Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTLGIYXPCISQKP 98
Db 174 CDSTRLCVOSTHVDIRLTEDLMGTLGIYXPCISQKP 211

RESULT 30
US-10-899-771-1
; Sequence 1, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeic protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E7 from Human papilloma virus type
; OTHER INFORMATION: 16)
; US-10-899-771-1

Query Match          99.0%; Score 512; DB 5; Length 220;
Best Local Similarity 96.9%; Pred. No. 5e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMLDLPETTDLYXXQLNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 114 MHGDPPTLHEYMLDLPETTDLYCYEQUNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 173

Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTLGIYXPCISQKP 98
Db 174 CDSTRLCVOSTHVDIRLTEDLMGTLGIYXPCISQKP 211

RESULT 31
US-10-000-903-12
; Sequence 12, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
```

APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-12

Query Match 99.0%; Score 512; DB 4; Length 239;
Best Local Similarity 96.9%; Pred. No. 5.5e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHRYMDLOPETTDLYXXYXQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 133 MHGDTPLHRYMDLOPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 192
Qy 61 CDSTLRICVQSTHVDIRTLBLLMGTLGIYXPCSQKP 98
Db 193 CDSTLRICVQSTHVDIRTLBLLMGTLGIYXPCSQKP 230

RESULT 32
US-10-899-771-12
Sequence 12, Application US/10899771
Publication No. US20050031638A1
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 239
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimaeic protein (C)Iyta from Streptococcus
OTHER INFORMATION: pneumoniae and E7 from Human papilloma virus type
OTHER INFORMATION: 16)
US-10-899-771-12

Query Match 99.0%; Score 512; DB 5; Length 239;
Best Local Similarity 96.9%; Pred. No. 5.5e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHRYMDLOPETTDLYXXYXQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 133 MHGDTPLHRYMDLOPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 192
Qy 61 CDSTLRICVQSTHVDIRTLBLLMGTLGIYXPCSQKP 98
Db 193 CDSTLRICVQSTHVDIRTLBLLMGTLGIYXPCSQKP 230

RESULT 33
US-10-530-253-7
Sequence 7, Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:
APPLICANT: Cassecci, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 248
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-10-530-253-7

Query Match 99.0%; Score 512; DB 5; Length 248;
Best Local Similarity 96.9%; Pred. No. 5.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHRYMDLOPETTDLYXXYXQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHRYMDLOPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Qy 61 CDSTLRICVQSTHVDIRTLBLLMGTLGIYXPCSQKP 98
Db 61 CDSTLRICVQSTHVDIRTLBLLMGTLGIYXPCSQKP 98

RESULT 34
US-11-192-923A-2
Sequence 2, Application US/11192923A
Publication No. US20060018928A1
GENERAL INFORMATION:
APPLICANT: PANG, XIAOWU
TITLE OF INVENTION: VIRUS-LIKE PARTICLE CONTAINING A DENGUE VIRUS
FILE REFERENCE: 116620-003
CURRENT APPLICATION NUMBER: US/11/192,923A
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: CN 03115272.4
PRIOR FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: CN 03115273.2
PRIOR FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 2
LENGTH: 256
TYPE: PRT
ORGANISM: Human papillomavirus
US-11-192-923A-2

Query Match 99.0%; Score 512; DB 6; Length 256;
Best Local Similarity 96.9%; Pred. No. 6e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHRYMDLOPETTDLYXXYXQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHRYMDLOPETTDLYCYEQNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Qy 61 CDSTLRICVQSTHVDIRTLBLLMGTLGIYXPCSQKP 98
Db 61 CDSTLRICVQSTHVDIRTLBLLMGTLGIYXPCSQKP 98

RESULT 35
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 99.0%; Score 512; DB 3; Length 266;
Best Local Similarity 96.9%; Pred. No. 6,3e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
DB 161 MHGDTPLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 220
OY 61 CDSTLRUCVOSTHVDIRTELDLMGTIGIVPICSQKP 98
DB 221 CDSTLRUCVOSTHVDIRTELDLMGTIGIVPICSQKP 258

RESULT 36
US-10-267-311-33
; Sequence 33, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-33

Query Match 99.0%; Score 512; DB 4; Length 295;
Best Local Similarity 96.9%; Pred. No. 7,2e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
DB 198 MHGDTPLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 257
OY 61 CDSTLRUCVOSTHVDIRTELDLMGTIGIVPICSQKP 98

DB 258 CDSTLRUCVOSTHVDIRTELDLMGTIGIVPICSQKP 295

RESULT 37
US-10-679-956-33
; Sequence 33, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-679-956-33

Query Match 99.0%; Score 512; DB 5; Length 295;
Best Local Similarity 96.9%; Pred. No. 7,2e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
DB 198 MHGDTPLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 257
OY 61 CDSTLRUCVOSTHVDIRTELDLMGTIGIVPICSQKP 98
DB 258 CDSTLRUCVOSTHVDIRTELDLMGTIGIVPICSQKP 295

RESULT 38
US-10-267-311-25
; Sequence 25, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-25

Query Match 99.0%; Score 512; DB 4; Length 324;
Best Local Similarity 96.9%; Pred. No. 8,1e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMLDLPETTDLYXXYQNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 227 MGGDTPLHEHYMLDLPETTDLYCYEQNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 286
Qy 61 CDSTLRLCVQSTHYDITRTLEDLMGTIGIYCPICQKP 98
Db 287 CDSTLRLCVQSTHYDITRTLEDLMGTIGIYCPICQKP 324

RESULT 39
US-10-679-956-25
; Sequence 25, Application US/10679956
; Publication No. US20050098841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-679-956-25

Query Match 99.0%; Score 512; DB 5; Length 324;
Best Local Similarity 96.9%; Pred. No. 8.1e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMLDLPETTDLYXXYQNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 227 MGGDTPLHEHYMLDLPETTDLYCYEQNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 286
Qy 61 CDSTLRLCVQSTHYDITRTLEDLMGTIGIYCPICQKP 98
Db 287 CDSTLRLCVQSTHYDITRTLEDLMGTIGIYCPICQKP 324

RESULT 40
US-10-472-724-10
; Sequence 10, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified H5 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-10

Query Match 99.0%; Score 512; DB 4; Length 334;
Best Local Similarity 96.9%; Pred. No. 8.4e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMLDLPETTDLYXXYQNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 229 MGGDTPLHEHYMLDLPETTDLYCYEQNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 288
Qy 61 CDSTLRLCVQSTHYDITRTLEDLMGTIGIYCPICQKP 98
Db 289 CDSTLRLCVQSTHYDITRTLEDLMGTIGIYCPICQKP 326

RESULT 41
US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernarde
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match 99.0%; Score 512; DB 4; Length 371;
Best Local Similarity 96.9%; Pred. No. 9.5e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDTPLHEHYMLDLPETTDLYXXYQNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 265 MGGDTPLHEHYMLDLPETTDLYCYEQNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 324
Qy 61 CDSTLRLCVQSTHYDITRTLEDLMGTIGIYCPICQKP 98
Db 325 CDSTLRLCVQSTHYDITRTLEDLMGTIGIYCPICQKP 362

RESULT 42
US-10-899-771-6
; Sequence 6, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6

```

; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenza B and B6E7 fusion from Human Papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-6

Query Match          99.0%; Score 512; DB 5; Length 371;
Best Local Similarity 96.9%; Pred. No. 9.5e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGPTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
Db 265 MGGPTPLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 324

Qy 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICSKP 98
Db 325 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICSKP 362

RESULT 43
US-10-000-903-14
; Sequence 14, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000.903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-14

Query Match          99.0%; Score 512; DB 4; Length 390;
Best Local Similarity 96.9%; Pred. No. 1e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGPTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
Db 284 MGGPTPLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 343

Qy 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICSKP 98
Db 344 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICSKP 381

RESULT 44
US-10-899-771-14
; Sequence 14, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a Cpg Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899.771
; CURRENT FILING DATE: 2004-07-27
```

```

; PRIOR APPLICATION NUMBER: US/09/581.976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-14

Query Match          99.0%; Score 512; DB 5; Length 390;
Best Local Similarity 96.9%; Pred. No. 1e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGPTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
Db 284 MGGPTPLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 343

Qy 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICSKP 98
Db 344 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICSKP 381

RESULT 45
US-10-296-770-7
; Sequence 7, Application US/10296770
; Publication No. US20030104570A1
; GENERAL INFORMATION:
; APPLICANT: Cabazon Silva, Teresa Elisa Virginia
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; TITLE OF INVENTION: Triple Fusion Proteins Comprising
; TITLE OF INVENTION: Ubiquitin Fused Between Thiorodoxin and a polypeptide of
; FILE REFERENCE: B45221
; CURRENT APPLICATION NUMBER: US/10/296.770
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/EP01/06952
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: GB 0015619.0
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: GB 0026484.6
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Chimeric (E. coli - human)
US-10-296-770-7

Query Match          99.0%; Score 512; DB 4; Length 421;
Best Local Similarity 96.9%; Pred. No. 1.1e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGPTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
Db 315 MGGPTPLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 374

Qy 61 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICSKP 98
Db 375 CDSTLRFCVOSTHVDIRTELDLMGTGIVXPICSKP 412

RESULT 46
US-10-267-311-19
```

```
; Sequence 19, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; US-10-267-311-19
```

```
Query Match          99.0%; Score 512; DB 4; Length 493;
Best Local Similarity 96.9%; Pred. No. 1.4e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGAGQAEPRRAHYNIVTFCK 60
Db 396 MHGDTPLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGAGQAEPRRAHYNIVTFCK 455
Qy 61 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 98
Db 456 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 493
```

```
RESULT 47
US-10-679-956-19
; Sequence 19, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; US-10-679-956-19
```

```
Query Match          99.0%; Score 512; DB 5; Length 493;
Best Local Similarity 96.9%; Pred. No. 1.4e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGAGQAEPRRAHYNIVTFCK 60
Db 396 MHGDTPLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGAGQAEPRRAHYNIVTFCK 455
Qy 61 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 98
```

```
Db 456 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 493
```

```
RESULT 48
US-10-267-311-17
; Sequence 17, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; US-10-267-311-17
```

```
Query Match          99.0%; Score 512; DB 4; Length 639;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGAGQAEPRRAHYNIVTFCK 60
Db 542 MHGDTPLHEYMLDLOPETTDLYCYEQLNDSSEDEIDGAGQAEPRRAHYNIVTFCK 601
Qy 61 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 98
Db 602 CDSTLRLCVOSTHYDRTLEDLMLGTLGIYCPICSKP 639
```

```
RESULT 49
US-10-679-956-17
; Sequence 17, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; US-10-679-956-17
```

```
Query Match          99.0%; Score 512; DB 5; Length 639;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEYMLDLOPETTDLYXXQLNDSSEDEIDGAGQAEPRRAHYNIVTFCK 60
```

Db 542 MHGDTPLHEYMLDQPEETDLYCYEQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 601
Qy 61 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 98
Db 602 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 639

RESULT 50

US-10-267-311-51
; Sequence 51, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-51

Query Match 99.0%; Score 512; DB 4; Length 641;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDQPEETDLYCYEQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 544 MHGDTPLHEYMLDQPEETDLYCYEQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 603

Qy 61 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 98
Db 604 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 641

RESULT 51

US-10-679-956-51
; Sequence 51, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-679-956-51

Query Match 99.0%; Score 512; DB 5; Length 641;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDQPEETDLYCYEQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 544 MHGDTPLHEYMLDQPEETDLYCYEQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 603

Qy 61 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 98
Db 604 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 641

RESULT 52

US-10-267-311-53
; Sequence 53, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-53

Query Match 99.0%; Score 512; DB 4; Length 647;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDQPEETDLYCYEQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 550 MHGDTPLHEYMLDQPEETDLYCYEQUNDSESEDEIDGPAGQAEPPRAHYNIVTFCK 609

Qy 61 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 98
Db 610 CDSTRLCVOGTHVDIRTLBDMGTGIVXPICQKP 647

RESULT 53

US-10-679-956-53
; Sequence 53, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 647
; TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-679-956-53

Query Match 99.0%; Score 512; DB 5; Length 647;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPETTDLYXXQNLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
Db 550 MHGDTPLHEHYMDLQPETTDLYCYEQNLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 609
Qy 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVXPICSQKP 98
Db 610 CDSTLRLCVOSTHVDIRLTEDLMGTGIVCPICSQKP 647

RESULT 54

US-10-530-253-5
Sequence 5, Application US/10530253
Publication No. US20060014926A1

GENERAL INFORMATION:
APPLICANT: Casaretti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 248
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-10-530-253-5

Query Match 98.8%; Score 511; DB 5; Length 248;
Best Local Similarity 95.9%; Pred. No. 7.6e-53;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPETTDLYXXQNLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
Db 151 LHGDTPLHEHYMDLQPETTDLYCYEQNLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 210
Qy 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVXPICSQKP 98
Db 211 CDSTLRLCVOSTHVDIRLTEDLMGTGIVCPICSQKP 248

RESULT 55

US-10-530-253-3
Sequence 3, Application US/10530253
Publication No. US20060014926A1

GENERAL INFORMATION:
APPLICANT: Casaretti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03

NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 248
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-10-530-253-3

Query Match 98.6%; Score 510; DB 5; Length 248;
Best Local Similarity 95.9%; Pred. No. 1e-52;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPETTDLYXXQNLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
Db 151 LHGDTPLHEHYMDLQPETTDLYCYEQNLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 210
Qy 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVXPICSQKP 98
Db 211 CDSTLRLCVOSTHVDIRLTEDLMGTGIVCPICSQKP 248

RESULT 56

US-10-530-253-1
Sequence 1, Application US/10530253
Publication No. US20060014926A1

GENERAL INFORMATION:
APPLICANT: Casaretti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 248
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-10-530-253-1

Query Match 98.5%; Score 509; DB 5; Length 248;
Best Local Similarity 95.9%; Pred. No. 1.3e-52;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMDLQPETTDLYXXQNLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 60
Db 151 LHGDTPLHEHYMDLQPETTDLYCYEQNLNDSSEDEIDGPAGAEPPRAHYNIVTFCK 210
Qy 61 CDSTLRLCVOSTHVDIRLTEDLMGTGIVXPICSQKP 98
Db 211 CDSTLRLCVOSTHVDIRLTEDLMGTGIVCPICSQKP 248

RESULT 57

US-10-201-764-19
Sequence 19, Application US/10201764
Publication No. US20030166140A1

GENERAL INFORMATION:
APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: TBA
CURRENT APPLICATION NUMBER: US/10/201,764
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/566,420
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,752

;; PRIOR FILING DATE: 1999-05-06
;; PRIOR APPLICATION NUMBER: 60/132,750
;; PRIOR FILING DATE: 1999-05-06
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 19
;; LENGTH: 98
;; TYPE: PRT
;; ORGANISM: Human papillomavirus type E7
US-10-201-764-19

Query Match 98.1%; Score 507; DB 4; Length 98;
Best Local Similarity 95.9%; Pred. No. 7.4e-53;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60
Db 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60
Qy 61 CDSTLRCLCVOSTHVDIRLTEDLMLGTLGIYXPICSQKP 98
Db 61 CDSTLRCLCVOSTHVDIRLTEDLMLGTLGIYXPICSQKP 98

RESULT 58
US-10-681-410-19
;; Sequence 19, Application US/10681410
;; Publication No. US20040096426A1
;; GENERAL INFORMATION:
;; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
;; FILE REFERENCE: TBA
;; CURRENT APPLICATION NUMBER: US/10/681,410
;; CURRENT FILING DATE: 2003-10-08
;; PRIOR APPLICATION NUMBER: US/10/201,764
;; PRIOR FILING DATE: 2002-07-22
;; PRIOR APPLICATION NUMBER: US/09/566,420
;; PRIOR FILING DATE: 2000-05-05
;; PRIOR APPLICATION NUMBER: 60/132,752
;; PRIOR FILING DATE: 1999-05-06
;; PRIOR APPLICATION NUMBER: 60/132,750
;; PRIOR FILING DATE: 1999-05-06
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 19
;; LENGTH: 98
;; TYPE: PRT
;; ORGANISM: Human papillomavirus type E7
US-10-681-410-19

Query Match 98.1%; Score 507; DB 4; Length 98;
Best Local Similarity 95.9%; Pred. No. 7.4e-53;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60
Db 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60
Qy 61 CDSTLRCLCVOSTHVDIRLTEDLMLGTLGIYXPICSQKP 98
Db 61 CDSTLRCLCVOSTHVDIRLTEDLMLGTLGIYXPICSQKP 98

RESULT 59
US-10-484-063-26
;; Sequence 26, Application US/10484063
;; Publication No. US20050048467A1
;; GENERAL INFORMATION:
;; APPLICANT: SASSTRY, K. JAGANNADHA
;; APPLICANT: TORTOLEERO-LUNA, GUILLEMO
;; APPLICANT: FOLLEN, MICHELE
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

;; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
;; FILE REFERENCE: UTSC:560US
;; CURRENT APPLICATION NUMBER: US/10/484,063
;; CURRENT FILING DATE: 2004-01-16
;; PRIOR APPLICATION NUMBER: PCT/US02/23198
;; PRIOR FILING DATE: 2002-07-19
;; PRIOR APPLICATION NUMBER: 60/306,809
;; PRIOR FILING DATE: 2001-07-20
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 26
;; LENGTH: 98
;; TYPE: PRT
;; ORGANISM: Human papillomavirus type 16
US-10-484-063-26

Query Match 98.1%; Score 507; DB 5; Length 98;
Best Local Similarity 95.9%; Pred. No. 7.4e-53;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60
Db 1 MHGDPPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 60
Qy 61 CDSTLRCLCVOSTHVDIRLTEDLMLGTLGIYXPICSQKP 98
Db 61 CDSTLRCLCVOSTHVDIRLTEDLMLGTLGIYXPICSQKP 98

RESULT 60
US-10-472-724-4
;; Sequence 4, Application US/10472724
;; Publication No. US20040171806A1
;; GENERAL INFORMATION:
;; APPLICANT: Cid-Arregui, Angel
;; APPLICANT: Zur Hausen, Harald
;; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
;; FILE REFERENCE: 4121-154
;; CURRENT APPLICATION NUMBER: US/10/472,724
;; CURRENT FILING DATE: 2003-09-17
;; PRIOR APPLICATION NUMBER: PCT/EP02/03271
;; PRIOR FILING DATE: 2002-03-22
;; PRIOR APPLICATION NUMBER: EP 01107271.7
;; PRIOR FILING DATE: 2001-03-23
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: Patentin version 3.2
;; SEQ ID NO 4
;; LENGTH: 111
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic Construct
US-10-472-724-4

Query Match 98.1%; Score 507; DB 4; Length 111;
Best Local Similarity 96.9%; Pred. No. 8.6e-53;
Matches 94; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 HGDPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 61
Db 7 HGDPTLHEWMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAEPPRAHNYITVFCCK 66
Qy 62 DSTLRCLCVOSTHVDIRLTEDLMLGTLGIYXPICSQKP 98
Db 67 DSTLRCLCVOSTHVDIRLTEDLMLGTLGIYXPICSQKP 103

RESULT 61
US-10-392-113-29
;; Sequence 29, Application US/10392113
;; Publication No. US20030224993A1
;; GENERAL INFORMATION:
;; APPLICANT: Land, Hartmut

```
APPLICANT: Deleu, Laurent
TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
FILE REFERENCE: 21108.000503
CURRENT FILING DATE: 2003-03-17
PRIORITY FILING DATE: 2003-03-17
PRIORITY FILING DATE: 2002-03-15
PRIORITY FILING DATE: 2001-10-15
PRIORITY FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 98
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/Note =
US-10-392-113-29
```

```
Query Match          97.5%; Score 504; DB 4; Length 98;
Best Local Similarity 95.9%; Pred. No. 1.7e-52;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEMYMDLOPETTDLYXXQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEMYMDLOPETTDLYCYEQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Dy 61 CDSTLRLCVOSTHVDIRTLLEDLMGTGIVCPICSOXP 98
Db 61 CDSTLRLCVOSTHVDIRTLLEDLMGTGIVCPICSOXP 98
```

```
RESULT 62
US-10-267-311-8
Sequence 8, Application US/10267311
Publication No. US20030050469A1
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT FILING DATE: 2002-10-09
PRIORITY FILING DATE: 2002-10-09
PRIORITY FILING DATE: 2000-07-10
PRIORITY FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 98
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-267-311-8
```

```
Query Match          97.3%; Score 503; DB 4; Length 98;
Best Local Similarity 95.9%; Pred. No. 2.2e-52;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEMYMDLOPETTDLYXXQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEMYMDLOPETTDLYCYEQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Dy 61 CDSTLRLCVOSTHVDIRTLLEDLMGTGIVCPICSOXP 98
Db 61 CDSTLRLCVOSTHVDIRTLLEDLMGTGIVCPICSOXP 98
```

```
RESULT 63
US-10-679-956-8
Sequence 8, Application US/10679956
Publication No. US20050089841A1
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT FILING DATE: 2003-10-06
PRIORITY FILING DATE: 2003-10-06
PRIORITY FILING DATE: 2000-07-10
PRIORITY FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 98
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-679-956-8
```

```
Query Match          97.3%; Score 503; DB 5; Length 98;
Best Local Similarity 95.9%; Pred. No. 2.2e-52;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEMYMDLOPETTDLYXXQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEMYMDLOPETTDLYCYEQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Dy 61 CDSTLRLCVOSTHVDIRTLLEDLMGTGIVCPICSOXP 98
Db 61 CDSTLRLCVOSTHVDIRTLLEDLMGTGIVCPICSOXP 98
```

```
RESULT 64
US-10-267-311-29
Sequence 29, Application US/10267311
Publication No. US20030050469A1
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT FILING DATE: 2002-10-09
PRIORITY FILING DATE: 2002-10-09
PRIORITY FILING DATE: 2000-07-10
PRIORITY FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 648
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-267-311-29
```

```
Query Match          97.3%; Score 503; DB 4; Length 648;
Best Local Similarity 95.9%; Pred. No. 2.3e-51;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 MHGDTPLHEMYMDLOPETTDLYXXQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Dy 1 MHGDTPLHEMYMDLOPETTDLYCYEQNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
```

Db 1 MDGDTPLHEHYMLDLPETTDLYCYEQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Qy 61 CDSTRLCVOSTHVDIRTLIEDLMGTGIVXPCISQKP 98
Db 61 CDSTRLCVOSTHVDIRTLIEDLMGTGIVCPCISQKP 98

RESULT 65
US-10-679-956-29
; Sequence 29, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-679-956-29

Query Match 97.3%; Score 503; DB 5; Length 648;
Best Local Similarity 95.9%; Pred. No. 2.3e-51;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMLDLPETTDLYXXYQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MDGDTPLHEHYMLDLPETTDLYCYEQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Qy 61 CDSTRLCVOSTHVDIRTLIEDLMGTGIVXPCISQKP 98
Db 61 CDSTRLCVOSTHVDIRTLIEDLMGTGIVCPCISQKP 98

RESULT 66
US-10-267-311-41
; Sequence 41, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-41

Query Match 97.3%; Score 503; DB 4; Length 711;

Best Local Similarity 95.9%; Pred. No. 2.6e-51;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMLDLPETTDLYXXYQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MDGDTPLHEHYMLDLPETTDLYCYEQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Qy 61 CDSTRLCVOSTHVDIRTLIEDLMGTGIVXPCISQKP 98
Db 61 CDSTRLCVOSTHVDIRTLIEDLMGTGIVCPCISQKP 98

RESULT 67
US-10-679-956-41
; Sequence 41, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-679-956-41

Query Match 97.3%; Score 503; DB 5; Length 711;
Best Local Similarity 95.9%; Pred. No. 2.6e-51;
Matches 94; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMLDLPETTDLYXXYQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MDGDTPLHEHYMLDLPETTDLYCYEQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Qy 61 CDSTRLCVOSTHVDIRTLIEDLMGTGIVXPCISQKP 98
Db 61 CDSTRLCVOSTHVDIRTLIEDLMGTGIVCPCISQKP 98

RESULT 68
US-10-267-311-45
; Sequence 45, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-45

```

Query Match	97.3%	Score 503	DB 4	Length 724
Best Local Similarity	95.9%	Pred. No. 2.6e-51		
Matches 94; Conservative	0	Mismatches 4	Indels 0	Gaps 0

DQ 1 MHGDIPTLHEWMLDLPETTDLYXXYQLNDSSSEDEIDGPAGQAHPDRAHYNIIVTFCKK 60
 |||||
DP 1 MDGDPTLHEWMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAHPDRAHYNIIVTFCKK 60

[illegible]

RESULT 69
US-10-679

US-10-679-956-45
; Sequence 45, Application US/10679956
; Publication No. US20050089841A1
Journal INFORMATION

Query Match	97.3%	Score 503	DB 51	Length 724
Best Local Similarity	95.9%	Pred No. 2.6e-51		
Matches 94	Conservative 0	Mismatches 4	Indels 0	Gaps 0

QY 1 MHGDFPTLHEHYMLDLOPETTDLYXXYQLNDSSSEEDIDSPAGQAPDRAHYNIIVTFCK 600

Db 1 MDGDFPTLHEHYMLDLOPETTDLYCYEQNLNDSSSEEDIDSPAGQAPDRAHYNIIVTFCK 600

Qy 61 CQSTLRICVQSTHVDIRTELEDMGTGIVPICSKKP 98
|||
Db 61 CQSTLRICVQSTHVDIRTELEDMGTGIVPICSKKP 98

```

RESULT 70
US-10-115-440-7
: Sequence 7, Application US/10115440
: Publication No. US20040086845A1
: GENERAL INFORMATION:
: APPLICANT: WU, Tzy-Choon
: APPLICANT: HUNG, Chien-Fu
: TITLE OF INVENTION: SUPERIOR MOLECULAR VACCINE LINKING THE TRANSLLOCATION DOMAIN OF A
: TITLE OF INVENTION: BACTERIAL TOXIN TO AN ANTIGEN

```

;; PRIOR FILING DATE: 2000-02-09
;; PRIOR APPLICATION NUMBER: US 09/421,608
; PRIOR FILING DATE: 1999-10-20

Query Match	96.7%;	Score 500;	DB 4;	Length 99;
Best Local Similarity	96.9%;	Pred. No. 5,2e-52;		
Matches 93; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 1 MHGDPPTLHEYMLDLOPETTDLYXXYXQUNDSSSEDEIDGPAGQAEPRRAHNYIVTFCKK 600

Db 1 MHGDPPTLHEYMLDLOPETTDLYCYEQLUNDSSSEDEIDGPAGQAEPRRAHNYIVTFCKK 600

```

QY      61 CDSILRLCYGVSTHVDIRILEDLNGTIGIIVPICSQ 96
        |||||
DB      61 CDSILRLCYGVSTHVDIRILEDLNGTIGIIVPICSQ 96

```

RESULT 71
US-10-115

US-10-115-440-5
; Sequence 5, Application US/10115440
; Publication No. US20040086845A1
CURRENT INFORMATION

Query Match	96.7%;	Score 500;	DB 4;	Length 289;
Best Local Similarly	96.9%;	Pred. NO. 1.9e-51;		
Matches 93;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

[illegible]

QY	61	CDSTLRKCVQSTHVDIRITLEDLNGTGLVXPICQ	96
Db	234	CDSTLRKCVQSTHVDIRITLEDLNGTGLVCPICQ	263

RESULT 72
US-11-072-268-2
; Sequence 2, Application US/11072288
; Publication No. US20050159386A1
; GENERAL INFORMATION:
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: BALLOU, Jean-Marc
; APPLICANT: BIZOURNE, Nadine

TITLE OF INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNOGENIC
 TITLE OF INVENTION: POLYPEPTIDE WITH MODIFIED CELL LOCATION
 FILE REFERENCE: 017753-122
 CURRENT APPLICATION NUMBER: US/11/072,288
 CURRENT FILING DATE: 2005-03-07
 PRIOR APPLICATION NUMBER: US/09/462,993
 PRIOR FILING DATE: 2000-04-17
 PRIOR APPLICATION NUMBER: PCT/FR98/01576
 PRIOR FILING DATE: 1998-07-17
 PRIOR APPLICATION NUMBER: FR 97/09152
 PRIOR FILING DATE: 1997-07-18
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: PatentIn Ver. 2.2
 SEQ ID NO 2
 LENGTH: 185
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Derived from human papillomavirus, strain
 OTHER INFORMATION: HPV-16, E7 fusion signals of the rabies
 OTHER INFORMATION: glycoprotein, clone E7-TMR.
 US-11-072-288-2

Query Match	92.5%	Score 478;	DB 6;	Length 185;
Best Local Similarity	92.9%	Pred. No. 5e-49;		
Matches	91;	Conservative	0;	Mismatches 1;
				Indels 6;
				Gaps 1;

```
Oy      1 MHGDFPTLHEXWLDQRETTDLYXXYKQLNDSSEDEIGBPAGQAEPDRAHNYIVTFCK 60  
        |||||  
Db      26 MHGDFPTLHEXWLDQRETT-----QLNDSSEDEIDGPAGQAEPDRAHNYIVTFCK 79
```

Qy	61	CDSTLR	CVQSTH	VDIR	LTLEDL	MGTL	GI	VPIC	SQKP	98
Db	80	CDSTLR <td>CVQSTH <td>VDIR <td>LTLEDL <td>MGTL <td>GI <td>VPIC <td>SQKP</td> <td>117</td> </td></td></td></td></td></td>	CVQSTH <td>VDIR <td>LTLEDL <td>MGTL <td>GI <td>VPIC <td>SQKP</td> <td>117</td> </td></td></td></td></td>	VDIR <td>LTLEDL <td>MGTL <td>GI <td>VPIC <td>SQKP</td> <td>117</td> </td></td></td></td>	LTLEDL <td>MGTL <td>GI <td>VPIC <td>SQKP</td> <td>117</td> </td></td></td>	MGTL <td>GI <td>VPIC <td>SQKP</td> <td>117</td> </td></td>	GI <td>VPIC <td>SQKP</td> <td>117</td> </td>	VPIC <td>SQKP</td> <td>117</td>	SQKP	117

```

RESULT 73
US-10-530-253-30
; Sequence 30, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Cassecci, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Human papillomavirus type 35
US-10-530-253-30

```

Query Match	73.8%;	Score 381.5;	DB 5;	Length 99;
Best Local Similarity	73.5%;	Pred. No. 9.4e-38;		
Matches 72; Conservative	11;	Mismatches 14;	Indels 1;	Gaps 1;

```
Oy      1 MHGDFPTLHEXMLDLOBETTDLDXXYXQLNDS-EEDELDGPAGCAEPDRAHYNIVTFCC 59  
        ||| : | : ||| : | | | | | | | | | | | | | | | | : ||| | |  
Db      1 MHGETTLQDYVLDLEBEATDLCYEQLCDSSSEEBEDTIDGPAGCAKPTSNINIVTSCC 60
```

```
Qy      60 KCDSTLRLCVQSTHVDIRLTEDLLMGTLGIVXPICSQK 97
      ||::|||||:|||||:|||||:|||||:
Db      61 KCEATLRLCVQSTHVDIRKLEDDLLMGTGIVCPGCSQR 98
```

RESULT 74

```

: Sequence: 28, Application US/10530253
: Publication No. US20060014926A1
: GENERAL INFORMATION:
: APPLICANT: Casasetti, Maria C.
: APPLICANT: Smith, Larry
: APPLICANT: Jeffrey K. Pullen
: APPLICANT: Susan P. McElhinney
: TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
: FILE REFERENCE: 00630/100M137-US2
: CURRENT APPLICATION NUMBER: US/10/530,253
: CURRENT FILING DATE: 2005-04-04
: PRIOR APPLICATION NUMBER: PCT/US2003/031726
: PRIOR FILING DATE: 2003-10-02
: PRIOR APPLICATION NUMBER: US 60/415,929
: PRIOR FILING DATE: 2002-10-03
: NUMBER OF SEQ ID NOS: 65
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 28
: LENGTH: 98
: TYPE: PRT
: ORGANISM: Human papillomavirus type 31
: US-10-530-253-28

```

Query Match	72.0%;	Score 372;	DB 5;	length 98;
Best Local Similarity	71.1%;	Pred. No. 1.3e-36;		
Matches 69;	Conservative 12;	Mismatches 16;	Indels 0;	Gaps 0;

```
QY      1 MHGDTPTLHXYMLDLOPETTDLYXXYXOLNDSSEDEIDGPAGCAEPDRAHINYITFCCK 600
      | : | | | : | | | | | | | : | | | | | | | | | | | | | | | : | | | | | :
Db      1 MRGEIPTLODYVLDLOPEATIDHCYEOLPDSSSEEDVIDSPAGCAEPDRTSNINYITFCCK 600
```

```
QY      61 CDSTLRICVQSTHYDIRTLEDLLMGTLGIVXPCISQK 97
      | | | | | | | | | | : | | | | | | | :
Db      61 CKSTLRICVQSTHYDIRILOELMGSPGIVCNCSTR 97
```

```

RESULT 75
US-10-530-253-29
: Sequence 29, Application US/10530253
: Publication No. US20060014926A1
: GENERAL INFORMATION:
: APPLICANT: Cassecci, Maria C.
: APPLICANT: Smith, Larry
: APPLICANT: Jeffrey K. Pullen
: APPLICANT: Susan P. McElhinney
: TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
: FILE REFERENCE: 00630/100M137-US2
: CURRENT APPLICATION NUMBER: US/10/530,253
: CURRENT FILING DATE: 2005-04-04
: PRIOR APPLICATION NUMBER: PCT/US2003/031726
: PRIOR FILING DATE: 2003-10-02
: PRIOR APPLICATION NUMBER: US 60/415,929
: PRIOR FILING DATE: 2002-10-03
: NUMBER OF SEQ ID NOS: 65
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 29
: LENGTH: 97
: TYPE: PRT
: ORGANISM: Human papillomavirus type 33
US-10-530-253-29

```

Query Match	57.1%;	Score 295;	DB 5;	length 97;
Best Local Similarity	57.7%;	Pred. No. 2.3e-27;		
Matches	56;	Conservative	25;	Indels 0;
		Mismatches	25;	Gaps 0;

QY

1 MGGDTPTLHXYMLDLPETTDLYXXYYXQLNDSSEEDRIDGPAGOAEPDRAHYNIVTFCKK 60
| | ||| :||| | ||| | ||| : : : | ||| | ||| |
1 MRGHPPTLKRYVLDLYPEPTDLYCYEOLSDSSDEDEGLDRPDGOAPADAYIYTTCCHT 60

Db

61 CDSTRLCVQSTHVDIRLTLEDLMGTGIVXPICSQK 97

Db 61 CATTIVRLCVNSTASDLRTIQQLLMGIVNIVCPTCAQQ 97

RESULT 76
US-10-530-253-34

; Sequence 34, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530, 253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Human papillomavirus type 52
US-10-530-253-34

Query Match 56.9%; Score 294; DB 5; Length 99;
Best Local Similarity 57.1%; Pred. No. 3.2e-27;
Matches 56; Conservative 17; Mismatches 23; Indels 2; Gaps 1;

Qy 1 MHGDTPLHEMYMDLQ-PEETDLYXXYQXNDSSSEED--IDGPAGQAPPPRAHNYIVTFC 58
Db 1 MRRGKATIKDYIIDLQ-ETDTHCYEQDGSDEEDTDGVDPRPGQAEQATSNYYIVTTC 60

Qy 59 CKDSTRLCVQSTHVDIRITLEDLMGTGIVXPICQ 96
Db 61 HSCDSTRLCINHTATDRLTQQLGLGVCPGCR 98

RESULT 77
US-10-530-253-36

; Sequence 36, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530, 253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type 58
US-10-530-253-36

Query Match 56.0%; Score 289.5; DB 5; Length 98;
Best Local Similarity 57.1%; Pred. No. 1.1e-26;
Matches 56; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MHGDTPLHEMYMDLQ-PEETDLYXXYQXNDSSSEED--IDGPAGQAPPPRAHNYIVTFC 59
Db 1 MRRGKATIKDYIIDLQ-ETDTHCYEQDGSDEEDTDGVDPRPGQAEQATSNYYIVTTC 60

Db 1 MRRGKATIKDYIIDLQ-PEETDLYXXYQXNDSSSEED--IDGPAGQAPPPRAHNYIVTFC 60
Qy 60 CKDSTRLCVQSTHVDIRITLEDLMGTGIVXPICQ 97
Db 61 TCGIVRLCINSTYTDVRLTQQLMGITCTIVCPSCAQ 98

RESULT 78
US-10-367-057-12

; Sequence 12, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cutbill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 12
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-12

Query Match 47.4%; Score 245; DB 5; Length 98;
Best Local Similarity 53.0%; Pred. No. 2.5e-21;
Matches 53; Conservative 14; Mismatches 29; Indels 4; Gaps 3;

Qy 1 MHGDTPLHEMYMDLQ-PEETDLYXXYQXNDSSSEED--DEIDGPAGQAPPPRAHNYIVTFC 58
Db 1 MRRGKATIKDYIIDLQ-ETDTHCYEQDGSDEEDTDGVDPRPGQAEQATSNYYIVTTC 60

Qy 59 CKDSTRLCVQSTHVDIRITLEDLMGTGIVXPICQ 98
Db 59 CGCDNVRLVVECTDGIROLQDLGLTINIVCPICAPKP 98

RESULT 79
US-10-751-845-126

; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Artificial fusion sequence
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match 41.6%; Score 215; DB 5; Length 117;
Best Local Similarity 52.2%; Pred. No. 1.2e-17;

```
Matches 48; Conservative 0; Mismatches 2; Indels 42; Gaps 2;
Qy 7 TLHEYMDLPETTDLYXXYQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCKCDSTLR 66
Db 68 TLHEYMDLPETTDLYSY-----QAEPRAHYNIIVTF----- 100
Qy 67 LCQSTHVDIRTLLEDLMGTIGIVPICSQKP 98
Db 101 -----LIMGTLGIVCPICSQKP 117

RESULT 80
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 41.6%; Score 215; DB 5; Length 236;
Best Local Similarity 52.2%; Pred. No. 3e-17;
Matches 48; Conservative 0; Mismatches 2; Indels 42; Gaps 2;
Qy 7 TLHEYMDLPETTDLYXXYQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCKCDSTLR 66
Db 68 TLHEYMDLPETTDLYSY-----QAEPRAHYNIIVTF----- 100
Qy 67 LCQSTHVDIRTLLEDLMGTIGIVPICSQKP 98
Db 101 -----LIMGTLGIVCPICSQKP 117

RESULT 81
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158

Matches 48; Conservative 0; Mismatches 2; Indels 42; Gaps 2;
Qy 7 TLHEYMDLPETTDLYXXYQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCKCDSTLR 66
Db 68 TLHEYMDLPETTDLYSY-----QAEPRAHYNIIVTF----- 100
Qy 67 LCQSTHVDIRTLLEDLMGTIGIVPICSQKP 98
Db 101 -----LIMGTLGIVCPICSQKP 117

RESULT 82
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 41.6%; Score 215; DB 5; Length 261;
Best Local Similarity 52.2%; Pred. No. 3.3e-17;
Matches 48; Conservative 0; Mismatches 2; Indels 42; Gaps 2;
Qy 7 TLHEYMDLPETTDLYXXYQLNDSSEDEIDGPAGQAEPRAHYNIIVTFCKCDSTLR 66
Db 93 TLHEYMDLPETTDLYSY-----QAEPRAHYNIIVTF----- 125
Qy 67 LCQSTHVDIRTLLEDLMGTIGIVPICSQKP 98
Db 126 -----LIMGTLGIVCPICSQKP 142

RESULT 83
US-10-530-253-32
; Sequence 32, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M17-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
```



```

:
: CURRENT FILING DATE: 2005-04-04
: PRIOR APPLICATION NUMBER: PCT/US2003/091726
: PRIOR FILING DATE: 2003-10-02
: PRIOR APPLICATION NUMBER: US 60/415,929
: PRIOR FILING DATE: 2002-10-03
: NUMBER OF SEQ ID NOS: 65
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 32
:   LENGTH: 106
:   TYPE: prt
: ORGANISM: Human papillomavirus type 45
: US-10-530-253-32

```

Query Match	41.2%	Score 213	DB 5;	length 106;
Best Local Similarity	43.8%	Pred. No. 1.9e-17;		
Matches 46;	Conservative 15;	Mismatches 32;	Indels 12;	Gaps 3

```

OY      1 MHGDTTLHEHWLMDLOPET----TDLXXXXQNDSSSEEBEIDG-----PAGQAEPRDA 50
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      1 MHGPRETLQEIVLHLEPQNDLPVDLLCYEQLSSEEBEENDEADGVSHAQLTPARRAEQR- 59

```

```

Oy      51 HNYIVTFCCKDSTLRKLVQSTHVDIRITLEDLLMGTLGIVXPICS 95
        :|: ||||| :|:|: |:|||:|: ||| |:|:
Db      60 -HKILCVCKCDGRITLVSSAEDRLTQLFLSTLSFVCPWCA 103

```

```

RESULT 84
US-10-433-091-4
: Sequence 4, Application US/10433091
: Publication No. US20040101535A1
: GENERAL INFORMATION:
: APPLICANT: MULLER, RAINER
: APPLICANT: NIELAND, JOHN
: APPLICANT: GABELSBERGER, JOSEF
: APPLICANT: HERBST, RUTH
: TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
: TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS TYPE 18
: FILE REFERENCE: 037067/0115
: CURRENT APPLICATION NUMBER: US/10/433,091
: CURRENT FILING DATE: 2003-11-25
: PRIOR APPLICATION NUMBER: PCT/EP01/14038
: PRIOR FILING DATE: 2001-11-30
: PRIOR APPLICATION NUMBER: DE 100 59 630.4
: PRIOR FILING DATE: 2000-12-01
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 105
: TYPE: PR1
: ORGANISM: Human papillomavirus type 18
US-10-433-091-4

```

Query Match	39.2%	Score 202.5	DB 4	Length 105
Best Local Similarity	39.6%	Pred. No. 3.5e-16		
Matches 42	Conservative 21	Mismatches 32	Indels 11	Gaps 3

```

Oy      1 MHGDTPLHEWMLDLQPET---TDLYXXYQLNDSEEBDELDG-----PAGQAEPRRAH 51
      ||| : : : : ||| : : : : ||| : : : : ||| : : : :
Db      1 MHGPKATLQDILVHLEPQNEIPVDLLCHEQSDSEENDELDGVNHQLPARAEPR-- 56

```

QY 52 YNIVTFCKCDSTLRLCVGFTHVDIRTEDELLMGILGIVXPICBQK 97
::|||:::||::||::||::||
DB 59 HTMLCMCKCEARIKLVNESSADDLRAFGQLFLNTLTSFVCPCWCSAQ 104

```

RESULT 85
US-10-530-253-27
; Sequence 27, Application US/10530255-27
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casaretti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen

```

```

1  APPLICANT: Susan P. McElhinney
2  TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
3  FILE REFERENCE: 00630/100m137-US2
4  CURRENT APPLICATION NUMBER: US/10/530,253
5  CURRENT FILING DATE: 2005-04-04
6  PRIOR APPLICATION NUMBER: PCT/US2003/031726
7  PRIOR FILING DATE: 2003-10-02
8  PRIOR APPLICATION NUMBER: US 60/415,929
9  PRIOR FILING DATE: 2002-10-03
10 NUMBER OF SEQ ID NOS: 65
11 SOFTWARE: PatentIn version 3.1
12 SEQ ID NO 27
13     LENGTH: 105
14     TYPE: PRT
15 ORGANISM: Human papillomavirus type 18
16 US-10-530-253-27

```

Query Match	39.2%;	Score 202.5;	DB 5	Length 105;
Best Local Similarity	39.6%;	Prod. No. 3.5e-16;		
Matches	42;	Conservative	21;	Mismatches 32;
				Indels 11;
				Gaps 3

```

QY      1 MHGDPPTLHEMLDLQPET---TDLYXXXXQLNDSSEBEIDG-----PAGQAEPPRAH 5
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      1 MHGPRTLQDVLVLTLPQNEIFVDLLCHEQLSDSEEBENDEIDGVNHQHLPRARAEPR-- 56

```

QY 52 YNITFECCKDSTLRCLCQSTHVDIRTLBEDLMGTGIVXPCISQK 97
::|||:::||::|::|::|::|::|:
Db 59 HTMLCMCKCEARIKLVESSADDLRAFOQLFLNTLSFVCPWCASQ 104

```

RESULT 86
US-10-000-903-19
? Sequence 19, Application US/10000903
? Publication No. US20020182221A1
? GENERAL INFORMATION:
? APPLICANT: Bruck, Claudine
? APPLICANT: Cabezon Silva, Teresa
? APPLICANT: Delisse, Anne-Marie Eva Bernande
? APPLICANT: Gerard, Catherine Marie Ghislaine
? APPLICANT: Lombardo-Bencheikh, Angela
? TITLE OF INVENTION: Vaccine
? FILE REFERENCE: B45107
? CURRENT APPLICATION NUMBER: US/10/000,903
? CURRENT FILING DATE: 2001-10-01
? PRIOR APPLICATION NUMBER: PCT/EP98/05285
? PRIOR FILING DATE: 1998-08-17
? PRIOR APPLICATION NUMBER: GB 9717953.5
? PRIOR FILING DATE: 1997-08-22
? NUMBER OF SEQ ID NOS: 23
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 19
? LENGTH: 227
? TYPE: PR1
? ORGANISM: Homo sapien
US-10-000-903-19

```

Query Match	39.0%	Score 201.5	DB 4	Length 227
Best Local Similarity	39.6%	Pred. No. 1.2e-15		
Matches 42	Conservative 20	Mismatches 33	Indels 11	Gaps 3

```

QY      1 MHGDTPTLHYMLDQPET---TDLYXXQJNDSSSEDEIDG-----PAGAAEPDRAH 51
      |||  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :  |||  :
Db      114 MHGRATLDQIVLHLEPQNEIPVDLLGHQQSDSSEENDEIDGVNHQLPAAEAEPQR-- 174

```

```

QY      52 YNIVFCCCKDSTRLRCQVSTHVDIRTEDELMGTLGIVXPICSOQ 97
        : :: |||:: : |::: |::: |::: |::: |::: |:::
DB      172 HTMLCMCKCEARIELVVESSADDLRAFOQLFLINTLSFVCPWCASQ 217

```

RESULT 87
US-10-899-771-19
; Sequence 19, Application US/10899771
; Publication No. US20050031638A1

```

; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a Cpg Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899, 771
; PRIOR FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581, 976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and mutated E7 from Human papilloma
; OTHER INFORMATION: virus type 18)
; US-10-899-771-19

```

```

Query Match          39.0%; Score 201.5; DB 5; Length 227;
Best Local Similarity 39.6%; Pred. No. 1.2e-15;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

```

```

Qy 1 MHGDPPLHEMYMLDLOPET---TDLYXXYXQOLNDSSEEDIDG-----PAGQAEPPRAH 51
Db 114 MHGKATLQDVLHLEPQNEIPVDLGHQQLSDSEENDEIDGVNHQHLPARRAEPQR-- 171

```

```

Qy 52 YNIVTFCCKDSTRLCVQSTHVDIRTLIEDLMLGTGIVXPISQK 97
Db 172 HTMLCMCKCEARIELVVESSADDLRAFOQLFNTLSFVCPWCASQ 217

```

```

RESULT 88
US-10-000-903-23
; Sequence 23, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000, 903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-000-903-23

```

```

Query Match          38.8%; Score 200.5; DB 4; Length 383;
Best Local Similarity 39.6%; Pred. No. 3e-15;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

```

```

Qy 1 MHGDPPLHEMYMLDLOPET---TDLYXXYXQOLNDSSEEDIDG-----PAGQAEPPRAH 51
Db 270 MHGKATLQDVLHLEPQNEIPVDLGHQQLSDSEENDEIDGVNHQHLPARRAEPQR-- 327

```

```

Qy 52 YNIVTFCCKDSTRLCVQSTHVDIRTLIEDLMLGTGIVXPISQK 97
Db 328 HTMLCMCKCEARIELVVESSADDLRAFOQLFNTLSFVCPWCASQ 373

```

```

RESULT 89
US-10-899-771-23
; Sequence 23, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a Cpg Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899, 771
; PRIOR FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581, 976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 18)
; US-10-899-771-23

```

```

Query Match          38.8%; Score 200.5; DB 5; Length 383;
Best Local Similarity 39.6%; Pred. No. 3e-15;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

```

```

Qy 1 MHGDPPLHEMYMLDLOPET---TDLYXXYXQOLNDSSEEDIDG-----PAGQAEPPRAH 51
Db 270 MHGKATLQDVLHLEPQNEIPVDLGHQQLSDSEENDEIDGVNHQHLPARRAEPQR-- 327

```

```

Qy 52 YNIVTFCCKDSTRLCVQSTHVDIRTLIEDLMLGTGIVXPISQK 97
Db 328 HTMLCMCKCEARIELVVESSADDLRAFOQLFNTLSFVCPWCASQ 373

```

```

RESULT 90
US-10-800-023-28
; Sequence 28, Application US/10800023
; Publication No. US20040258688A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Ralph
; APPLICANT: Nussenzweig, Michel
; APPLICANT: Hawiger, Daniel
; APPLICANT: Bonifaz, Laura
; TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
; TITLE OF INVENTION: of the Immune Response Therefrom
; FILE REFERENCE: 600-1-081CONCIP1
; CURRENT APPLICATION NUMBER: US/10/800, 023
; CURRENT FILING DATE: 2004-03-14
; PRIOR APPLICATION NUMBER: 09/925, 284
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/586, 704
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: PCT/US96/01383
; PRIOR FILING DATE: 1996-01-31
; PRIOR APPLICATION NUMBER: 08/381, 528
; PRIOR FILING DATE: 1995-01-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28

```

[illegible]

```

US-10-530-253-37
Query Match      37.8%; Score 195.5; DB 5; Length 107;
Best Local Similarity 43.4%; Pred. No. 2.5e-15;
Matches 46; Conservative 17; Mismatches 30; Indels 13; Gaps 4;

Qy      1 MHGPRPTLHEXYMLDLP---ETDLYXXYXOL--NDSSSEEDIDGP-----ACQAEPDR 49
       ||| :|||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 1:|||||
Db      1 MHGPRATLCDVLVDPEPNTVEVDLVCEQLPSDSSEKEXEKPVGVAHPLLARAEQR 60
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:

Qy      50 AHNVVTFCKCSDTLRLCVOSTHVDIRTELDLMGLTGIYXPICS 95
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      61 --HNIVCVCKCNNOQLGVETSGDLRALQQLFMDLTLSFVCPCIA 104

RESULT 93
US-10-472-724-8
; Sequence 8, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271..7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-8

Query Match      37.8%; Score 195.5; DB 4; Length 118;
Best Local Similarity 39.0%; Pred. No. 2.8e-15;
Matches 41; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

Qy      2 HGDPTLHEXYMLDLPET--TDLYXXYLNDSSSEBDEIDG-----PAQAEPDRAY 52
       ||| :|||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 1:|||||
Db      7 HGPRATLCDVLVDPEPNTVEVDLVCEQLPSDSSEKEXEKPVGVAHPLLARAEQR--H 64
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:

Qy      53 NIVTFCKCSDTLRLCVOSTHVDIRTELDLMGLTGIYXPICSO 97
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      65 TMLCWCKCEARIELVRESSADLRAPQOLFMTLSFVCPCWCAQO 109

RESULT 94
US-10-000-903-16
; Sequence 16, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Benchekh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0

```

SEQ ID NO 16
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-16

Query Match 37.2%; Score 192.5; DB 4; Length 227;
Best Local Similarity 38.7%; Pred. No. 1.4e-14;
Matches 41; Conservative 20; Mismatches 34; Indels 11; Gaps 3;

QY 1 MHGDTPTLHEMYLDLOPET---TDLYXXYQLNDSSEDEIDG-----PAGQAEPPRAH 51
DB 114 MHGKATLQDVLVLEPQNEIPVDLCHESQLDSSEENDEIDEVNHQHLPARRAEPOR-- 171

QY 52 YNITPCKCDSTRLCVQSTHVDIRTELDLMTGLGIVXPICSOX 97
DB 172 HTMLCMCKCEARIELVVESSADDLRARQQLPLNTLSFVCPWCASQ 217

RESULT 95

US-10-899-771-16
Sequence 16; Application US/10899771
Publication No. US20050031638A1
GENERAL INFORMATION:

APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a Cpg Oligonucleotide
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16

LENGTH: 227
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
OTHER INFORMATION: Influenza B and E7 from Human papilloma virus type
OTHER INFORMATION: 18)
US-10-899-771-16

Query Match 37.2%; Score 192.5; DB 5; Length 227;
Best Local Similarity 38.7%; Pred. No. 1.4e-14;
Matches 41; Conservative 20; Mismatches 34; Indels 11; Gaps 3;

QY 1 MHGDTPTLHEMYLDLOPET---TDLYXXYQLNDSSEDEIDG-----PAGQAEPPRAH 51
DB 114 MHGKATLQDVLVLEPQNEIPVDLCHESQLDSSEENDEIDEVNHQHLPARRAEPOR-- 171

QY 52 YNITPCKCDSTRLCVQSTHVDIRTELDLMTGLGIVXPICSOX 97
DB 172 HTMLCMCKCEARIELVVESSADDLRARQQLPLNTLSFVCPWCASQ 217

RESULT 96

US-10-530-253-35
Sequence 35; Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:

APPLICANT: Casasetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2

CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 105
TYPE: PRT
ORGANISM: Human papillomavirus type 56
US-10-530-253-35

Query Match 34.5%; Score 178.5; DB 5; Length 105;
Best Local Similarity 40.8%; Pred. No. 2.7e-13;
Matches 42; Conservative 17; Mismatches 35; Indels 9; Gaps 3;

QY 1 MHGDTPTLHEMYLDLOPET-TDLYXXYQLNDSSEDEIDGAPGQAEPPRAH-----Y 52
DB 1 MHGKATLQDVLVLEPQNEIPVDLCHESQLDSSEENDEIDEVNHQHLPARRAEPOR-- 171

QY 53 YNITPCKCDSTRLCVQSTHVDIRTELDLMTGLGIVXPICSOX 95
DB 60 LHVPCCECKRFVYQLDIQSTKEDLRVYQQLMGALVTVCPLCA 102

RESULT 97

US-10-530-253-33
Sequence 33; Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:

APPLICANT: Casasetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Susan P. McElhinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33
LENGTH: 101
TYPE: PRT
ORGANISM: Human papillomavirus type 51
US-10-530-253-33

Query Match 34.4%; Score 178; DB 5; Length 101;
Best Local Similarity 41.0%; Pred. No. 2.9e-13;
Matches 41; Conservative 16; Mismatches 37; Indels 6; Gaps 3;

QY 1 MHGDTPTLHEMYLDLOPET-TDLYXXYQLNDSSEDEIDGAPGQAEPPRAH-----YNIV 55
DB 1 MHGKATLQDVLVLEPQNEIPVDLCHESQLDSSEENDEIDEVNHQHLPARRAEPOR-- 171

QY 56 YNITPCKCDSTRLCVQSTHVDIRTELDLMTGLGIVXPICSOX 95
DB 60 APCRCSSVVQLAVESGDTLRVYQQLMGELSLVCPCCA 99

QY 56 YNITPCKCDSTRLCVQSTHVDIRTELDLMTGLGIVXPICSOX 95
DB 60 APCRCSSVVQLAVESGDTLRVYQQLMGELSLVCPCCA 99

RESULT 98

US-10-530-253-31
Sequence 31; Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:

APPLICANT: Casasetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen

```
; APPLICANT: Susan P. McElhiney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Human papillomavirus type 39
; US-10-530-253-31

Query Match          32.9%; Score 170; DB 5; Length 109;
Best Local Similarity 39.1%; Pred. No. 3e-12;
Matches 43; Conservative 16; Mismatches 31; Indels 20; Gaps 4;

QY 1 MHGDTPLHRYMDLQF---ETTDLYXXYQLNDSSEEDIDGP-----AGQA 45
DB 1 MRGKPTLQEIIVDLCPYNEIQPDVLCVHQGLGES---EDEIDPDHANNHQLLRD 57
QY 46 EPDRAHNYITFCCKDSTLRCLCVQSTHVDIRLTEDLMTGLGIYXPIC 95
DB 58 EPQR--HTIQSCCKCNNTLQLVVEASRDTRLQQLFMDSLGFVCPWCA 105

RESULT 99
US-10-530-253-38
; Sequence 38, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Cassetti, Maria C.
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhiney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Human papillomavirus type 68
; US-10-530-253-38

Query Match          31.8%; Score 164.5; DB 5; Length 110;
Best Local Similarity 34.0%; Pred. No. 1.4e-11;
Matches 36; Conservative 20; Mismatches 39; Indels 11; Gaps 2;

QY 1 MHGDTPLHRYMDLQF---ETTDLYXXYQLNDSSEEDIDGPAGAB-----PDR 49
DB 1 MRGKPTLQEIIVDLCPYNEIQPDVLCVHQGLGSDDEIDPDHANNHQLLRDQ 60
QY 50 AHYNIYVFCCKDSTLRCLCVQSTHVDIRLTEDLMTGLGIYXPIC 95
DB 61 QRRIQGLCKCKNKALQLVVEASRDNLRTLQQLFMDSLGFVCPWCA 106

RESULT 100
US-10-475-203A-14
; Sequence 14, Application US/10475203A
; Publication No. US20040241177A1
; GENERAL INFORMATION:
```

```
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: E1679-00002
; CURRENT APPLICATION NUMBER: US/10/475,203A
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/AU02/00486
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: AU PR4468/01
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide encoded by SEQ ID NO: 13
; US-10-475-203A-14

Query Match          30.2%; Score 156; DB 5; Length 517;
Best Local Similarity 40.9%; Pred. No. 9.7e-10;
Matches 36; Conservative 13; Mismatches 33; Indels 6; Gaps 3;

QY 16 QPETTDLY---XXYQLNDSSEEDIDG--PAGQ--AEPDRAHNYITFCCKDSTLRCLCV 69
DB 429 EKEKPDYKMLSTWVNLKESSELDQYPLGKFKLLQSHGHFQIYVCCCGCSNRLV 488
QY 70 QSTHVDIRLTEDLMTGLGIYXPIC 97
DB 489 QCTETDIRVYQQLLGTINIVCICAPK 516
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Search completed: May 27, 2006, 05:37:53
Job time : 103.936 secs

This Page Blank (uspto)

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OM protein - protein search, using sw model

Run on: May 27, 2006, 05:33:42 ; Search time 6.69076 Seconds

(Without alignments)
163.129 Million cell updates/sec

Title: US-10-530-253-14ED

Perfect score: 517
Sequence: 1 MHDDPTIHHYMDLDPEFTT.....LEDLMLGTGLIVPICSGKP 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New*

1: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US09_NEW_PUB.pap:*
2: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US07_NEW_PUB.pap:*
3: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US08_NEW_PUB.pap:*
4: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US08_NEW_PUB.pap:*
5: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US08_NEW_PUB.pap:*
6: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US10_NEW_PUB.pap:*
7: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US11_NEW_PUB.pap:*
8: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US60_NEW_PUB.pap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512	99.0	98	US-10-511-814-8	Sequence 8, Appli
2	511	98.8	98	US-10-511-814-1	Sequence 11, Appli
3	478	92.5	92	US-10-512-190-2	Sequence 2, Appli
4	62.5	12.1	148	US-11-293-697-2678	Sequence 2678, Ap
5	60.5	11.7	1287	US-10-505-928-341	Sequence 341, App
6	60	11.6	468	US-11-293-697-4473	Sequence 4473, App
7	58.5	11.3	462	US-10-953-349-39521	Sequence 39521, A
8	58.5	11.3	616	US-10-953-349-39520	Sequence 39520, A
9	58.5	11.3	646	US-10-953-349-39519	Sequence 39519, A
10	57.5	11.1	233	US-10-953-349-27426	Sequence 27426, A
11	57.5	11.1	296	US-10-953-349-27425	Sequence 27425, A
12	57.5	11.1	353	US-10-953-349-27424	Sequence 27424, A
13	57.5	11.1	446	US-10-953-349-39537	Sequence 39537, A
14	57.5	11.1	464	US-10-953-349-39536	Sequence 39536, A
15	57.5	11.1	499	US-10-953-349-3781	Sequence 3781, Ap
16	57.5	11.1	552	US-10-953-349-3780	Sequence 3780, Ap
17	57.5	11.1	618	US-10-953-349-39535	Sequence 39535, A
18	57	11.0	300	US-11-242-111-23	Sequence 23, Appli
19	57	11.0	314	US-09-981-845-1	Sequence 1, Appli
20	55.5	10.7	286	US-10-953-349-23406	Sequence 23406, A
21	55.5	10.7	293	US-10-953-349-23405	Sequence 23405, A
22	55.5	10.7	538	US-10-953-349-5452	Sequence 5452, Ap
23	55.5	10.7	544	US-10-953-349-5451	Sequence 5451, Ap
24	55.5	10.7	574	US-10-953-349-5450	Sequence 5450, Ap
25	55.5	10.7	878	US-10-468-193-32	Sequence 32, Appli

26	54.5	10.5	58	US-10-525-126-177	Sequence 177, App
27	54.5	10.5	88	US-10-525-126-215	Sequence 215, App
28	54.5	10.5	88	US-10-525-126-174	Sequence 174, App
29	54.5	10.5	88	US-10-525-126-175	Sequence 175, App
30	54.5	10.5	88	US-10-525-126-212	Sequence 212, App
31	54.5	10.5	88	US-10-525-126-213	Sequence 213, App
32	54.5	10.5	88	US-10-525-126-284	Sequence 284, App
33	54.5	10.5	88	US-10-525-126-299	Sequence 299, App
34	54.5	10.5	88	US-10-525-126-300	Sequence 300, App
35	54.5	10.5	255	US-10-953-349-20549	Sequence 20549, A
36	54.5	10.5	259	US-10-953-349-20548	Sequence 20548, A
37	54.5	10.5	489	US-11-293-697-2988	Sequence 2988, Ap
38	54	10.4	278	US-10-953-349-1526	Sequence 1526, Ap
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40	54	10.4	630	US-10-953-349-35808	Sequence 35808, A
41	54	10.4	676	US-10-953-349-35807	Sequence 35807, A
42	53.5	10.3	533	US-10-953-349-31198	Sequence 31198, A
43	53.5	10.3	639	US-10-953-349-23351	Sequence 23351, A
44	53.5	10.3	656	US-10-953-349-23350	Sequence 23350, A
45	53.5	10.3	664	US-10-953-349-23349	Sequence 23349, A
46	53	10.3	253	US-10-953-349-34172	Sequence 34172, A
47	53	10.3	283	US-10-953-349-34171	Sequence 34171, A
48	53	10.3	286	US-10-953-349-34170	Sequence 34170, A
49	53	10.3	377	US-10-953-349-12021	Sequence 12021, A
50	53	10.3	423	US-11-293-697-3292	Sequence 3292, Ap
51	53	10.3	749	US-10-505-928-443	Sequence 443, App
52	52.5	10.2	109	US-10-953-349-15959	Sequence 15959, A
53	52.5	10.2	275	US-11-293-697-3886	Sequence 3886, Ap
54	52.5	10.2	288	US-10-953-349-11222	Sequence 11222, A
55	52.5	10.2	1912	US-10-511-937-2561	Sequence 2561, Ap
56	52	10.1	90	US-10-525-126-296	Sequence 296, App
57	52	10.1	97	US-10-953-349-15960	Sequence 15960, A
58	52	10.1	324	US-10-953-349-21798	Sequence 21798, A
59	52	10.1	348	US-10-953-349-21797	Sequence 21797, A
60	52	10.1	352	US-10-953-349-31968	Sequence 31968, A
61	52	10.1	357	US-10-953-349-31967	Sequence 31967, A
62	52	10.1	405	US-10-953-349-31966	Sequence 31966, A
63	52	10.1	507	US-10-514-462-4	Sequence 4, Appli
64	52	10.1	634	US-11-293-697-3174	Sequence 3174, Ap
65	52	10.1	1067	US-10-514-462-2	Sequence 2, Appli
66	52	10.1	61	US-10-525-126-302	Sequence 302, App
67	51.5	10.0	145	US-10-953-349-6871	Sequence 6871, Ap
68	51.5	10.0	158	US-10-953-349-6870	Sequence 6870, Ap
69	51.5	10.0	159	US-11-297-160-7	Sequence 7, Appli
70	51.5	10.0	315	US-10-953-349-24841	Sequence 24841, A
71	51.5	10.0	323	US-10-953-349-24840	Sequence 24840, A
72	51.5	10.0	335	US-11-121-154-195	Sequence 195, App
73	51.5	10.0	500	US-10-953-349-22956	Sequence 22956, A
74	51	9.9	121	US-10-953-349-16871	Sequence 16871, A
75	51	9.9	549	US-10-953-349-16870	Sequence 16870, A
76	51	9.9	557	US-10-953-349-16869	Sequence 16869, A
77	51	9.9	585	US-11-293-697-4398	Sequence 4398, App
78	51	9.9	744	US-10-953-349-23157	Sequence 23157, A
79	51	9.8	176	US-10-953-349-23156	Sequence 23156, A
80	50.5	9.8	218	US-10-953-349-23155	Sequence 23155, A
81	50.5	9.8	225	US-10-953-349-36029	Sequence 36029, A
82	50.5	9.8	343	US-10-953-349-36028	Sequence 36028, A
83	50.5	9.8	359	US-10-953-349-36027	Sequence 36027, A
84	50.5	9.8	382	US-10-953-349-39397	Sequence 39397, A
85	50.5	9.8	57	US-10-953-349-39396	Sequence 39396, A
86	50	9.7	81	US-10-953-349-27383	Sequence 27383, Ap
87	50	9.7	205	US-10-953-349-38511	Sequence 38511, A
88	50	9.7	211	US-10-953-349-38510	Sequence 38510, A
89	50	9.7	212	US-10-953-349-27382	Sequence 27382, Ap
90	50	9.7	222	US-10-511-937-2618	Sequence 2618, Ap
91	50	9.7	233	US-10-953-349-12546	Sequence 12546, A
92	50	9.7	233	US-10-953-349-38510	Sequence 38510, A
93	50	9.7	438	US-10-953-349-8835	Sequence 8835, App
94	50	9.7	438	US-10-953-349-8834	Sequence 8834, App
95	50	9.7	476	US-10-953-349-8833	Sequence 8833, App
96	50	9.7	516	US-10-953-349-8832	Sequence 8832, App
97	50	9.7	527	US-10-953-349-13398	Sequence 13398, A
98	50	9.7	548	US-10-953-349-13397	Sequence 13397, A

99 50 9.7 634 6 US-10-953-349-13396 Sequence 13396, A
100 50 9.7 878 7 US-11-293-697-3814 Sequence 3814, Ap

ALIGNMENTS

RESULT 1
US-10-511-814-8

; Sequence 8, Application US/10511814
; Publication No. US20060088472A1
; GENERAL INFORMATION:
; APPLICANT: McCance, Dennis
; APPLICANT: Westbrock, III, Thomas F.
; TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
; FILE REFERENCE: 21108.0016U2
; CURRENT APPLICATION NUMBER: US/10/511.814
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US03/12667
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,245
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
US-10-511-814-8

Query Match 99.0%; Score 512; DB 6; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.3e-50;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMLDLOPETTDLYXXYXQUNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEHYMLDLOPETTDLYCYEQUNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60

Qy 61 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSKP 98
Db 61 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSKP 98

RESULT 2
US-10-511-814-11

; Sequence 11, Application US/10511814
; Publication No. US20060088472A1
; GENERAL INFORMATION:
; APPLICANT: McCance, Dennis
; APPLICANT: Westbrock, III, Thomas F.
; TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
; FILE REFERENCE: 21108.0016U2
; CURRENT APPLICATION NUMBER: US/10/511.814
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US03/12667
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,245
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
US-10-511-814-11

Query Match 98.8%; Score 511; DB 6; Length 98;

Best Local Similarity 95.9%; Pred. No. 3e-50;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEHYMLDLOPETTDLYXXYXQUNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEHYMLDLOPETTDLYCYEQUNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60

Qy 61 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSKP 98
Db 61 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSKP 98

RESULT 3
US-10-512-190-2

; Sequence 2, Application US/10512190
; Publication No. US20060099219A1
; GENERAL INFORMATION:
; APPLICANT: Halliez, Sophie
; APPLICANT: Burny, Arsene
; APPLICANT: Jacquet, Alain
; APPLICANT: Bollet, Alex
; TITLE OF INVENTION: MUTATED HPV-16 E7 POLYPEPTIDE, PHARMACEUTICAL COMPOSITION
; FILE REFERENCE: 9997.50USWO
; CURRENT APPLICATION NUMBER: US/10/512.190
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: PCT/BE03/000073
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 60/410,461
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: FR 0205173
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: FR 0304170
; PRIOR FILING DATE: 2003-04-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutated (recombinant) HPV-16 E7
US-10-512-190-2

Query Match 92.5%; Score 478; DB 6; Length 92;
Best Local Similarity 92.9%; Pred. No. 1.3e-46;
Matches 91; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

Qy 1 MHGDTPLHEHYMLDLOPETTDLYXXYXQUNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDTPLHEHYMLDLOPETTDLYXXYXQUNDSSSEEDIDGPAGQAEPPRAHYNIVTFCK 54

Qy 61 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSKP 98
Db 55 CDSTLRFCVOSTHVDIRTTLEDLMGTGIVXPICSKP 92

RESULT 4
US-11-293-697-2678

; Sequence 2678, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: Helix Research Institute
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293.697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2678
; LENGTH: 148


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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2678
Query Match
Best Local Similarity 12.1%; Score 62.5; DB 7; Length 148;
Matches 19; Conservative 5; Mismatches 21; Indels 17; Gaps 2;

QY 31 SSEDEIDGPAQAE-----DRAHYIVTFCKCDSTLRLCVOSTHVDIR 77
Db 50 SSSPDSDDGAPPEPTGSSGCTGWSCLSPVHFHMGMECP-----ILCRSPHLRLR 105
QY 78 TL 79
Db 106 GL 107

RESULT 5
US-10-505-928-341
; Sequence 341, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 341
; LENGTH: 1287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-341
Query Match
Best Local Similarity 11.7%; Score 60.5; DB 6; Length 1287;
Matches 19; Conservative 11; Mismatches 23; Indels 27; Gaps 3;

QY 23 YXXQLNDSSSEDEIDGPA-----GOAPDRAHYIVTFCKCD 62
Db 1126 YGLQSSDSDSEDEPPDNDKSEYLLNQLNSIPQLGQKSPKNDHILN-CSI 1184
QY 63 STLRLCVOSTHVDIRLTLEDL 82
Db 1185 SV-----GTNADTPVLRNI 1198

RESULT 6
US-11-293-697-4473
; Sequence 4473, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4473
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4473
Query Match
Best Local Similarity 11.6%; Score 60; DB 7; Length 468;
Matches 29; Conservative 17; Mismatches 30; Indels 52; Gaps 7;
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QY 16 QPETDLYXXQLNDSSSE-----EBDEIDGPAQ-----QAE----- 47
Db 35 EPQDLDLVPPRPRLNSAEAPQSLHPSRGVWNELPQSGQFSQYGRSRTFOSQHPPT 94
QY 48 -----DRAHYIVTFCKCDSTLRLCVOSTHVDIRLTLEDL-----MGTIGIVXP- 92
Db 95 SSNGELPYVNSSAGSNCT--CNCOSTLQAILQ-----ELKTRKMLNQLQAVGQNRQPP 148
QY 93 ---ICSQK 97
Db 149 ISLICSR 156

RESULT 7
US-10-953-349-39521
; Sequence 39521, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39521
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39521
Query Match
Best Local Similarity 11.3%; Score 58.5; DB 6; Length 462;
Matches 24; Conservative 15; Mismatches 30; Indels 35; Gaps 5;

QY 6 PTHRYMLDQPETDLYXXQLNDSSSE---ED-----EIDGPAQAEPPRAHYNI 54
Db 351 PAVHMASVLDIKGAYDV-----LRNSSRFLBDVYRNPGPLQFEGGADSKP----- 398
QY 55 VTFCKCDSTLRLCVOSTHV--DIRTLEDLMLGTLGIVXPICSQ 96
Db 399 -----ISLCVEDQDMGRIKLQETLEKYSIVKFGCCQ 432

RESULT 8
US-10-953-349-39520
; Sequence 39520, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39520
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39520
Query Match
Best Local Similarity 11.3%; Score 58.5; DB 6; Length 616;
Matches 24; Conservative 15; Mismatches 30; Indels 35; Gaps 5;

QY 6 PTHRYMLDQPETDLYXXQLNDSSSE---ED-----EIDGPAQAEPPRAHYNI 54
Db 505 PAVHMASVLDIKGAYDV-----LRNSSRFLBDVYRNPGPLQFEGGADSKP----- 552
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Qy 55 VTFCCKCDSTRLCVOSTHV--DIRTLEDLMGTGLGVXPICSQ 96
Db 553 -----ISLCEVDODYNGRIKGLQEVYLEKXSIYKPCSCQ 586

RESULT 9
US-10-953-349-39519
; Sequence 39519, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39519
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39519

Query Match 11.1%; Score 58.5; DB 6; Length 646;
Best Local Similarity 23.1%; Pred. No. 33;
Matches 24; Conservative 15; Mismatches 30; Indels 35; Gaps 5;
Qy 6 PTLHEWMLDLOPETTDLYXXYQANDSSEEDIDGPAQAEPRRAHYNIVTFCCCKDST 54
Db 535 PAVHMASVDLKGKAYDV-----LRONSSRFLEEDYRNPGPLQEGFGADSKP----- 582
Qy 55 VTFCCKCDSTRLCVOSTHV--DIRTLEDLMGTGLGVXPICSQ 96
Db 583 -----ISLCEVDODYNGRIKGLQEVYLEKXSIYKPCSCQ 616

RESULT 10
US-10-953-349-27426
; Sequence 27426, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27426
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-27426

Query Match 11.1%; Score 57.5; DB 6; Length 233;
Best Local Similarity 27.6%; Pred. No. 14;
Matches 16; Conservative 11; Mismatches 24; Indels 7; Gaps 2;
Qy 8 LHEWMLDLOPETTDLYXXYQANDSSEEDIDGPAQAEPRRAHYNIVTFCCCKDST 64
Db 85 IQEYVLGEYDPDADAYHDNHTSESADBDHYKD-----TSKRHYHVYVYTNGTVCDDL 136

RESULT 11
US-10-953-349-27425
; Sequence 27425, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27425
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-27425

FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27425
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-27425

Query Match 11.1%; Score 57.5; DB 6; Length 296;
Best Local Similarity 27.6%; Pred. No. 18;
Matches 16; Conservative 11; Mismatches 24; Indels 7; Gaps 2;
Qy 8 LHEWMLDLOPETTDLYXXYQANDSSEEDIDGPAQAEPRRAHYNIVTFCCCKDST 64
Db 148 IQEYVLGEYDPDADAYHDNHTSESADBDHYKD-----TSKRHYHVYVYTNGTVCDDL 199

RESULT 12
US-10-953-349-27424
; Sequence 27424, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27424
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-27424

Query Match 11.1%; Score 57.5; DB 6; Length 353;
Best Local Similarity 27.6%; Pred. No. 22;
Matches 16; Conservative 11; Mismatches 24; Indels 7; Gaps 2;
Qy 8 LHEWMLDLOPETTDLYXXYQANDSSEEDIDGPAQAEPRRAHYNIVTFCCCKDST 64
Db 205 IQEYVLGEYDPDADAYHDNHTSESADBDHYKD-----TSKRHYHVYVYTNGTVCDDL 256

RESULT 13
US-10-953-349-39537
; Sequence 39537, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39537
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39537

Query Match 11.1%; Score 57.5; DB 6; Length 446;
Best Local Similarity 23.8%; Pred. No. 29;
Matches 24; Conservative 15; Mismatches 33; Indels 29; Gaps 4;
Qy 6 PTLHEWMLDLOPETTDLYXXYQANDSSEEDIDGPAQAEPRRAHYNIVTF 57
Db 6 PTLHEWMLDLOPETTDLYXXYQANDSSEEDIDGPAQAEPRRAHYNIVTF 57

```
Db      333 PAVHMASVDLKGKAYDV--LRQNSSSTLEDDVYRNPGPLQFEGPGADSKP----- 380
Qy      58 CCKCDSTLRICVOSTHV--DIRTLEDLLMGTGIVXPICSQ 96
      381 -----ISLCVEDDQDYMGRIKLQETLEKVKRIIVRGCSQ 414

RESULT 14
US-10-953-349-39536
; Sequence 39536, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39536
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39536

Query Match      11.1%; Score 57.5; DB 6; Length 464;
Best Local Similarity 23.8%; Pred. No. 30;
Matches 24; Conservative 15; Mismatches 33; Indels 29; Gaps 4;

Qy      6 PTHHEYMLDQPTTLDYXXQUNDSEED-----RIDPGAGAEPRRAHYNIYTF 57
      351 PAVHMASVDLKGKAYDV--LRQNSSSTLEDDVYRNPGPLQFEGPGADSKP----- 388
Db      58 CCKCDSTLRICVOSTHV--DIRTLEDLLMGTGIVXPICSQ 96
      399 -----ISLCVEDDQDYMGRIKLQETLEKVKRIIVRGCSQ 432

RESULT 15
US-10-953-349-3781
; Sequence 3781, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3781
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3781

Query Match      11.1%; Score 57.5; DB 6; Length 499;
Best Local Similarity 28.8%; Pred. No. 33;
Matches 15; Conservative 8; Mismatches 18; Indels 11; Gaps 3;

Qy      28 LNDSESEDEIDGPAGAEPRRAHYNIYTFCC-KCOST-----LRLCVQSTH 73
      13 LNDDEDDDDDCDW-----EPVQAPMEFVKWCVCVCTMSNGDMVHCICGEH 59
Db

RESULT 16
US-10-953-349-3780
; Sequence 3780, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.

Db      28 LNDSESEDEIDGPAGAEPRRAHYNIYTFCC-KCOST-----LRLCVQSTH 73
      13 LNDDEDDDDDCDW-----EPVQAPMEFVKWCVCVCTMSNGDMVHCICGEH 59
Db

RESULT 17
US-10-953-349-39535
; Sequence 39535, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39535
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39535

Query Match      11.1%; Score 57.5; DB 6; Length 618;
Best Local Similarity 23.8%; Pred. No. 41;
Matches 24; Conservative 15; Mismatches 33; Indels 29; Gaps 4;

Qy      6 PTHHEYMLDQPTTLDYXXQUNDSEED-----RIDPGAGAEPRRAHYNIYTF 57
      505 PAVHMASVDLKGKAYDV--LRQNSSSTLEDDVYRNPGPLQFEGPGADSKP----- 552
Db      58 CCKCDSTLRICVOSTHV--DIRTLEDLLMGTGIVXPICSQ 96
      553 -----ISLCVEDDQDYMGRIKLQETLEKVKRIIVRGCSQ 586
Db

RESULT 18
US-11-242-111-23
; Sequence 23, Application US/11242111
; Publication No. US2006008862A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M
; TITLE OF INVENTION: DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTION
; FILE REFERENCE: NIEB-01001US1 MCF/MLB
; CURRENT APPLICATION NUMBER: US/11/242,111
; CURRENT FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: 60/614,746
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 60/651,344
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 300
```

TYPE: PRT
ORGANISM: HUMAN
US-11-242-111-23

Query Match 11.0%; Score 57; DB 7; Length 300;
Best Local Similarity 24.4%; Pred. No. 21;
Matches 11; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 9 HEWMLDQPTTDLVXXQLNDSSEEDIDGPAQAEPRAHYN 53
DB 68 HDHWDMDDEDHVDSDSDSDVDVDTSDSHQSDSHS 112

RESULT 19
US-09-981-845-1
Sequence 1, Application US/09981845
Publication No. US2006010501A1
GENERAL INFORMATION:
APPLICANT: Ashkar, Samy
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Osteoporosis-Coated Surfaces and Methods of Use
FILE REFERENCE: CMC 779
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 60/241,248
PRIOR FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: US 60/327,273
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-09-981-845-1

Query Match 11.0%; Score 57; DB 1; Length 314;
Best Local Similarity 24.4%; Pred. No. 22;
Matches 11; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 9 HEWMLDQPTTDLVXXQLNDSSEEDIDGPAQAEPRAHYN 53
DB 82 HDHWDMDDEDHVDSDSDSDVDVDTSDSHQSDSHS 126

RESULT 20
US-10-953-349-23406
Sequence 23406, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23406
LENGTH: 286
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-23406

Query Match 10.7%; Score 55.5; DB 6; Length 286;
Best Local Similarity 31.4%; Pred. No. 30;
Matches 11; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

QY 37 EIDGPAQAEPRAHYNIV---TFCCCKDSTLRLC 68
DB 188 KVDGPGMSYGIKRVYSVQGNDFCGACGATAGTC 222

RESULT 21
US-10-953-349-23405
Sequence 23405, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23405
LENGTH: 293
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-23405

Query Match 10.7%; Score 55.5; DB 6; Length 293;
Best Local Similarity 31.4%; Pred. No. 30;
Matches 11; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

QY 37 EIDGPAQAEPRAHYNIV---TFCCCKDSTLRLC 68
DB 195 KVDGPGMSYGIKRVYSVQGNDFCGACGATAGTC 229

RESULT 22
US-10-953-349-5452
Sequence 5452, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5452
LENGTH: 538
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-5452

Query Match 10.7%; Score 55.5; DB 6; Length 538;
Best Local Similarity 27.7%; Pred. No. 59;
Matches 26; Conservative 11; Mismatches 32; Indels 25; Gaps 5;

QY 14 DLDPTTDLVXXQLNDSSEEDIDGPAQAEPD-----RAHYNIVTFCCCK 61
DB 149 DEEPE---HDARFLPTBEELEEARP-----PDLPKTRLEIVRAKNAKAFPK- 198

QY 62 DSTLRLCVQSTHVDIRT---LEDLMLGTGIVXP 92
DB 199 DTRKACVEQLKADLGSYGYNFLLGTIVEMFP 232

RESULT 23
US-10-953-349-5451
Sequence 5451, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3

SEQ ID NO 5451
LENGTH: 544
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-5451

Query Match 10.7%; Score 55.5; DB 6; Length 544;
Best Local Similarity 27.7%; Pred. No. 60;

Matches 26; Conservative 11; Mismatches 32; Indels 25; Gaps 5;

QY 14 DLQPTTDLXXYYQLNDSSEEDIDGPAGQAEPD-----RAHNYIVTFCCKC 61
DB 155 DEEPE-----HDARLPTREELEEARGP-----PDLPLKTRLEIYRALKNFRAPRK- 204

QY 62 DSTLRLCVQSTHVDIRT--LEDLLMGTGIVXP 92
DB 205 DTRKACVEQLKADLGSYGNSFLIGTLVEMFP 238

RESULT 24
US-10-953-349-5450
Sequence 5450, Application US/10953349
Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nicholas et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

PRIOR FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PatentIn version 3.3

SEQ ID NO 5450

LENGTH: 574

TYPE: PRT

ORGANISM: Arabidopsis thaliana
US-10-953-349-5450

Query Match 10.7%; Score 55.5; DB 6; Length 574;
Best Local Similarity 27.7%; Pred. No. 63;

Matches 26; Conservative 11; Mismatches 32; Indels 25; Gaps 5;

QY 14 DLQPTTDLXXYYQLNDSSEEDIDGPAGQAEPD-----RAHNYIVTFCCKC 61
DB 185 DEEPE-----HDARLPTREELEEARGP-----PDLPLKTRLEIYRALKNFRAPRK- 234

QY 62 DSTLRLCVQSTHVDIRT--LEDLLMGTGIVXP 92
DB 235 DTRKACVEQLKADLGSYGNSFLIGTLVEMFP 268

RESULT 25

US-10-468-193-32
Sequence 32, Application US/10468193
Publication No. US20060100416A1

GENERAL INFORMATION:
APPLICANT: Paili, Subba R.

APPLICANT: Creese, Dean E.

APPLICANT: Fujimoto, T.

APPLICANT: Kumar, Mohan B.

TITLE OF INVENTION: Novel Substitution Mutant Receptor and Their Use in a Nuclear

FILE REFERENCE: A01247-US

CURRENT APPLICATION NUMBER: US/10/468,193

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/313,925

PRIOR FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: PCT/US02/05090

PRIOR FILING DATE: 2002-02-20

NUMBER OF SEQ ID NOS: 113

SOFTWARE: PatentIn version 3.2

SEQ ID NO 32
LENGTH: 878

TYPE: PRT
ORGANISM: Drosophila melanogaster
US-10-468-193-32

Query Match 10.7%; Score 55.5; DB 6; Length 878;
Best Local Similarity 24.8%; Pred. No. 1e+02;

Matches 27; Conservative 14; Mismatches 35; Indels 33; Gaps 7;

QY 14 DLQPTTDLXXYYQLNDSSEEDIDGPAGQAEPD-----DPA---HNYIVT----- 56
DB 230 DLSP-SSSLNGY-SANESCDKSKKGPAPRVOEELCLVGDRAAGYHVALTCGCKGF 287

QY 57 -----FCCCKDSTLRLCVQSTHVDIRTLEDLLMGTGIVXPIC 94
DB 288 FRRSVTKSAVYCKFG--RACEMDMYRRKQCEKIKKCLAVGMREPC 333

RESULT 26
US-10-525-126-177

Sequence 177, Application US/10525126
Publication No. US20060093596A1

GENERAL INFORMATION:
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA

TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM

FILE REFERENCE: 6899-6/PAR

CURRENT APPLICATION NUMBER: US/10/525,126

PRIOR FILING DATE: 2005-02-18

PRIOR APPLICATION NUMBER: PCT/CA03/01323

PRIOR FILING DATE: 2003-08-22

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR FILING DATE: 2002-08-22

NUMBER OF SEQ ID NOS: 329

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 177

LENGTH: 58

TYPE: PRT

ORGANISM: Unknown Organism

FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Hepcidin peptide

US-10-525-126-177

Query Match 10.5%; Score 54.5; DB 6; Length 58;
Best Local Similarity 22.2%; Pred. No. 6.7; Indels 15; Gaps 1;

Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

QY 32 SEEDIEDIDGPAGQAEPD-----RAHNYIVTFCCKC 61
DB 2 TEEVESIDSEVGEHQPGGTSNMLPMHFRKRSQSHSLCKWCNC 46

RESULT 27

US-10-525-126-215

Sequence 215, Application US/10525126
Publication No. US20060093596A1

GENERAL INFORMATION:
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA

TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM

FILE REFERENCE: 6899-6/PAR

CURRENT APPLICATION NUMBER: US/10/525,126

PRIOR FILING DATE: 2005-02-18

PRIOR APPLICATION NUMBER: PCT/CA03/01323

PRIOR FILING DATE: 2003-08-22

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR FILING DATE: 2002-08-22

NUMBER OF SEQ ID NOS: 329

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 215

LENGTH: 58

TYPE: PRT

ORGANISM: Salmo salar

US-10-525-126-215

Query Match 10.5%; Score 54.5; DB 6; Length 58;
Best Local Similarity 22.2%; Pred. No. 6.7;
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

Qy 32 SEEDSIDSPVGEHQPGGTSMNLPMHFRFRKQSHSLCRAWCCNC 61
Db 2 TEEVESIDSPVGEHQPGGTSMNLPMHFRFRKQSHSLCRAWCCNC 46

RESULT 28

US-10-525-126-174
; Sequence 174, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; FILE REFERENCE: 6899-6/PAR
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: US/10/525,126
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 174
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Hepcidin peptide
; US-10-525-126-174

Query Match 10.5%; Score 54.5; DB 6; Length 88;
Best Local Similarity 22.2%; Pred. No. 11;
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

Qy 32 SEEDSIDSPVGEHQPGGTSMNLPMHFRFRKQSHSLCRAWCCNC 61
Db 32 TEEVESIDSPVGEHQPGGTSMNLPMHFRFRKQSHSLCRAWCCNC 76

RESULT 29

US-10-525-126-175
; Sequence 175, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 175
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Hepcidin peptide
; US-10-525-126-175

Query Match 10.5%; Score 54.5; DB 6; Length 88;

Best Local Similarity 22.2%; Pred. No. 11;
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

Qy 32 SEEDSIDSPVGEHQPGGTSMNLPMHFRFRKQSHSLCRAWCCNC 61
Db 32 TEEVESIDSPVGEHQPGGTSMNLPMHFRFRKQSHSLCRAWCCNC 76

RESULT 30

US-10-525-126-212
; Sequence 212, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 212
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Hippoglossus hippoglossus
; US-10-525-126-212

Query Match 10.5%; Score 54.5; DB 6; Length 88;
Best Local Similarity 22.2%; Pred. No. 11;
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

Qy 32 SEEDSIDSPVGEHQPGGTSMNLPMHFRFRKQSHSLCRAWCCNC 61
Db 32 TEEVESIDSPVGEHQPGGTSMNLPMHFRFRKQSHSLCRAWCCNC 76

RESULT 31

US-10-525-126-213
; Sequence 213, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 213
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Salmo salar
; US-10-525-126-213

Query Match 10.5%; Score 54.5; DB 6; Length 88;
Best Local Similarity 22.2%; Pred. No. 11;
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

Qy 32 SEEDSIDSPVGEHQPGGTSMNLPMHFRFRKQSHSLCRAWCCNC 61
Db 32 TEEVESIDSPVGEHQPGGTSMNLPMHFRFRKQSHSLCRAWCCNC 76

RESULT 32

```
US-10-525-126-284
; Sequence 284, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 284
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Type1 Hepcidin
; OTHER INFORMATION: sequence
US-10-525-126-284

Query Match 10.5%; Score 54.5; DB 6; Length 88;
Best Local Similarity 22.2%; Pred. No. 11;
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

QY 32 SEEDRIDGPAQAEPD-----RAHYIVTFCKC 61
DB 32 TEVESIDSPVGEHQPGGTSMNLPMHFRKROSHSLCRWCNC 76

RESULT 33
US-10-525-126-299
; Sequence 299, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 299
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Hippoglossus hippoglossus
US-10-525-126-299

Query Match 10.5%; Score 54.5; DB 6; Length 88;
Best Local Similarity 22.2%; Pred. No. 11;
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

QY 32 SEEDRIDGPAQAEPD-----RAHYIVTFCKC 61
DB 32 TEVESIDSPVGEHQPGGTSMNLPMHFRKROSHSLCRWCNC 76

RESULT 34
US-10-525-126-300
; Sequence 300, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
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; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 300
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Salmo salar
US-10-525-126-300

Query Match 10.5%; Score 54.5; DB 6; Length 88;
Best Local Similarity 22.2%; Pred. No. 11;
Matches 10; Conservative 9; Mismatches 11; Indels 15; Gaps 1;

QY 32 SEEDRIDGPAQAEPD-----RAHYIVTFCKC 61
DB 32 TEVESIDSPVGEHQPGGTSMNLPMHFRKROSHSLCRWCNC 76

RESULT 35
US-10-953-349-20549
; Sequence 20549, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20549
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20549

Query Match 10.5%; Score 54.5; DB 6; Length 255;
Best Local Similarity 27.7%; Pred. No. 34;
Matches 13; Conservative 7; Mismatches 26; Indels 1; Gaps 1;

QY 2 HGDPTLHEVMDLOPETTDLYXXQLNDSSEEDRIDGPAQAEPD 48
DB 94 HNPENAKAVKFDI-PEEDDYTDDELDPDDDDDFDDEPDDEMD 139

RESULT 36
US-10-953-349-20548
; Sequence 20548, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20548
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20548

Query Match 10.5%; Score 54.5; DB 6; Length 269;
```

Best Local Similarity 27.7%; Pred. No. 36;
Matches 13; Conservative 7; Mismatches 26; Indels 1; Gaps 1;

QY 2 HCGPTLHEHYMDLPETDLYXXQXQNDSEEDIEDGPAGQAEPP 48
DB 108 HNPENKAVKFDI-PEEDDDYTDLDLDDFDDDDDFDDEDDMD 153

RESULT 37

US-11-293-697-2988
; Sequence 2988, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2988
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-293-697-2988

Query Match 10.5%; Score 54.5; DB 7; Length 489;
Best Local Similarity 24.7%; Pred. No. 69;
Matches 20; Conservative 10; Mismatches 26; Indels 25; Gaps 3;

QY 8 LHEHYMDLPETDLYXXQXQNDSEEDIEDGPAGQAEPPRAHNYIVTFCCKDSTLR 67
DB 187 LQELREKLRPPAYD-----KPIILTKPPAAQKDLIGVCC---DLVL 226

QY 68 CVQSTHVDIRTL-----EDLL 83
DB 227 AQLTHIELDRVSSIVPEDLM 247

RESULT 38
US-10-953-349-1526
; Sequence 1526, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1526
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

US-10-953-349-1526

Query Match 10.4%; Score 54; DB 6; Length 278;
Best Local Similarity 27.4%; Pred. No. 42;
Matches 20; Conservative 10; Mismatches 29; Indels 14; Gaps 2;

QY 7 TLHEHYMDLPETDLYXXQXQNDSEEDIEDGPAGQAEPPRAHNYIVTFCCKDSTLR 66
DB 62 TLNEPTIGDKLESIDLNGEKVN--SESNRDSAPGDDKPTTASVNV----- 107

QY 67 LCVQSTHVDIRTL 79
DB 108 LKQALHADRSLL 120

RESULT 39
US-10-518-414-1
; Sequence 1, Application US/10518414
; Publication No. US20060093588A1
; GENERAL INFORMATION:
; APPLICANT: Chr. Hansen A/S
; APPLICANT: Maarten van den Brink, Johannes
; APPLICANT: Harboe, Marianne K
; APPLICANT: Petersen, Steen Guldager
; APPLICANT: Rahbek-Nielsen, Henrik
; TITLE OF INVENTION: IMPROVED METHOD OF PRODUCING AN ASPARTIC PROTEASE POLYPEPTIDE IN
; FILE REFERENCE: P103IUS00
; CURRENT APPLICATION NUMBER: US/10/518,414
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PA 2002 0092
; PRIOR FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Bos taurus

US-10-518-414-1

Query Match 10.4%; Score 54; DB 6; Length 323;
Best Local Similarity 28.4%; Pred. No. 50;
Matches 29; Conservative 13; Mismatches 30; Indels 30; Gaps 8;

QY 4 DPTLHEHYMDLP-----PETDLYXXQXQNDSEEDIEDGPAGQAEPPRA-HNYIV 55
DB 89 DTVTVSN-IVDIOQTGVLSTQEPGDVFTYA-----EPGGILGMAYPSLASEYSIP 137

QY 56 TPCKCKDSTL--RLCVQ---STHVDIRTLIEDLMTGLGIYXP 92
DB 138 VF---DNMMNRHLVADLFFSYMDRNGQESML--TLGAIDP 173

RESULT 40
US-10-953-349-35808
; Sequence 35808, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35808
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays

US-10-953-349-35808

Query Match 10.4%; Score 54; DB 6; Length 630;
Best Local Similarity 28.6%; Pred. No. 1e+02;
Matches 18; Conservative 10; Mismatches 27; Indels 8; Gaps 3;

QY 13 LDLPET--TDLYXXQXQNDSEEDIEDGPAGQAEPPRAHNYIVTFCCKDSTLR 70
DB 32 VELRAETDSDEVYAQIMLQPTQSEPTSPDRPRPERC--NHSFC-----KTLGLASDT 85

QY 71 STH 73
DB 86 STH 88

RESULT 41
US-10-953-349-35807
; Sequence 35807, Application US/10953349

Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35807
LENGTH: 676
TYPE: PRT
ORGANISM: Zea mays subsp. mays
US-10-953-349-35807

Query Match 10.4%; Score 54; DB 6; Length 676;
Best Local Similarity 28.6%; Pred. No. 1.1e+02;
Matches 18; Conservative 10; Mismatches 27; Indels 8; Gaps 3;

QY 13 LDLPET-TDLYXXQLNDSSEEDIDGPAGQAEPRAHYNIWTFCKCDSTLRICVQ 70
Db 78 VELRAETDSEVYQAQWLPQTESPTSPDPPEPERC-NHSPC---KTLTASPT 131

QY 71 STH 73
Db 132 STH 134

RESULT 42
US-10-953-349-31198
Sequence 31198, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31198
LENGTH: 533
TYPE: PRT
ORGANISM: Trifolium aestivum
US-10-953-349-31198

Query Match 10.3%; Score 53.5; DB 6; Length 533;
Best Local Similarity 36.2%; Pred. No. 97;
Matches 17; Conservative 6; Mismatches 21; Indels 3; Gaps 1;

QY 49 RAHNYITFCCKDSTLRICVQSTHVDIRTLIEDLMTGLGVXPRCS 95
Db 4 RSPANVTKOSKCRPRTRVPGSGSCHRPILDRQLTGLV--ICS 47

RESULT 43
US-10-953-349-23351
Sequence 23351, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23351
LENGTH: 639
TYPE: PRT

ORGANISM: Glycine max
US-10-953-349-23351

Query Match 10.3%; Score 53.5; DB 6; Length 639;
Best Local Similarity 27.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 7; Mismatches 31; Indels 5; Gaps 2;

QY 30 DSSEEDER-DGPAGQAEPRAHYNIWTFCKCDSTLRICVQSTHVDIRTLIEDL 83
Db 19 EEEEEEVWDWEGEGEGERSEFVCLFCDNRYSGSLFDHCASLHRDPFTIRRTL 77

RESULT 44
US-10-953-349-23350
Sequence 23350, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23350
LENGTH: 656
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-23350

Query Match 10.3%; Score 53.5; DB 6; Length 656;
Best Local Similarity 27.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 7; Mismatches 31; Indels 5; Gaps 2;

QY 30 DSSEEDER-DGPAGQAEPRAHYNIWTFCKCDSTLRICVQSTHVDIRTLIEDL 83
Db 36 EEEEEEVWDWEGEGEGERSEFVCLFCDNRYSGSLFDHCASLHRDPFTIRRTL 94

RESULT 45
US-10-953-349-23349
Sequence 23349, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23349
LENGTH: 664
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-23349

Query Match 10.3%; Score 53.5; DB 6; Length 664;
Best Local Similarity 27.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 7; Mismatches 31; Indels 5; Gaps 2;

QY 30 DSSEEDER-DGPAGQAEPRAHYNIWTFCKCDSTLRICVQSTHVDIRTLIEDL 83
Db 44 EEEEEEVWDWEGEGEGERSEFVCLFCDNRYSGSLFDHCASLHRDPFTIRRTL 102

RESULT 46
US-10-953-349-34172
Sequence 34172, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:

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; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34172
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34172

Query Match          10.3%; Score 53; DB 6; Length 263;
Best Local Similarity 25.0%; Pred. No. 51;
Matches 25; Conservative 9; Mismatches 34; Indels 32; Gaps 4;

Qy 27 QUNDSSEDEIDGPAGQAP-----DRAHY-----NIVTFCKCDST 64
Db 32 QVSDALRLHDEIMQPGSLPEPKAIALIEHIRTGEGELDRHQLDGLDNSMWDGGRV 91
Qy 65 LRLCVGSTHVDIRLTEDLL-----MGTIGIYXPICSQ 96
Db 92 LLYCVQHNYPDAAI--DLLKQIREKDEWSTYMWVDQVFCQ 129

RESULT 47
US-10-953-349-34171
; Sequence 34171, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34171
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34171

Query Match          10.3%; Score 53; DB 6; Length 283;
Best Local Similarity 25.0%; Pred. No. 55;
Matches 25; Conservative 9; Mismatches 34; Indels 32; Gaps 4;

Qy 27 QUNDSSEDEIDGPAGQAP-----DRAHY-----NIVTFCKCDST 64
Db 52 QVSDALRLHDEIMQPGSLPEPKAIALIEHIRTGEGELDRHQLDGLDNSMWDGGRV 111
Qy 65 LRLCVGSTHVDIRLTEDLL-----MGTIGIYXPICSQ 96
Db 112 LLYCVQHNYPDAAI--DLLKQIREKDEWSTYMWVDQVFCQ 149

RESULT 48
US-10-953-349-34170
; Sequence 34170, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34170
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; LENGTH: 286
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34170

Query Match          10.3%; Score 53; DB 6; Length 286;
Best Local Similarity 25.0%; Pred. No. 56;
Matches 25; Conservative 9; Mismatches 34; Indels 32; Gaps 4;

Qy 27 QUNDSSEDEIDGPAGQAP-----DRAHY-----NIVTFCKCDST 64
Db 55 QVSDALRLHDEIMQPGSLPEPKAIALIEHIRTGEGELDRHQLDGLDNSMWDGGRV 114
Qy 65 LRLCVGSTHVDIRLTEDLL-----MGTIGIYXPICSQ 96
Db 115 LLYCVQHNYPDAAI--DLLKQIREKDEWSTYMWVDQVFCQ 152

RESULT 49
US-10-953-349-12021
; Sequence 12021, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12021
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (224)..(224)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (228)..(228)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (252)..(252)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; NAME/KEY: misc_feature
; LOCATION: (314)..(314)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (325)..(325)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-12021

Query Match          10.3%; Score 53; DB 6; Length 377;
Best Local Similarity 21.4%; Pred. No. 76;
Matches 27; Conservative 19; Mismatches 40; Indels 40; Gaps 7;

Qy 5 TPT-LHEWMLDLPETTDLYXXYL-----NDSSEDEIDGPAGQ-----AEPDRA 50
Db 34 TPSNSHPKLLHPRBSVSESTQKAPAVLGESEEDDDDDPSAELSYVDPTDPESI 93
Qy 51 HYNIVTFCKC-----CDSTLRLCVGSYH-----VDIRLTEDLLMGR--- 86
Db 94 TEMELDFCSRPIIDARGKVMELVCDKTSL--QYTKYPPNNVINSTILKDAIVASDQ 151
Qy 87 LGIYXP 92
Db 152 LGVPLP 157
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RESULT 50
US-11-293-697-3292
; Sequence 3292, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3292
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3292

Query Match      10.3%; Score 53; DB 7; Length 423;
Best Local Similarity 23.5%; Pred. No. 86;
Matches 23; Conservative 10; Mismatches 29; Indels 36; Gaps 3;

Qy      22 LYYXQLND-----SEEDDEIDGPAGQAE-----DRAHYNIYT 56
Db      291 LVYVNOQNDVYRLKIRSESVPLFGPPLPTPPVFTDQHFQDFDPLVYLINGEKATLETPT 350
Qy      57 FCCKCDSTLRLCVOSTYVNDI-----RTLEDLL 83
Db      351 FAQKRRITLMLIRSLHQDLMPDLHKMLMRSSDVL 388

RESULT 51
US-10-505-928-443
; Sequence 443, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 443
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-443

Query Match      10.3%; Score 53; DB 6; Length 749;
Best Local Similarity 34.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 8; Mismatches 17; Indels 8; Gaps 3;

Qy      3 GDTPTLHEVMDLQPETTDLYXXYQLND-----SEEDDEIDGPAGQAE 48
Db      484 GRAGKHNFMLGLNLTNS--YPLSPUSDFAFQDSFDDDELD--AAVADPD 529

RESULT 52
US-10-953-349-15959
; Sequence 15959, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCED-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
```

```
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 15959
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-15959

Query Match      10.2%; Score 52.5; DB 6; Length 109;
Best Local Similarity 24.2%; Pred. No. 22;
Matches 16; Conservative 10; Mismatches 33; Indels 7; Gaps 2;

Qy      3 GDT---PTLHEVMDLQPETTDLYXXYQ-----LNDSEEDDEIDGPAGQAEPPRAHYNIY 55
Db      9 GETDMLQWQDAMDLSKALDFDVTETAIKIRFTIKKEDRMHGPMQCVGTDFGSFV 68
Qy      56 TPCCCK 61
Db      69 THCCGC 74

RESULT 53
US-11-293-697-3886
; Sequence 3886, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3886
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3886

Query Match      10.2%; Score 52.5; DB 7; Length 275;
Best Local Similarity 30.0%; Pred. No. 61;
Matches 18; Conservative 8; Mismatches 19; Indels 15; Gaps 4;

Qy      44 QAEPPRAHYNIYVFCCKDSTLRLCVOST---HVDIR-TLEDLLM-----GTIGIYXPIC 94
Db      180 QAKPSRLH-----GSHCDFTYTLPPQNGTIKLYKELRCPLDDELVLVSSGSGKSYPLC 233

RESULT 54
US-10-953-349-11222
; Sequence 11222, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCED-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 11222
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11222

Query Match      10.2%; Score 52.5; DB 6; Length 288;
Best Local Similarity 27.8%; Pred. No. 64;
Matches 15; Conservative 9; Mismatches 19; Indels 11; Gaps 2;
```

Qy 15 LQPTTDLXXYYXQLNDSSEDEIDG-----PAGQAEPPRAHNYITVFC 58
Db 232 IEPETEYEESEDEDEDEVMGLENVNSRCVQGDRE-NRGLLWESFC 264

RESULT 55
US-10-511-937-2561
; Sequence 2561, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2561
; LENGTH: 1912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2561

Query Match 10.2%; Score 52.5; DB 6; Length 1912;
Best Local Similarity 29.6%; Pred. No. 5.1e+02;
Matches 16; Conservative 9; Mismatches 14; Indels 15; Gaps 4;
Qy 30 DSSEDEIDGPAQAEPPRAHNYITVFC-----CDSTLRICVOSTHV 74
Db 426 DNSEGEIIEVGGDLLEEDDH--MEFCRVCKXGGLCCDT----CPSSYHI 473
RESULT 56
US-10-525-126-296
; Sequence 296, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01123
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 296
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Oryzias latipes
US-10-525-126-296

Query Match 10.1%; Score 52; DB 6; Length 90;
Best Local Similarity 20.0%; Pred. No. 20;
Matches 13; Conservative 8; Mismatches 24; Indels 20; Gaps 1;

Qy 4 DFTLHEVMDLQPETTDLXXYYXQLNDSSEDEIDGPAQAEPPRAHNYITVFCCKDS 63
Db 40 DTVAAARHEHNSMCPWML-----PNHRRKQSHISMCTMCKCK 79

Qy 64 TLRIC 68
Db 80 NYKGC 84
RESULT 57
US-10-953-349-15960
; Sequence 15960, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579P052
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15960
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-15960

Query Match 10.1%; Score 52; DB 6; Length 97;
Best Local Similarity 23.7%; Pred. No. 22;
Matches 14; Conservative 9; Mismatches 32; Indels 4; Gaps 1;

Qy 7 TLHEVMDLQPETTDLXXYYXQ-----LNDSESEDEIDGPAQAEPPRAHNYITVFCCKC 61
Db 4 TMOQDAMDILASKALDFPDVTIAIKIARFKRPFDRMHGPEWQCI VGTDFGSSFTVHCCKC 62

RESULT 58
US-10-953-349-21799
; Sequence 21799, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579P052
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21799
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21799

Query Match 10.1%; Score 52; DB 6; Length 324;
Best Local Similarity 21.5%; Pred. No. 83;
Matches 17; Conservative 13; Mismatches 29; Indels 20; Gaps 3;

Qy 10 EYMLDQPETTDLXXYYXQLNDSSEDEIDGPAQAEPPRAHNYITVFCCKCDSTLRICV 69
Db 113 EHKLDMPFTASERKSF-----KKHBDLNDP-----IOFGCQVSKPLP-P 152
Qy 70 QSTHVDIRITLEDILMGTLG 88
Db 153 EERKTEVDLQSSQSGSLG 171

RESULT 59
US-10-953-349-21798
; Sequence 21798, Application US/10953349

```
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21798
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-21798

Query Match          10.1%; Score 52; DB 6; Length 348;
Best Local Similarity 21.5%; Pred. No. 90;
Matches 17; Conservative 13; Mismatches 29; Indels 20; Gaps 3;

QY 10 EYMLDLPETTDLYXXYQLNDSSEEDIDGPAQAEPDRAHNYIVTFCKCDSTLRVCV 69
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 137 EHKLDMDPTASERKSF-----KHEBLNDP-----IQFCGQCVSKLPL-P 176
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 70 QSTHVDIRLTEDLLMGTIG 88
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 EERKTEVDLQSSQSGSLG 195
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 60
US-10-953-349-21797
; Sequence 21797, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21797
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-21797

Query Match          10.1%; Score 52; DB 6; Length 352;
Best Local Similarity 21.5%; Pred. No. 91;
Matches 17; Conservative 13; Mismatches 29; Indels 20; Gaps 3;

QY 10 EYMLDLPETTDLYXXYQLNDSSEEDIDGPAQAEPDRAHNYIVTFCKCDSTLRVCV 69
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 141 EHKLDMDPTASERKSF-----KHEBLNDP-----IQFCGQCVSKLPL-P 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 70 QSTHVDIRLTEDLLMGTIG 88
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 EERKTEVDLQSSQSGSLG 199
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 61
US-10-953-349-31968
; Sequence 31968, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31968
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Trilicium aestivum
; US-10-953-349-31968

Query Match          10.1%; Score 52; DB 6; Length 357;
Best Local Similarity 24.7%; Pred. No. 92;
Matches 19; Conservative 9; Mismatches 33; Indels 16; Gaps 2;

QY 1 MHGDTPLHEYMDLPETTDLYXXYQLNDSSEEDIDGPAQAEPDRAHNYI--VTFC 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 249 VHQFAPTYNEYVL-----YHNHGESAPTKPSSGSAVPSVADVLAGITVM 294
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 59 CKCDSTLRCLCVOSTHVD 75
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 295 PPSNSPVTSSVSNHVD 311
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 62
US-10-953-349-31967
; Sequence 31967, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31967
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Trilicium aestivum
; US-10-953-349-31967

Query Match          10.1%; Score 52; DB 6; Length 405;
Best Local Similarity 24.7%; Pred. No. 11e+02;
Matches 19; Conservative 9; Mismatches 33; Indels 16; Gaps 2;

QY 1 MHGDTPLHEYMDLPETTDLYXXYQLNDSSEEDIDGPAQAEPDRAHNYI--VTFC 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 VHQFAPTYNEYVL-----YHNHGESAPTKPSSGSAVPSVADVLAGITVM 342
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 59 CKCDSTLRCLCVOSTHVD 75
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 343 PPSNSPVTSSVSNHVD 359
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 63
US-10-953-349-31966
; Sequence 31966, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31966
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Trilicium aestivum
; US-10-953-349-31966

Query Match          10.1%; Score 52; DB 6; Length 475;
Best Local Similarity 24.7%; Pred. No. 1.3e+02;
```

Matches 19; Conservative 9; Mismatches 33; Indels 16; Gaps 2;
Qy 1 MHGPTLHEMLDLOPETTDLYXXQLNDSSEDELDGAGAPRAHNY--VFPC 58
Db 367 VHOFAPTYNEVTL-----YNHGESAPTKFPGSVAVSDVDELAGITVM 412
Qy 59 CKCDSTLRCLCVQSTHVD 75
Db 413 PPSNSPVTSSVSSSHVD 429

RESULT 64
US-10-514-462-4
; Sequence 4, Application US/10514462
; Publication No. US20060088909A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic
; FILE REFERENCE: 050508-2210
; CURRENT APPLICATION NUMBER: US/10/514,462
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: 60/381,557
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 507
; TYPE: PRT
; ORGANISM: RVFV GC
US-10-514-462-4

Query Match 10.1%; Score 52; DB 6; Length 507;
Best Local Similarity 30.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 9; Mismatches 25; Indels 8; Gaps 3;
Qy 37 EIDGPAQAPDRAHNYIVTFCCCKDSTLRCLCVQSTHVDIRTL----EDLLMGTLGIYXP 92
Db 329 EVDVFGAANVSCDAFLNL-TGCTSCNAGARVCLSTGTGSLSAHMKD---GSLHIVLP 384

RESULT 65
US-11-293-3174
; Sequence 3174, Application US/112933697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3174
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3174

Query Match 10.1%; Score 52; DB 7; Length 634;
Best Local Similarity 34.4%; Pred. No. 1.7e+02;
Matches 21; Conservative 9; Mismatches 21; Indels 10; Gaps 4;
Qy 29 NDSSEDELDG---AGQAPDRAHNYIVTFCCCKD---STL--RLCVQSTHVDIRTL 79
Db 183 HEMMEBEREIPKPSVVAAPGAPKKEHNVV-FIGHVDAGKSTIGQIMVLTGMVDKRTL 241
Qy 80 E 80
Db 242 E 242

RESULT 66
US-10-514-462-2
; Sequence 2, Application US/10514462
; Publication No. US20060088909A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic
; FILE REFERENCE: 050508-2210
; CURRENT APPLICATION NUMBER: US/10/514,462
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: 60/381,557
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1067
; TYPE: PRT
; ORGANISM: RVFV Glycoprotein a.a.
US-10-514-462-2

Query Match 10.1%; Score 52; DB 6; Length 1067;
Best Local Similarity 30.0%; Pred. No. 3e+02;
Matches 18; Conservative 9; Mismatches 25; Indels 8; Gaps 3;
Qy 37 EIDGPAQAPDRAHNYIVTFCCCKDSTLRCLCVQSTHVDIRTL----EDLLMGTLGIYXP 92
Db 889 EVDVFGAANVSCDAFLNL-TGCTSCNAGARVCLSTGTGSLSAHMKD---GSLHIVLP 944

RESULT 67
US-10-525-126-302
; Sequence 302, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 302
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Oncoerhynchus mykiss
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (37)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (55)
; OTHER INFORMATION: Variable amino acid
US-10-525-126-302

Query Match 10.0%; Score 51.5; DB 6; Length 61;
Best Local Similarity 24.4%; Pred. No. 15;
Matches 11; Conservative 8; Mismatches 11; Indels 15; Gaps 2;
Qy 32 SDEEDIDGPAQAE-----PDR-----AHYNIYTFCCCK 61
Db 5 TEEVGSIDSPVGHQPGGESMRLPEHFRPKRXSHSLCWCNC 49

RESULT 68
US-10-953-349-6871

```

: Sequence 6871, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nikolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1579PU52
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 6871
: LENGTH: 145
: TYPE: PR1
: ORGANISM: Arabidopsis thaliana
US-10-953-349-6871

```

	Query Match	10.0%	Score 51.5;	DB 6;	length 145;
	Best Local Similarity	30.4%	Pred. No. 39;		
	Matches	14;	Conservative	7;	Mismatches 24; Indels 1; Gaps 1
QY	13 LDLDQPERTDLKXXXYQNDSSEED-ETDGPACAGAPPDAAHNIYTF	57			
	: :				
Db	20 IKLDPFTNLRAFDLPKRPPTATIDNARPKRGSKPLSTETVTF	65			
	: :				

```

RESULT 69
US-10-953-349-6870
: Sequence 6870, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 6870
: LENGTH: 158
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
: US-10-953-349-6870

```

Query Match	10.0%	Score 51.5;	DB 6;	Length 158;
Best Local Similarity	30.4%	Pred. No. 43;		
Matches	14;	Conservative	7;	Mismatches 24; Indels 1; Gaps 1
QY	13	LDLQPETDLYXXQINDSSEED-ETGPGACGAPPDRAHYIVTF	57	
Db	33	IKLPETITNLPAFLQPKPPATIDNAPKPGTGEKPLSTETVTF	78	

RESULT 70
US-11-297-160-7
Sequence 7, Application US/11297160
Publication No. US20060088888A1
GENERAL INFORMATION:
APPLICANT: Wang, Xin wei
APPLICANT: Harris, Curtis C.
APPLICANT: Fornace Jr., Albert J.
APPLICANT: Coursen, Jill D.
APPLICANT: Zhan, Qimian
APPLICANT: The Government of the United States of America
as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
FILE REFERENCE: 015280-367100US
CURRENT APPLICATION NUMBER: US/11/297,160
CURRENT FILING DATE: 2005-12-07
PRIOR APPLICATION NUMBER: US/10/600,158

```

:
: PRIOR FILING DATE: 2003-06-20
: PRIOR APPLICATION NUMBER: US/09/534, 811
: PRIOR FILING DATE: 2000-03-24
: PRIOR APPLICATION NUMBER: US 60/126, 069
: PRIOR FILING DATE: 1999-03-25
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 159
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: human growth arrest and DNA-damage-inducible
: OTHER INFORMATION: protein (hGADD45gamma)
: US-11-297-160-7

```

Query Match	10.0%	Score 51.5;	DB 7;	Length 159;
Best Local Similarity	24.7%;	Pred. No.43;		
Matches 19;	Conservative 13;	Mismatches 24;	Indels 21;	Gaps 4;

```
QY      47 PDRAHYNIV-TECCCKD 62
        :|::: |||:|
DB      75 --QIHFTLIQAFCCEEND 89
```

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RESULT 71
US-10-953-349-24841
: Sequence 24841, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nikolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERAPY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 24841
:
: LENGTH: 315
:
: TYPE: PRT
: ORGANISM: Glycine max
: US-10-953-349-24841

```

Query Match	10.0%	Score 51.5;	DB 6;	Length 315;
Best Local Similarity	23.5%	Pred. No. 91;		
Matches	20;	Conservative	7;	Mismatches 15;
			Indels	43;
			Gaps	4;
QY	5	TPTLHEWLD-----LOPE--TTTLXXXXOLN-----DSSEEDRID	39	
		:::	:::	:::
Db	58	TKIVYINSLPAKKRWALQPSPPSNDVPAFDLNVETPSPNNHGFSEDSHSEDDGV	116	
		:::	:::	:::
QY	40	GPAGQAEPRDAHYNIIVTFCCCDST	64	
		:::	:::	:::
Db	117	-----LCCVCGST	124	

```

RESULT 72
US-10-953-349-24840
; Sequence: 24840, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252

```

SOFTWARE: Patentin version 3.3
SEQ ID NO 24840
LENGTH: 323
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-24840

Query Match 10.0%; Score 51.5; DB 6; Length 323;
Best Local Similarity 23.5%; Pred. No. 94;
Matches 20; Conservative 7; Mismatches 15; Indels 43; Gaps 4;

QY 5 TPTLHEMYLD-----LQPE---TTDLYXXQLN-----DSSEDEID 39
DB 66 TKTYVYNLSLPKAKRWALQPPSPNDVVPAPFDLNVETPSPNNHGFEEHSDSDGV- 124

QY 40 GPAGQAEPPDRAHNYIVTFCKCDST 64
DB 125 -----LCCVCQST 132

RESULT 73
US-11-121-154-195
Sequence 195, Application US/111211154
Publication No. US20060105914A1
GENERAL INFORMATION:
APPLICANT: TAYLOR, LARRY EDMUND
APPLICANT: WEINER, RONALD M.
APPLICANT: HUTCHESON, STEVEN WAYNE
APPLICANT: EKBORG, NATHAN A.
APPLICANT: HOWARD, MICHAEL
TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
FILE REFERENCE: 108172-00121
CURRENT APPLICATION NUMBER: US/11/121,154
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,971
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 214
SOFTWARE: Patentin version 3.3
SEQ ID NO 195
LENGTH: 500
TYPE: PRT
ORGANISM: Microbulbifer degradans
US-11-121-154-195

Query Match 10.0%; Score 51.5; DB 7; Length 500;
Best Local Similarity 42.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 6; Mismatches 8; Indels 5; Gaps 1;

QY 62 DSTLRLCVQSTHVDIRLEDLMTGTL---LGI 89
DB 219 EHTLRIVQAGNFNINWLELLAGTQOPDMLGV 251

RESULT 74
US-10-953-349-22956
Sequence 22956, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22956
LENGTH: 155
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-22956

Query Match 9.9%; Score 51; DB 6; Length 155;

Best Local Similarity 30.3%; Pred. No. 48;
Matches 20; Conservative 10; Mismatches 26; Indels 10; Gaps 4;

QY 31 SSEBEDIDGPAGQAEPPDRAHNYIVTFCKCDSTLRLCVQ--STHVDIRLEDLMTL- 87
DB 75 AQEGEGGLRDKPKR--RDHYH---TCYCLSGLSICQYWSKHPPSPPLNVLGPYS 127

QY 88 GIVXPI 93
DB 128 NLEPI 133

RESULT 75
US-10-953-349-22955
Sequence 22955, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22955
LENGTH: 171
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-22955

Query Match 9.9%; Score 51; DB 6; Length 171;
Best Local Similarity 30.3%; Pred. No. 53;
Matches 20; Conservative 10; Mismatches 26; Indels 10; Gaps 4;

QY 31 SSEBEDIDGPAGQAEPPDRAHNYIVTFCKCDSTLRLCVQ--STHVDIRLEDLMTL- 87
DB 91 AQEGEGGLRDKPKR--RDHYH---TCYCLSGLSICQYWSKHPPSPPLNVLGPYS 143

QY 88 GIVXPI 93
DB 144 NLEPI 149

RESULT 76
US-10-953-349-16871
Sequence 16871, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 16871
LENGTH: 549
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-16871

Query Match 9.9%; Score 51; DB 6; Length 549;
Best Local Similarity 31.4%; Pred. No. 1.9e+02;
Matches 16; Conservative 7; Mismatches 18; Indels 10; Gaps 1;

QY 22 LYXXYQLNDSSEBEDIDGPAGQAEPPDRAHNYIVTFCKCDSTLRLCVQST 72
DB 478 LHLSSKLSDDSNVCLDVD-----NNNIVTNACKCLSHDRCTDPSS 518

RESULT 77


```
US-10-953-349-16870
; Sequence 16870, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16870
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-16870

Query Match
Best Local Similarity 31.4%; Score 51; DB 6; Length 557;
Matches 16; Conservative 7; Mismatches 18; Indels 10; Gaps 1;

Qy 22 LYYXQLNDSSEEDIDGPAGAEPPRAHYNIVTFCKCDSTLRLCVQST 72
Db 486 LHSLSKLSDDSNVCLDVD-----NNNIVTNACKCLSRDRTCDPSS 526

RESULT 78
US-10-953-349-16869
; Sequence 16869, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16869
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-16869

Query Match
Best Local Similarity 31.4%; Score 51; DB 6; Length 585;
Matches 16; Conservative 7; Mismatches 18; Indels 10; Gaps 1;

Qy 22 LYYXQLNDSSEEDIDGPAGAEPPRAHYNIVTFCKCDSTLRLCVQST 72
Db 514 LHSLSKLSDDSNVCLDVD-----NNNIVTNACKCLSRDRTCDPSS 554

RESULT 79
US-11-293-697-4398
; Sequence 4398, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4398
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-11-293-697-4398

Query Match
Best Local Similarity 36.0%; Score 51; DB 7; Length 764;
Matches 18; Conservative 4; Mismatches 20; Indels 8; Gaps 3;

Qy 31 SSEEDEIDGPAGQ-----AEPRAHYNIVTFCKCDSTLRLCVQSTHV 74
Db 510 SCHEHMADDPKSKYLRFAEYVSHHPISCFYCEBER-RLCV-NTHV 557

RESULT 80
US-10-953-349-13813
; Sequence 13813, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13813
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13813

Query Match
Best Local Similarity 25.0%; Score 50.5; DB 6; Length 176;
Matches 18; Conservative 12; Mismatches 31; Indels 11; Gaps 4;

Qy 1 MHGDTPLHEWMLD---QPTDLYXXQLNDSSEEDIDGPAGAEPPRAHYNIVTF 57
Db 8 LHNENFGIHLMLSLYAKQDDSSLRLFLQSKFGKGP---NGPEFFYDPKYA----LRL 60

Qy 58 CCKCDSTLRLCV 69
Db 61 CLK-EKRMRACV 71

RESULT 81
US-10-953-349-23159
; Sequence 23159, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23159
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-23159

Query Match
Best Local Similarity 19.3%; Score 50.5; DB 6; Length 218;
Matches 26; Conservative 13; Mismatches 37; Indels 59; Gaps 5;

Qy 1 MHGDTPL-----LHEWMLD-----LOPET-----PLYYXQLN----- 29
Db 1 MYGDEITSLTITQYRMHELIMDSKSKELYSKIKAPSVTAHMLYDLGVRKRNSTPTL 60

Qy 30 -----DSSEEDIDGPAGAEPPRAHYNIVTFCKCDSTLRLCVQSTHVDIRTLED 81
Db 61 LLDITAGCDMEKKDEEDSFPNFGAEL-----VVTYHAKRLVQSG 100
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QY      82 LLMGTLGIVXPICSQ 96
      :| :||: | :|
Db      101 VLPSDIGITPYAAQ 115
```

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RESULT 82
US-10-953-349-36029
: Sequence 36029, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nikolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 36029
: LENGTH: 235
: TYPE: PRT
: ORGANISM: Zea mays subsp. mays
: US-10-953-349-36029

```

```

RESULT 83
US-10-953-349-23158
: Sequence 23158, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: FILE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 23158
: LENGTH: 343
: TYPE: PRT
: ORGANISM: Glycine max
: US-10-953-349-23158

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[illegible]

RESULT 84
US-10-953-349-36028
; Sequence 36028, Application US/10953349

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? Publication No. US20060107345A1
? GENERAL INFORMATION:
? APPLICANT: ALEXANDROV, Nikolai et al.
? TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
? TITLE OF INVENTION: ENCODED THERBY
? FILE REFERENCE: 2750-1579PUS2
? CURRENT APPLICATION NUMBER: US/10/953,349
? CURRENT FILING DATE: 2004-09-30
? NUMBER OF SEQ ID NOS: 40252
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 36028
? LENGTH: 369
? TYPE: prt
? ORGANISM: Zea mays subsp. mays
US-10-953-349-36028

```

```

RESULT 85
US-10-953-349-23157
; Sequence 23157, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23157
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-23157

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[illegible]

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RESULT 86
US-10-953-349-9399
; Sequence: 9399, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252

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; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9399
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9399

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```

Query Match          9.7%; Score 50; DB 6; Length 57;
Best Local Similarity 24.6%; Pred. No. 21;
Matches 15; Conservative 6; Mismatches 18; Indels 22; Gaps 2;

```

```

QY 3 GDPTLHEVMDLOPETTDLYXXQLNDSSEEDIEIGPAGQAPDRAHNYITFCCKCD 62
DB 9 GETTTETFTVLGVAFPMKNOY-----EASGESNNMEND-----ACKCG 46

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QY 63 S 63
DB 47 S 47

```

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RESULT 87
US-10-953-349-9398
; Sequence 9398, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9398
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9398

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```

Query Match          9.7%; Score 50; DB 6; Length 81;
Best Local Similarity 24.6%; Pred. No. 30;
Matches 15; Conservative 6; Mismatches 18; Indels 22; Gaps 2;

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```

QY 3 GDPTLHEVMDLOPETTDLYXXQLNDSSEEDIEIGPAGQAPDRAHNYITFCCKCD 62
DB 33 GETTTETFTVLGVAFPMKNOY-----EASGESNNMEND-----ACKCG 70

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QY 63 S 63
DB 71 S 71

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RESULT 88
US-10-953-349-27383
; Sequence 27383, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 27383
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Trillium aestivum
US-10-953-349-27383

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Query Match          9.7%; Score 50; DB 6; Length 205;
Best Local Similarity 21.3%; Pred. No. 84;

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Matches 20; Conservative 16; Mismatches 40; Indels 18; Gaps 3;

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QY 4 DPTLHEVMDLOPETTDLYXXQLNDSSEEDIEIGPAGQAPDRAHNYITFCCKCD 46
DB 7 DAPKLNQRMVSSLSKRTAAASHWHDLEIGPEAPLIRNAVVEITKGSVKYELDKTKGMIK 66

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QY 47 PDRAHNYITFCCKCDSTLR-LCVQSTHVDIRTL 79
DB 67 VDRILYSSVYPRHNYGFVPRTLCEDDGDPIDVLVL 100

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RESULT 89
US-10-953-349-38511
; Sequence 38511, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 38511
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38511

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```

Query Match          9.7%; Score 50; DB 6; Length 211;
Best Local Similarity 27.9%; Pred. No. 86;
Matches 17; Conservative 7; Mismatches 27; Indels 10; Gaps 1;

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QY 43 GQAPPD-----RAHNYITFCCKCDSTLR-LCVQSTHVDIRTLMDLMTGLGIYXP 92
DB 73 GQAPRERFVEVAIGVRHKNLVRLLGYCAEGQRILIVEYVONGNLHGQVGAIVSP 132

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QY 93 I 93
DB 133 I 133

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RESULT 90
US-10-953-349-27382
; Sequence 27382, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 27382
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Trillium aestivum
US-10-953-349-27382

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```

Query Match          9.7%; Score 50; DB 6; Length 231;
Best Local Similarity 21.3%; Pred. No. 95;
Matches 20; Conservative 16; Mismatches 40; Indels 18; Gaps 3;

```

```

QY 4 DPTLHEVMDLOPETTDLYXXQLNDSSEEDIEIGPAGQAPDRAHNYITFCCKCD 46
DB 33 DAPKLNQRMVSSLSKRTAAASHWHDLEIGPEAPLIRNAVVEITKGSVKYELDKTKGMIK 92

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```

QY 47 PDRAHNYITFCCKCDSTLR-LCVQSTHVDIRTL 79
DB 93 VDRILYSSVYPRHNYGFVPRTLCEDDGDPIDVLVL 126

```

```
RESULT 91
US-10-511-937-2618
; Sequence 2618, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2618
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2618

Query Match
Best Local Similarity 25.4%; Score 50; DB 6; Length 272;
Matches 16; Conservative 9; Mismatches 22; Indels 16; Gaps 3;

QY
9 HEYMLDLPQETTDLYXXQLNDSSSEDEIDGPAGQAPDRAHYNIVTFCKC-----DST 64
Db
222 HDVALPVGKQKQDLDL-----EBDSAGVGLHVDKDKVS---VEFCACARKKSSS 269
QY
65 LRL 67
Db
270 LKM 272

RESULT 92
US-10-953-349-12546
; Sequence 12546, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12546
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-12546

Query Match
Best Local Similarity 28.1%; Score 50; DB 6; Length 293;
Matches 18; Conservative 6; Mismatches 18; Indels 22; Gaps 3;

QY
17 PETTDLYXXQLNDSSSE-----EIDGPAGQAPDRAHYNIVTFCKCSTLRLCVQST 72
Db
18 PENITSL-----DRNNEKNAGWEFVSPNGE-----VFICKSDLEIGLCHQDK 59
```

```
QY
73 HVDI 76
Db
60 LEVEL 63

RESULT 93
US-10-953-349-38510
; Sequence 38510, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38510
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38510

Query Match
Best Local Similarity 27.9%; Score 50; DB 6; Length 343;
Matches 17; Conservative 7; Mismatches 27; Indels 10; Gaps 1;

QY
43 GOAEPD-----RAHYNIVTFCKCSTLRLCVQSTHVDIRLTEDLMTGLGIYP 92
Db
205 GOAEREFREVEAIGRVHKNLVLRLGYCAEGAQRILVVEYVNGMLEQWLHGDVGAVSP 264
QY
93 I 93
Db
265 L 265

RESULT 94
US-10-953-349-8835
; Sequence 8835, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8835
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8835

Query Match
Best Local Similarity 21.6%; Score 50; DB 6; Length 438;
Matches 19; Conservative 17; Mismatches 38; Indels 14; Gaps 2;

QY
15 LQPETTDLYXXQLNDSSSE-----SEDEIDGPAGQAPDRAHYNIVTFCKC 61
Db
118 LSVEMPEIEFARALDDAEAEIYRHRKPEVWMQGLIGVAGELKLRHAIYDRVCSKC 177
QY
62 DSTLRLCVQSTHVDIRLTEDLMTGLGI 89
Db
178 IASKRDEI-SQGIDSSSKDLMSINV 204

RESULT 95
US-10-953-349-8834
; Sequence 8834, Application US/10953349
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8834
LENGTH: 476
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-8834

Query Match
Best Local Similarity 9.7%; Score 50; DB 6; Length 476;
Matches 19; Conservative 17; Mismatches 38; Indels 14; Gaps 2;

QY 15 LQPTTDLVXXYXQLNDSF-----EEDIDGPAGAEPPRAHYNIVTFCKC 61
DB 156 LSVEMPEIEPARALDDAEBAIFRHFKEPVVMKQRLIGVGAELKLRARAIIDRYCSKC 215
QY 62 DSTLRUCVOSTHVDIRTLEDLMGTIGI 89
DB 216 IASKRDEI-SQGISSSSKDLMSINV 242

RESULT 96
US-10-953-349-8833
Sequence 8833, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8833
LENGTH: 516
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-8833

Query Match
Best Local Similarity 9.7%; Score 50; DB 6; Length 516;
Matches 19; Conservative 17; Mismatches 38; Indels 14; Gaps 2;

QY 15 LQPTTDLVXXYXQLNDSF-----EEDIDGPAGAEPPRAHYNIVTFCKC 61
DB 196 LSVEMPEIEPARALDDAEBAIFRHFKEPVVMKQRLIGVGAELKLRARAIIDRYCSKC 255
QY 62 DSTLRUCVOSTHVDIRTLEDLMGTIGI 89
DB 256 IASKRDEI-SQGISSSSKDLMSINV 282

RESULT 97
US-10-953-349-13398
Sequence 13398, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 13398
LENGTH: 527
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc feature
LOCATION: (9)..(9)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-13398

Query Match
Best Local Similarity 9.7%; Score 50; DB 6; Length 527;
Matches 18; Conservative 15; Mismatches 38; Indels 8; Gaps 2;

QY 27 QLNDSSEEDIED-GRAGAEPPRAHYNIVTFCKCDSTLRUCVOSTHVDIRT----- 78
DB 340 EVVKDRTSADSDSLASGKKDPFVRQELLIKSGLDSTLDICIESVGLIRSNLGEVYL 399
QY 79 LEDLMGTIGIYXPTCSOK 97
DB 400 YEVAATGSDGIMHPVLDK 418

RESULT 98
US-10-953-349-13397
Sequence 13397, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13397
LENGTH: 548
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc feature
LOCATION: (30)..(30)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-13397

Query Match
Best Local Similarity 9.7%; Score 50; DB 6; Length 548;
Matches 18; Conservative 15; Mismatches 38; Indels 8; Gaps 2;

QY 27 QLNDSSEEDIED-GRAGAEPPRAHYNIVTFCKCDSTLRUCVOSTHVDIRT----- 78
DB 361 EVVKDRTSADSDSLASGKKDPFVRQELLIKSGLDSTLDICIESVGLIRSNLGEVYL 420
QY 79 LEDLMGTIGIYXPTCSOK 97
DB 421 YEVAATGSDGIMHPVLDK 439

RESULT 99
US-10-953-349-13396
Sequence 13396, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 13396
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (116)..(116)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-13396

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Query Match          9.7%; Score 50; DB 6; Length 634;
Best Local Similarity 22.8%; Pred. No. 2.9e+02;
Matches 18; Conservative 15; Mismatches 38; Indels 8; Gaps 2;

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QY      27 QLNDSSEDEID-GPAGQAEPPDRAHNYIVFCCKCDSTLRLCVQSTHVDIRT----- 78
Db      447 EVNNDKTSADSDLAESGKDPFVRROELIKSGLADSLDICTESVGEIIRSNLKGKVL 506

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QY      79 LEDLIMGTGIVXPICSOX 97
Db      507 YEVAATGSGDGMHPVLDDX 525

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RESULT 100
US-11-293-697-3814
; Sequence 3814, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293, 697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3814
; LENGTH: 878
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3814

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Query Match          9.7%; Score 50; DB 7; Length 878;
Best Local Similarity 24.3%; Pred. No. 4.1e+02;
Matches 25; Conservative 15; Mismatches 39; Indels 24; Gaps 4;

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QY      5 TPTL--HEVMDLOPRTTLYXXQLN-----DSSEDEIDGPAGQAE--- 47
Db      591 TPBLSADELPDDIANETADIPHDLELNQEDFSDVLPRLPDDLQDPDFEFGKNGDLPTTE 650

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QY      48 ----DRAHNYIVFCCKCDSTLRLCVQSTHVDIRTLEDLIMG 85
Db      651 EAELELRALQAVTSL--ECLSTIGVLAQSDGVVQELSDRGIG 691

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Search completed: May 27, 2006, 05:38:15
Job time : 8.69076 secs

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